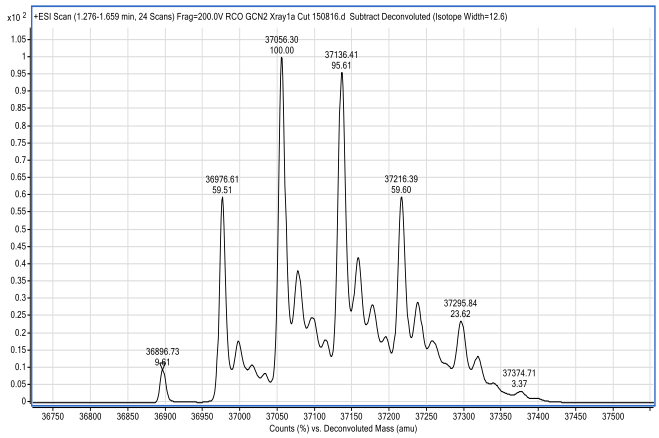
Supplementary Figures

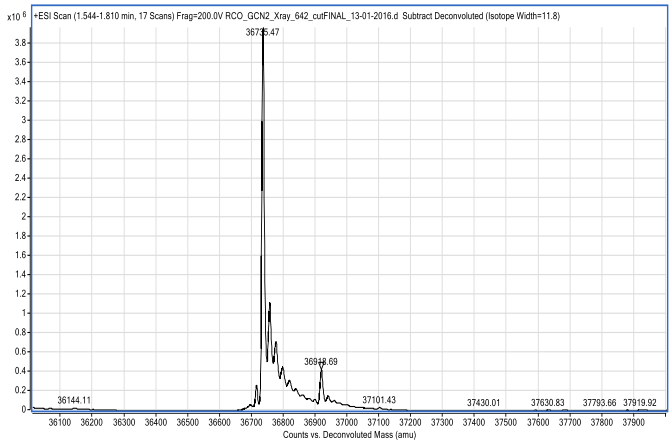
Supplementary Figure 1A

LC-MS of GCN2(S577-T1020,ΔA663-P788) to highlight multiple phosphorylations.



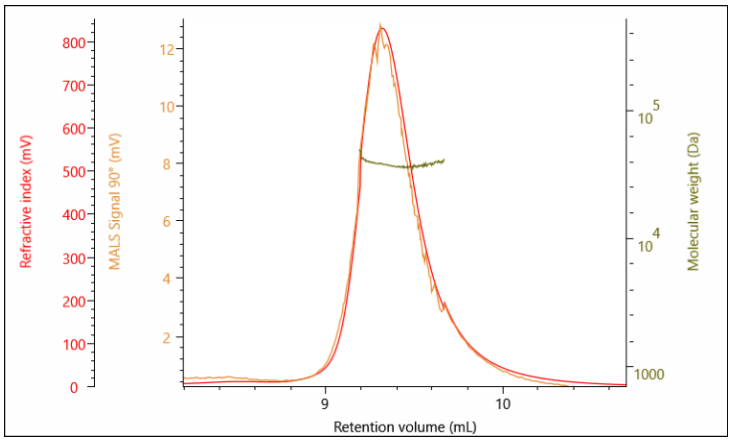
Supplementary Figure 1B

LC-MS of GCN2(S577-T1020,ΔA663-P788) to highlight lack of phosphorylations.



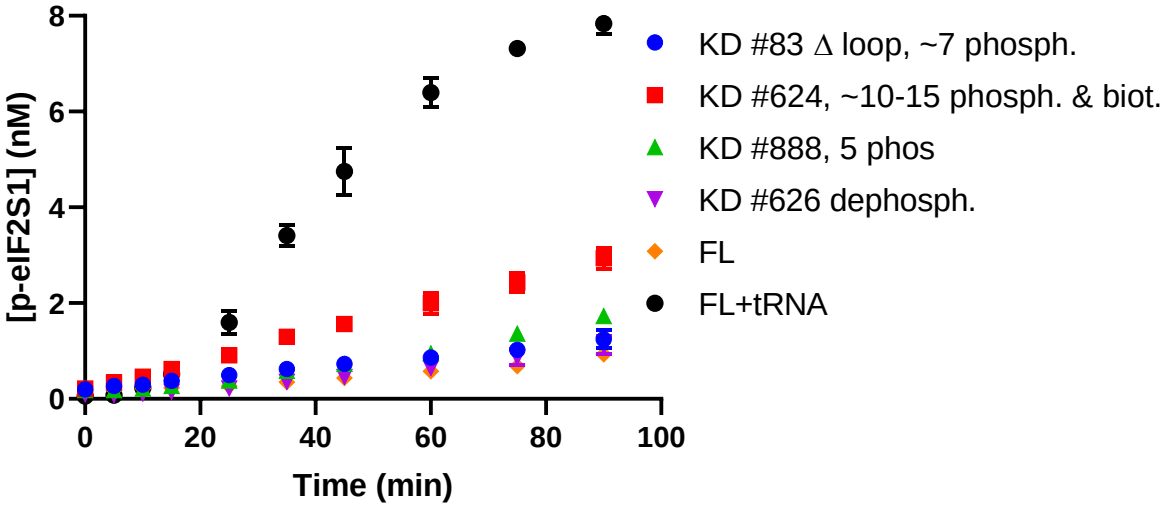
Supplementary Figure 2

SEC-MALS of human GCN2 Kinase Domain crystallization construct, GCN2 S577-T1020, ΔA663-P788 (2mg/mL), showing an average molecular weight of 38.5 kDa (consistent with a monomer)



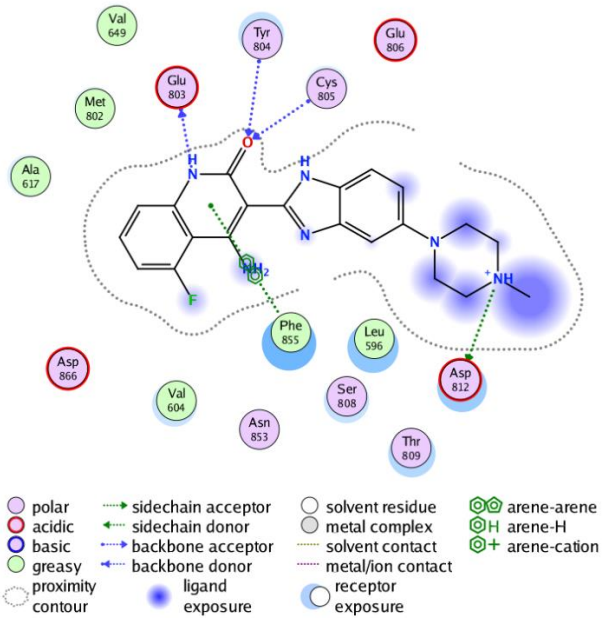
Supplementary Figure 3

Reaction progress curves for various GCN2 constructs determined according to the Biochemical Activity Assay session (Supplementary Materials). All four kinase domain constructs show relatively low levels of activity, with the highly phosphorylated construct #624 being most active, followed by partially phosphorylated, Δ loop & dephosphorylated KD constructs. Full length protein (FL) was tested at 4X lower concentration (5 nM) and showed minimal activity. However, in the presence of tRNA and after an ~20 minute lag which we attribute to an autophosphorylation step, the FL protein showed a dramatic increase in activity. (Datapoints above 5 nM p-eIF2S1 may be out of linear detection range). Data shown is an average of 3 independent experiments. Error bars are ± SEM.



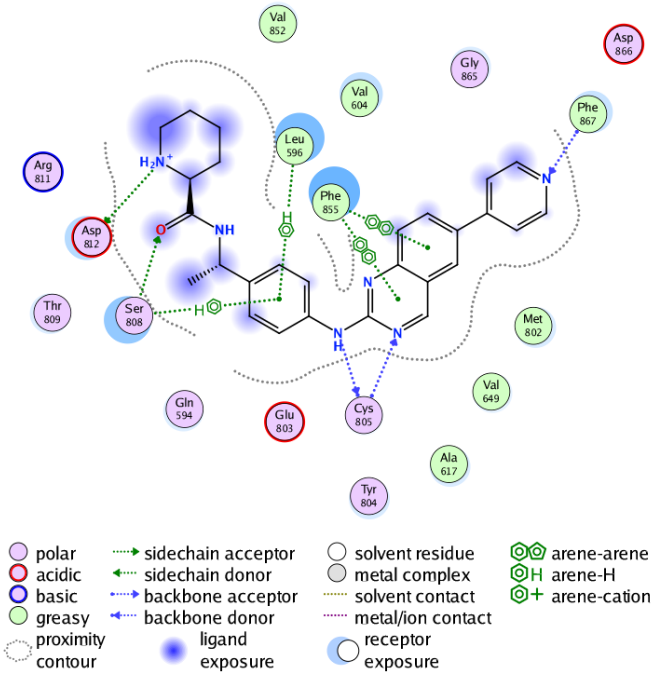
Supplementary Figure 4

Interaction map of Dovinitib:GCN2



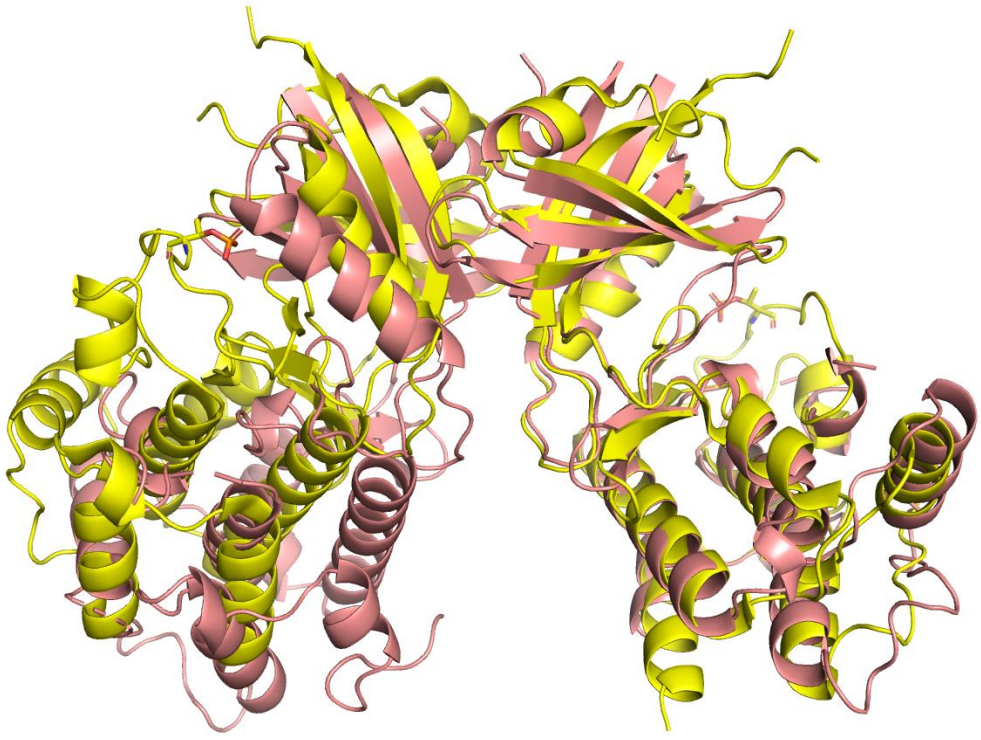
Supplementary Figure 5

Representative interactions of GCN2:(2S)-N-[(1S)-1-(4-{[6-(4-pyridinyl)-2-quinazolinyl]amino}phenyl)ethyl]-2 piperidinecarboxamide



Supplementary Figure 6

Human GCN2 (pink) adopts a dimeric arrangement similar to the one adopted by PKR (yellow)[13]. When compared to the parallel dimer of PKR, GCN2 is more closed.



Preliminary Full wwPDB X-ray Structure Validation Report (i)

Feb 20, 2019 – 09:53 am GMT

Deposition ID : D_1292100734
PDB ID : *(not yet assigned)*

This is a Preliminary Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB Deposition System during initial deposition but before annotation of the structure.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

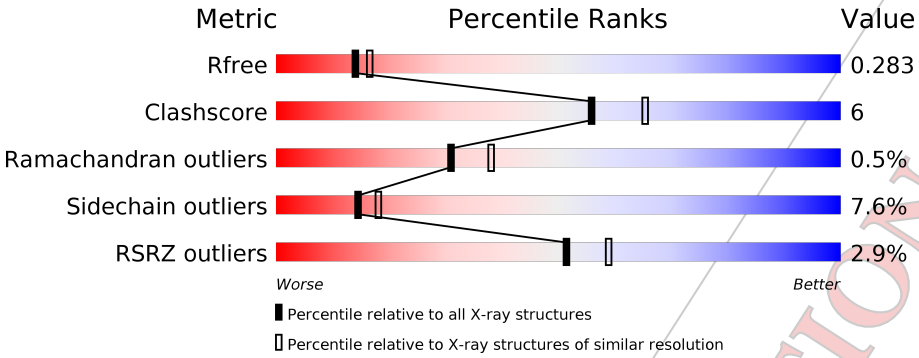
MolProbity	:	4.02b-467
Mogul	:	1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix)	:	1.13
EDS	:	2.1
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	111664	4477 (2.30-2.30)
Clashscore	122126	5072 (2.30-2.30)
Ramachandran outliers	120053	5022 (2.30-2.30)
Sidechain outliers	120020	5021 (2.30-2.30)
RSRZ outliers	108989	4374 (2.30-2.30)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	320	2% 64% 11% • 23%
1	B	320	3% 66% 11% • 22%
1	C	320	3% 65% 13% • 22%
1	D	320	2% 68% 11% • 21%
1	E	320	4% 59% 18% • 22%
1	F	320	% 65% 13% • 21%

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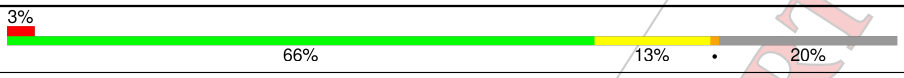
Mol	Chain	Length	Quality of chain
1	G	320	
1	H	320	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 16055 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called general control nonderepressible 2 (GCN2).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	245	Total	C	N	O	S	0	0	0
			1865	1205	314	339	7			
1	B	249	Total	C	N	O	S	0	0	0
			1934	1248	330	349	7			
1	C	249	Total	C	N	O	S	0	0	0
			1928	1249	326	346	7			
1	D	254	Total	C	N	O	S	0	0	0
			1993	1289	336	361	7			
1	E	249	Total	C	N	O	S	0	0	0
			1952	1262	334	349	7			
1	F	254	Total	C	N	O	S	0	0	0
			1990	1285	339	358	8			
1	G	257	Total	C	N	O	S	0	0	0
			2005	1293	339	365	8			
1	H	259	Total	C	N	O	S	0	0	0
			2024	1306	342	367	9			

- Molecule 2 is a ligand with the chemical component id INH but its atom names do not match the existing wwPDB Chemical Component Dictionary definition for INH. Consequently no firm identification of ligand chemistry can be made. Once the structure is annotated then an identification and diagram will be given here.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	I	1	Total	C	N	O	0	0
			34	27	6	1		
2	I	1	Total	C	N	O	0	0
			34	27	6	1		
2	I	1	Total	C	N	O	0	0
			34	27	6	1		
2	I	1	Total	C	N	O	0	0
			34	27	6	1		
2	I	1	Total	C	N	O	0	0
			34	27	6	1		

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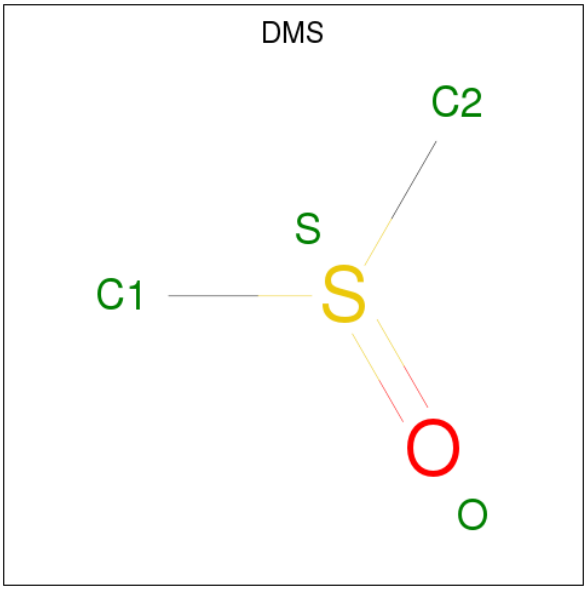
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	I	1	Total	C	N	O	0	0
			34	27	6	1		
2	I	1	Total	C	N	O	0	0
			34	27	6	1		
2	I	1	Total	C	N	O	0	0
			34	27	6	1		

- Molecule 3 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	K	1	Total	C	O	S	0	0
			4	2	1	1		
3	K	1	Total	C	O	S	0	0
			4	2	1	1		

- Molecule 4 is water.

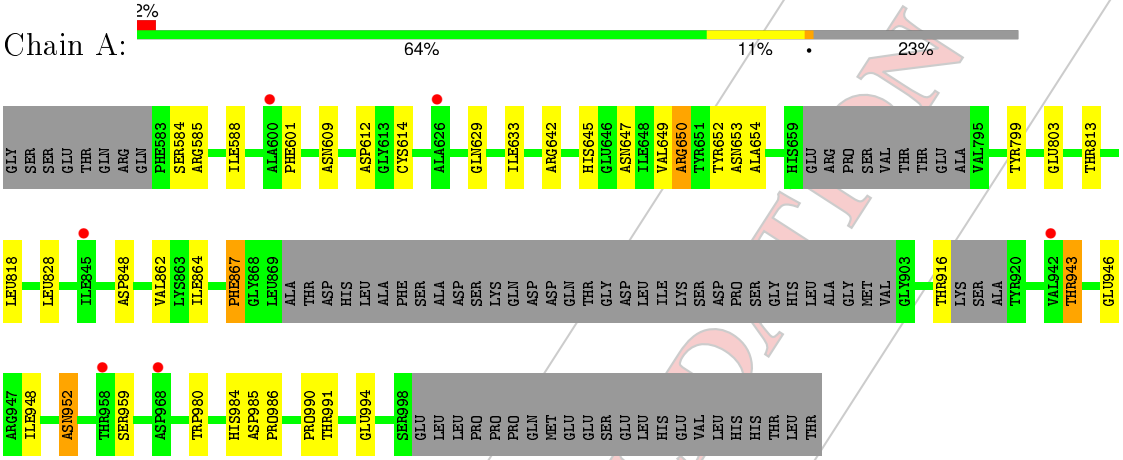
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	W	84	Total	O	0	0
			84	84		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometryand electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

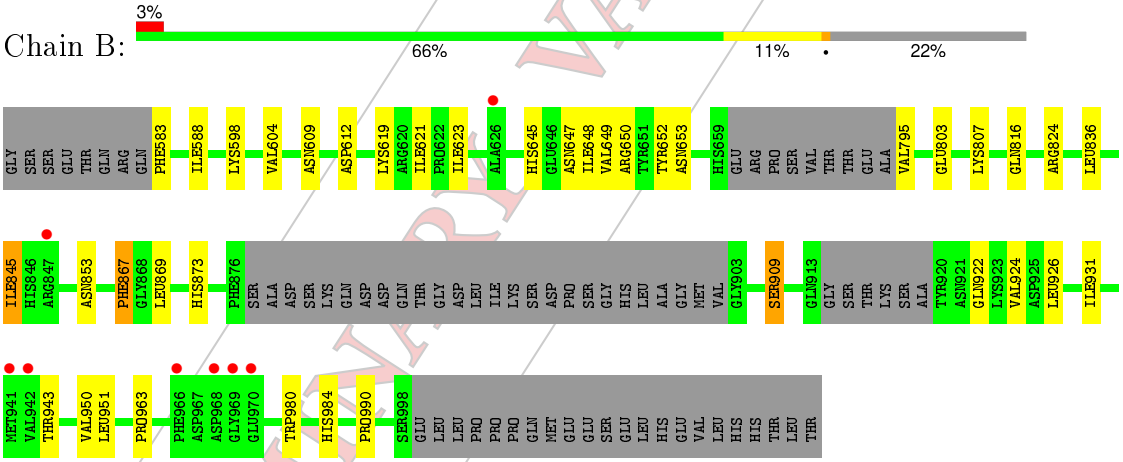
- Molecule 1: general control nonderepressible 2 (GCN2)

Chain A:



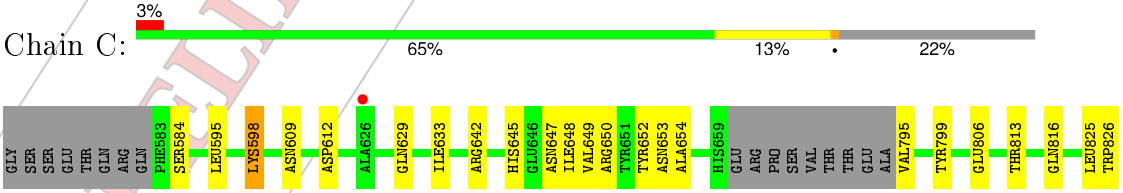
- Molecule 1: general control nonderepressible 2 (GCN2)

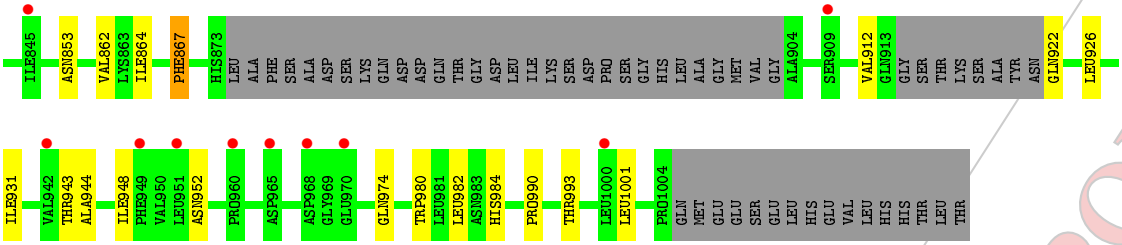
Chain B:



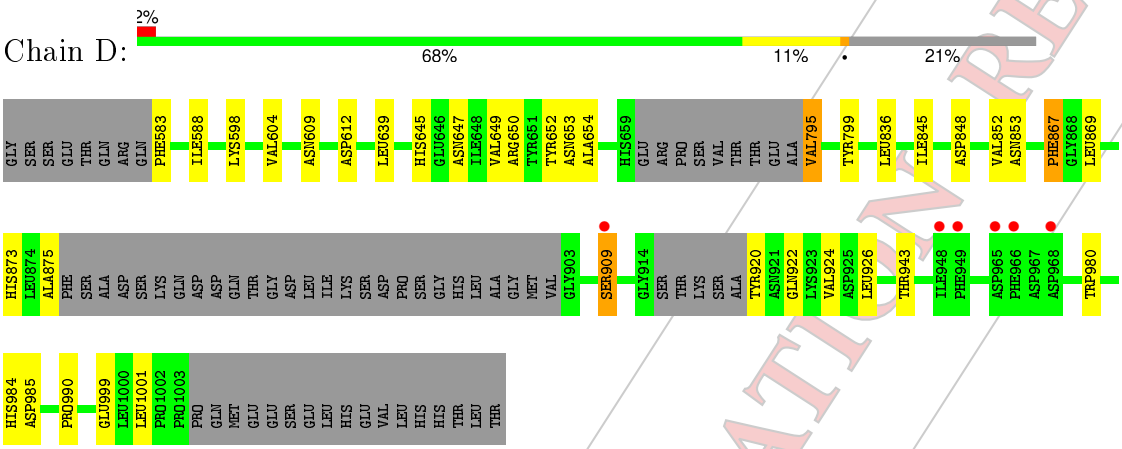
- Molecule 1: general control nonderepressible 2 (GCN2)

Chain C:

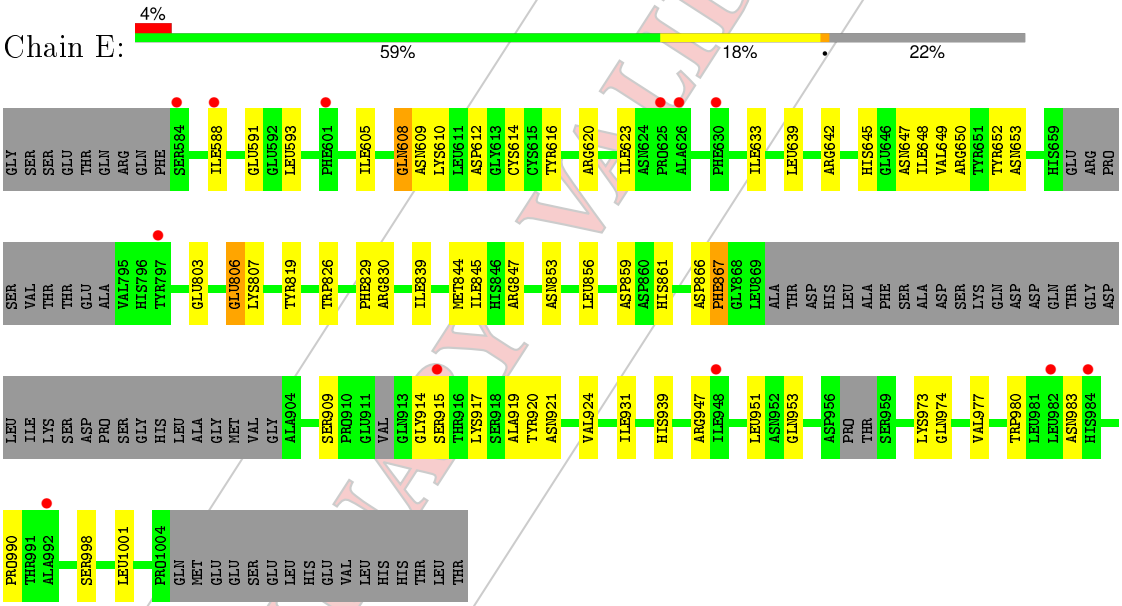




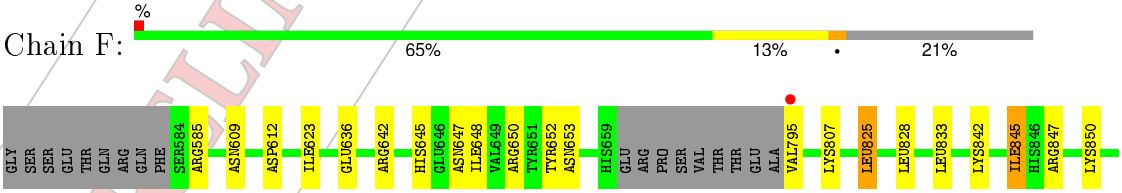
• Molecule 1: general control nonderepressible 2 (GCN2)

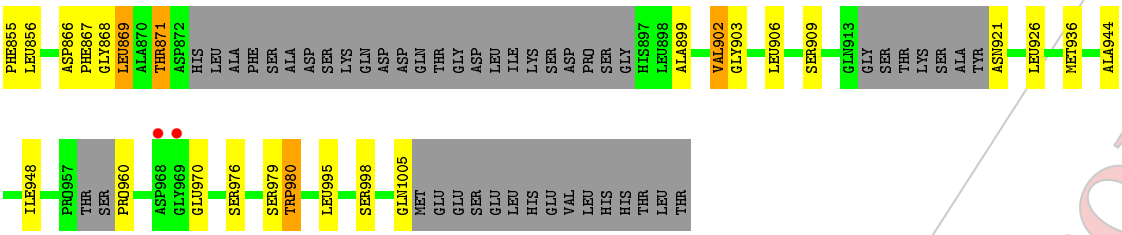


• Molecule 1: general control nonderepressible 2 (GCN2)



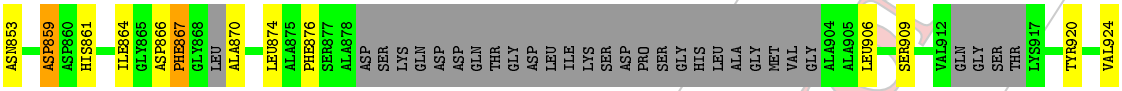
• Molecule 1: general control nonderepressible 2 (GCN2)

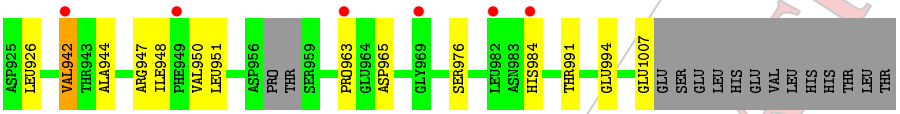




• Molecule 1: general control nonderepressible 2 (GCN2)

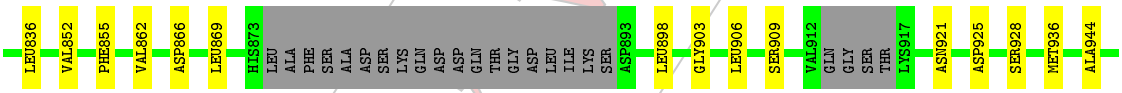
Chain G:





• Molecule 1: general control nonderepressible 2 (GCN2)

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	73.80Å 77.80Å 101.69Å 89.86° 90.05° 68.58°	Depositor
Resolution (Å)	39.43 – 2.30 39.43 – 2.30	Depositor EDS
% Data completeness (in resolution range)	96.5 (39.43-2.30) 95.8 (39.43-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.38 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.212 , 0.263 0.222 , 0.283	Depositor DCC
R_{free} test set	4728 reflections (5.24%)	wwPDB-VP
Wilson B-factor (Å^2)	38.5	Xtriage
Anisotropy	0.321	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 47.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.448 for -h,-k,l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	16055	wwPDB-VP
Average B, all atoms (Å^2)	50.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 43.06 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 1.8623e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: DMS, INH

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.50	0/1909	0.70	0/2598
1	B	0.52	0/1979	0.68	0/2686
1	C	0.49	0/1976	0.69	0/2686
1	D	0.52	0/2041	0.69	0/2770
1	E	0.51	0/1998	0.70	0/2709
1	F	0.53	0/2035	0.73	0/2759
1	G	0.51	0/2049	0.69	0/2779
1	H	0.52	0/2071	0.70	0/2809
All	All	0.51	0/16058	0.70	0/21796

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1865	0	1732	17	0
1	B	1934	0	1821	19	0
1	C	1928	0	1816	16	0
1	D	1993	0	1897	18	0
1	E	1952	0	1873	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	F	1990	0	1916	24	0
1	G	2005	0	1920	22	0
1	H	2024	0	1938	24	0
2	I	272	0	44	20	0
3	K	8	0	12	1	0
4	W	84	0	0	2	0
All	All	16055	0	14969	171	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (171) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:636:GLU:HG2	1:F:868:GLY:HA2	1.59	0.83
1:D:609:ASN:HD22	1:D:612:ASP:H	1.25	0.83
1:G:866:ASP:HB2	1:G:870:ALA:HA	1.58	0.83
1:G:609:ASN:HD22	1:G:612:ASP:H	1.28	0.81
1:H:645:HIS:HD2	1:H:647:ASN:H	1.30	0.80
1:B:853:ASN:ND2	1:B:867:PHE:H	1.82	0.76
1:D:853:ASN:ND2	1:D:867:PHE:H	1.84	0.76
1:F:855:PHE:CE2	2:I:4:INH:C14	2.70	0.75
1:B:853:ASN:HD22	1:B:867:PHE:H	1.33	0.74
1:E:920:TYR:HB3	1:E:924:VAL:HG21	1.70	0.74
1:D:639:LEU:HD12	1:D:875:ALA:HB1	1.69	0.73
1:C:609:ASN:HD22	1:C:612:ASP:H	1.36	0.72
1:A:649:VAL:HG23	1:A:803:GLU:HG2	1.72	0.72
1:H:609:ASN:HD22	1:H:612:ASP:H	1.37	0.70
1:F:645:HIS:HD2	1:F:647:ASN:H	1.39	0.70
1:B:609:ASN:HD22	1:B:612:ASP:H	1.39	0.70
1:H:645:HIS:CD2	1:H:647:ASN:H	2.09	0.70
1:B:604:VAL:HG23	1:B:869:LEU:HD21	1.75	0.69
1:A:609:ASN:HD22	1:A:612:ASP:H	1.39	0.68
1:F:609:ASN:HD22	1:F:612:ASP:H	1.39	0.68
1:E:609:ASN:HD22	1:E:612:ASP:H	1.40	0.67
1:D:645:HIS:HD2	1:D:647:ASN:H	1.41	0.66
1:B:645:HIS:HD2	1:B:647:ASN:H	1.43	0.66
1:D:795:VAL:HG11	1:F:1005:GLN:HB3	1.77	0.66
1:D:853:ASN:HD22	1:D:867:PHE:H	1.42	0.66
1:H:960:PRO:HG2	1:H:979:SER:HA	1.79	0.65
1:E:649:VAL:HG23	1:E:803:GLU:HG2	1.79	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:645:HIS:CD2	1:B:647:ASN:H	2.15	0.64
1:D:609:ASN:ND2	1:D:612:ASP:H	1.95	0.64
1:F:645:HIS:CD2	1:F:647:ASN:H	2.16	0.64
1:D:645:HIS:CD2	1:D:647:ASN:H	2.16	0.63
1:F:855:PHE:CZ	2:I:4:INH:C13	2.82	0.63
1:E:609:ASN:HB3	1:E:612:ASP:OD1	1.99	0.63
1:G:859:ASP:HB3	1:G:861:HIS:HD2	1.64	0.63
1:G:867:PHE:HA	2:I:3:INH:H48	1.80	0.62
1:H:619:LYS:HE2	1:H:621:ILE:HD11	1.81	0.62
1:G:609:ASN:ND2	1:G:612:ASP:H	1.96	0.61
1:E:593:LEU:HD11	1:E:608:GLN:HB2	1.83	0.61
1:D:604:VAL:HG23	1:D:869:LEU:HD21	1.83	0.61
1:C:816:GLN:HB3	1:H:806:GLU:HG2	1.82	0.60
1:F:648:ILE:HG22	1:F:866:ASP:OD2	2.01	0.60
1:A:645:HIS:HD2	1:A:647:ASN:H	1.49	0.60
1:G:609:ASN:HB3	1:G:612:ASP:OD1	2.01	0.60
1:F:855:PHE:CE2	2:I:4:INH:C15	2.85	0.59
1:E:645:HIS:HB3	1:E:648:ILE:HG12	1.85	0.59
1:G:650:ARG:HG2	1:G:652:TYR:CE1	2.38	0.59
1:C:645:HIS:HD2	1:C:647:ASN:H	1.49	0.59
1:B:909:SER:HB2	1:B:924:VAL:HG13	1.85	0.58
1:E:609:ASN:ND2	1:E:612:ASP:H	2.02	0.58
1:F:960:PRO:HG2	1:F:979:SER:HA	1.86	0.57
1:C:931:ILE:HG12	1:C:982:LEU:HD21	1.86	0.57
1:G:645:HIS:HD2	1:G:647:ASN:H	1.53	0.56
1:C:629:GLN:O	1:C:633:ILE:HG12	2.05	0.56
1:D:650:ARG:HG2	1:D:652:TYR:CE1	2.41	0.56
1:D:909:SER:HB2	1:D:924:VAL:HG13	1.87	0.56
1:H:855:PHE:CE1	2:I:2:INH:C14	2.89	0.55
1:C:645:HIS:CD2	1:C:647:ASN:H	2.24	0.55
1:G:645:HIS:CD2	1:G:647:ASN:H	2.24	0.55
1:B:845:ILE:HD11	1:B:922:GLN:HG2	1.88	0.55
1:H:648:ILE:HG23	1:H:866:ASP:OD2	2.06	0.55
1:D:583:PHE:N	1:D:588:ILE:HD11	2.22	0.55
1:B:645:HIS:HB3	1:B:648:ILE:HG12	1.88	0.54
1:F:855:PHE:CZ	2:I:4:INH:C14	2.90	0.54
1:G:944:ALA:O	1:G:948:ILE:HG12	2.09	0.53
1:F:944:ALA:O	1:F:948:ILE:HG12	2.10	0.52
1:G:920:TYR:HB3	1:G:924:VAL:HG21	1.90	0.52
1:C:649:VAL:HG12	1:C:864:ILE:O	2.09	0.52
1:B:816:GLN:HG3	1:E:806:GLU:HG3	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:591:GLU:HG3	1:E:610:LYS:HE2	1.92	0.52
1:B:619:LYS:HE2	1:B:621:ILE:HD11	1.91	0.51
2:I:5:INH:C4	2:I:5:INH:N2	2.73	0.51
1:H:593:LEU:HD11	1:H:608:GLN:HB2	1.92	0.51
1:E:845:ILE:HD13	1:E:847:ARG:HG3	1.92	0.51
1:G:853:ASN:ND2	1:G:866:ASP:O	2.43	0.51
1:E:844:MET:HA	1:E:914:GLY:HA3	1.93	0.50
2:I:4:INH:C4	2:I:4:INH:N2	2.75	0.50
1:C:853:ASN:ND2	1:C:867:PHE:H	2.09	0.49
1:C:826:TRP:CZ2	1:C:974:GLN:HG3	2.47	0.49
1:B:824:ARG:HD2	1:E:807:LYS:HD3	1.93	0.49
1:E:650:ARG:HG2	1:E:652:TYR:CE1	2.47	0.49
2:I:3:INH:C4	2:I:3:INH:N2	2.75	0.49
2:I:8:INH:N2	2:I:8:INH:C4	2.76	0.49
1:D:920:TYR:C	1:D:922:GLN:H	2.16	0.49
1:H:855:PHE:CZ	2:I:2:INH:C13	2.96	0.49
1:H:650:ARG:HG2	1:H:652:TYR:CE1	2.48	0.49
1:H:903:GLY:HA2	1:H:906:LEU:HD12	1.95	0.48
1:H:855:PHE:CE1	2:I:2:INH:C15	2.96	0.48
1:A:828:LEU:HD22	1:A:862:VAL:HG23	1.96	0.48
1:C:609:ASN:ND2	1:C:612:ASP:H	2.10	0.48
1:A:584:SER:O	1:A:588:ILE:HG12	2.13	0.48
1:H:831:GLU:HB3	1:H:862:VAL:HB	1.94	0.48
1:A:645:HIS:CD2	1:A:647:ASN:H	2.29	0.48
1:E:980:TRP:CZ2	1:E:990:PRO:HB3	2.48	0.48
1:G:602:GLY:HA3	1:G:621:ILE:HD13	1.96	0.48
1:H:898:LEU:O	1:H:903:GLY:HA3	2.14	0.48
1:F:650:ARG:HD2	4:W:4:HOH:O	2.14	0.48
1:G:866:ASP:O	1:G:867:PHE:CB	2.61	0.47
1:H:609:ASN:ND2	1:H:612:ASP:H	2.08	0.47
1:E:645:HIS:CD2	1:E:647:ASN:H	2.31	0.47
1:E:853:ASN:ND2	1:E:867:PHE:H	2.12	0.47
1:A:813:THR:HG22	1:A:818:LEU:HB2	1.96	0.47
1:E:645:HIS:HD2	1:E:647:ASN:H	1.61	0.47
2:I:6:INH:C4	2:I:6:INH:N2	2.75	0.47
1:C:650:ARG:HG2	1:C:652:TYR:CE1	2.50	0.47
1:E:931:ILE:HG23	1:E:951:LEU:HD22	1.97	0.47
1:B:649:VAL:HG13	1:B:803:GLU:HG2	1.97	0.47
1:D:639:LEU:CD1	1:D:875:ALA:HB1	2.40	0.47
1:F:825:LEU:CD2	1:F:936:MET:HB3	2.45	0.47
1:D:650:ARG:HD2	4:W:8:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:943:THR:HG22	1:A:946:GLU:H	1.80	0.46
1:B:980:TRP:CD1	1:B:990:PRO:HD3	2.50	0.46
1:F:650:ARG:HG2	1:F:652:TYR:CE1	2.50	0.46
1:H:833:LEU:HD11	1:H:995:LEU:HG	1.97	0.46
2:I:2:INH:C4	2:I:2:INH:N2	2.78	0.46
1:A:612:ASP:OD1	1:A:614:CYS:HB2	2.15	0.46
1:F:845:ILE:HG12	1:F:871:THR:CG2	2.46	0.46
1:A:629:GLN:O	1:A:633:ILE:HG12	2.16	0.46
1:G:649:VAL:HG12	1:G:864:ILE:O	2.16	0.46
1:E:866:ASP:O	2:I:5:INH:C17	2.64	0.46
1:D:980:TRP:CD1	1:D:990:PRO:HD3	2.51	0.46
1:E:826:TRP:CZ2	1:E:974:GLN:HG3	2.51	0.46
1:G:950:VAL:HG13	1:G:963:PRO:HG3	1.98	0.46
1:C:944:ALA:O	1:C:948:ILE:HG12	2.16	0.46
1:H:836:LEU:HD11	1:H:925:ASP:HB3	1.98	0.45
1:A:654:ALA:HA	1:A:799:TYR:O	2.17	0.45
1:H:944:ALA:O	1:H:948:ILE:HG12	2.16	0.45
1:G:906:LEU:HD13	1:G:951:LEU:HD12	1.98	0.45
1:B:950:VAL:HG13	1:B:963:PRO:HG3	1.97	0.45
1:F:833:LEU:HD11	1:F:995:LEU:HG	1.98	0.45
1:E:648:ILE:HD12	1:E:839:ILE:HD11	1.98	0.45
1:F:828:LEU:HD22	1:F:856:LEU:HD21	1.98	0.44
1:H:855:PHE:CZ	2:I:2:INH:C14	3.00	0.44
1:B:650:ARG:HG2	1:B:652:TYR:CE1	2.52	0.44
1:A:948:ILE:O	1:A:952:ASN:HB2	2.18	0.44
1:F:902:VAL:HG12	1:F:948:ILE:HD12	1.99	0.44
2:I:1:INH:C4	2:I:1:INH:N2	2.79	0.44
2:I:7:INH:C4	2:I:7:INH:N2	2.79	0.44
1:H:852:VAL:HG22	3:K:1:DMS:H21	2.00	0.44
1:C:595:LEU:HD21	1:C:598:LYS:HB2	2.00	0.44
1:F:976:SER:O	1:F:980:TRP:HB2	2.18	0.44
1:A:650:ARG:HG2	1:A:652:TYR:CE1	2.53	0.43
1:B:609:ASN:ND2	1:B:612:ASP:H	2.13	0.43
1:D:985:ASP:HB2	1:G:876:PHE:O	2.18	0.43
1:E:829:PHE:HE2	1:E:1001:LEU:HD11	1.83	0.43
1:F:903:GLY:HA2	1:F:906:LEU:HD12	2.01	0.42
1:H:812:ASP:OD1	2:I:2:INH:N5	2.52	0.42
1:B:583:PHE:HB3	1:B:588:ILE:HD11	2.01	0.42
1:D:654:ALA:HA	1:D:799:TYR:O	2.18	0.42
1:E:639:LEU:HD21	1:E:915:SER:HB2	2.00	0.42
1:F:845:ILE:HG12	1:F:871:THR:HG21	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:980:TRP:CZ2	1:C:990:PRO:HB3	2.54	0.42
1:G:645:HIS:HB3	1:G:648:ILE:HG12	2.02	0.42
1:E:973:LYS:O	1:E:977:VAL:HG23	2.19	0.42
1:F:847:ARG:HD3	1:F:869:LEU:CB	2.50	0.42
1:C:654:ALA:HA	1:C:799:TYR:O	2.20	0.42
1:C:645:HIS:HB3	1:C:648:ILE:HG12	2.02	0.42
1:B:931:ILE:HG23	1:B:951:LEU:HD22	2.02	0.41
1:E:819:TYR:CD1	1:E:939:HIS:HA	2.55	0.41
1:H:833:LEU:HD21	1:H:995:LEU:HD23	2.02	0.41
1:A:985:ASP:HA	1:A:986:PRO:HD2	1.76	0.41
1:E:614:CYS:HB3	1:E:616:TYR:CE2	2.56	0.41
1:A:649:VAL:HG12	1:A:864:ILE:O	2.20	0.41
1:A:991:THR:OG1	1:A:994:GLU:HB2	2.21	0.41
1:E:859:ASP:HB3	1:E:861:HIS:HD2	1.85	0.41
1:G:846:HIS:O	1:G:847:ARG:HB2	2.20	0.40
1:G:867:PHE:HA	2:I:3:INH:C13	2.47	0.40
1:G:991:THR:OG1	1:G:994:GLU:HB2	2.21	0.40
1:H:825:LEU:HD23	1:H:936:MET:HB3	2.03	0.40
1:A:980:TRP:CZ2	1:A:990:PRO:HB3	2.57	0.40
1:E:856:LEU:HD23	1:E:856:LEU:HA	1.91	0.40
1:F:899:ALA:CB	1:F:948:ILE:HD11	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	237/320 (74%)	221 (93%)	14 (6%)	2 (1%)	21 25
1	B	241/320 (75%)	230 (95%)	11 (5%)	0	100 100
1	C	241/320 (75%)	227 (94%)	14 (6%)	0	100 100
1	D	246/320 (77%)	234 (95%)	10 (4%)	2 (1%)	21 25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	E	239/320 (75%)	229 (96%)	8 (3%)	2 (1%)	21 25
1	F	244/320 (76%)	228 (93%)	13 (5%)	3 (1%)	14 15
1	G	245/320 (77%)	227 (93%)	17 (7%)	1 (0%)	36 45
1	H	247/320 (77%)	237 (96%)	10 (4%)	0	100 100
All	All	1940/2560 (76%)	1833 (94%)	97 (5%)	10 (0%)	31 38

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	848	ASP
1	D	848	ASP
1	E	917	LYS
1	F	902	VAL
1	F	970	GLU
1	A	867	PHE
1	D	873	HIS
1	E	919	ALA
1	G	942	VAL
1	F	869	LEU

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	184/284 (65%)	173 (94%)	11 (6%)	21 28
1	B	194/284 (68%)	181 (93%)	13 (7%)	18 23
1	C	194/284 (68%)	176 (91%)	18 (9%)	10 11
1	D	204/284 (72%)	190 (93%)	14 (7%)	17 22
1	E	200/284 (70%)	183 (92%)	17 (8%)	12 14
1	F	205/284 (72%)	188 (92%)	17 (8%)	12 15
1	G	206/284 (72%)	188 (91%)	18 (9%)	11 13
1	H	210/284 (74%)	197 (94%)	13 (6%)	20 27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1597/2272 (70%)	1476 (92%)	121 (8%)	14 18

All (121) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	585	ARG
1	A	601	PHE
1	A	642	ARG
1	A	650	ARG
1	A	653	ASN
1	A	867	PHE
1	A	916	THR
1	A	943	THR
1	A	952	ASN
1	A	959	SER
1	A	984	HIS
1	B	598	LYS
1	B	623	ILE
1	B	653	ASN
1	B	795	VAL
1	B	807	LYS
1	B	836	LEU
1	B	845	ILE
1	B	867	PHE
1	B	873	HIS
1	B	909	SER
1	B	926	LEU
1	B	943	THR
1	B	984	HIS
1	C	584	SER
1	C	598	LYS
1	C	642	ARG
1	C	653	ASN
1	C	795	VAL
1	C	806	GLU
1	C	813	THR
1	C	825	LEU
1	C	862	VAL
1	C	867	PHE
1	C	912	VAL
1	C	922	GLN
1	C	926	LEU

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Mol	Chain	Res	Type
1	C	943	THR
1	C	952	ASN
1	C	984	HIS
1	C	993	THR
1	C	1001	LEU
1	D	598	LYS
1	D	649	VAL
1	D	653	ASN
1	D	795	VAL
1	D	836	LEU
1	D	845	ILE
1	D	852	VAL
1	D	867	PHE
1	D	909	SER
1	D	926	LEU
1	D	943	THR
1	D	984	HIS
1	D	999	GLU
1	D	1001	LEU
1	E	588	ILE
1	E	605	ILE
1	E	608	GLN
1	E	620	ARG
1	E	623	ILE
1	E	633	ILE
1	E	642	ARG
1	E	653	ASN
1	E	806	GLU
1	E	830	ARG
1	E	867	PHE
1	E	909	SER
1	E	921	ASN
1	E	947	ARG
1	E	953	GLN
1	E	983	ASN
1	E	998	SER
1	F	585	ARG
1	F	623	ILE
1	F	642	ARG
1	F	653	ASN
1	F	795	VAL
1	F	807	LYS

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Mol	Chain	Res	Type
1	F	825	LEU
1	F	842	LYS
1	F	845	ILE
1	F	850	LYS
1	F	867	PHE
1	F	871	THR
1	F	909	SER
1	F	921	ASN
1	F	926	LEU
1	F	980	TRP
1	F	998	SER
1	G	585	ARG
1	G	598	LYS
1	G	620	ARG
1	G	636	GLU
1	G	642	ARG
1	G	813	THR
1	G	825	LEU
1	G	859	ASP
1	G	867	PHE
1	G	874	LEU
1	G	909	SER
1	G	926	LEU
1	G	942	VAL
1	G	947	ARG
1	G	965	ASP
1	G	976	SER
1	G	984	HIS
1	G	1007	GLU
1	H	585	ARG
1	H	642	ARG
1	H	648	ILE
1	H	653	ASN
1	H	807	LYS
1	H	813	THR
1	H	825	LEU
1	H	869	LEU
1	H	909	SER
1	H	921	ASN
1	H	928	SER
1	H	999	GLU
1	H	1003	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	609	ASN
1	A	645	HIS
1	A	853	ASN
1	A	984	HIS
1	B	609	ASN
1	B	624	ASN
1	B	645	HIS
1	B	853	ASN
1	C	609	ASN
1	C	645	HIS
1	C	853	ASN
1	D	609	ASN
1	D	645	HIS
1	D	853	ASN
1	E	609	ASN
1	E	645	HIS
1	E	853	ASN
1	E	861	HIS
1	E	913	GLN
1	E	921	ASN
1	F	609	ASN
1	F	645	HIS
1	F	853	ASN
1	G	609	ASN
1	G	645	HIS
1	G	853	ASN
1	G	861	HIS
1	H	609	ASN
1	H	645	HIS
1	H	853	ASN
1	H	921	ASN
1	H	974	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

Of 10 ligands modelled in this entry, 8 could not be matched to an existing wwPDB Chemical Component Dictionary definition at this stage - leaving 2 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	DMS	K	1	-	3,3,3	0.38	0	3,3,3	0.38	0
3	DMS	K	2	-	3,3,3	0.35	0	3,3,3	0.78	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	DMS	K	1	-	-	0/0/0/0	0/0/0/0
3	DMS	K	2	-	-	0/0/0/0	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	K	1	DMS	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	245/320 (76%)	-0.01	6 (2%) 59 66	23, 50, 89, 102	0
1	B	249/320 (77%)	-0.08	8 (3%) 47 55	23, 45, 76, 97	0
1	C	249/320 (77%)	0.11	11 (4%) 34 41	24, 51, 96, 111	0
1	D	254/320 (79%)	-0.02	6 (2%) 59 66	23, 46, 80, 99	0
1	E	249/320 (77%)	0.07	12 (4%) 30 38	28, 51, 83, 102	0
1	F	254/320 (79%)	-0.09	3 (1%) 79 83	23, 46, 76, 100	0
1	G	257/320 (80%)	0.07	11 (4%) 35 42	29, 52, 84, 100	0
1	H	259/320 (80%)	-0.15	1 (0%) 92 95	23, 46, 74, 110	0
All	All	2016/2560 (78%)	-0.01	58 (2%) 51 59	23, 49, 84, 111	0

All (58) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	584	SER	7.4
1	B	966	PHE	6.3
1	G	982	LEU	5.0
1	G	584	SER	4.8
1	F	795	VAL	4.4
1	B	968	ASP	4.3
1	C	968	ASP	4.3
1	G	626	ALA	3.8
1	C	626	ALA	3.7
1	E	625	PRO	3.7
1	G	963	PRO	3.6
1	D	968	ASP	3.5
1	G	984	HIS	3.4
1	C	960	PRO	3.3
1	F	968	ASP	3.3
1	A	626	ALA	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	970	GLU	3.2
1	E	984	HIS	3.2
1	F	969	GLY	3.1
1	E	626	ALA	3.1
1	C	942	VAL	3.1
1	D	966	PHE	3.0
1	C	1000	LEU	3.0
1	D	965	ASP	3.0
1	E	601	PHE	2.9
1	E	982	LEU	2.9
1	A	942	VAL	2.9
1	B	942	VAL	2.9
1	C	949	PHE	2.9
1	E	915	SER	2.8
1	E	630	PHE	2.8
1	G	601	PHE	2.8
1	G	949	PHE	2.8
1	B	969	GLY	2.7
1	E	992	ALA	2.6
1	H	600	ALA	2.5
1	A	845	ILE	2.5
1	G	969	GLY	2.5
1	G	942	VAL	2.5
1	D	909	SER	2.5
1	B	970	GLU	2.4
1	D	948	ILE	2.4
1	E	948	ILE	2.4
1	C	909	SER	2.3
1	C	951	LEU	2.3
1	A	600	ALA	2.3
1	B	847	ARG	2.3
1	E	797	TYR	2.2
1	C	965	ASP	2.2
1	C	845	ILE	2.2
1	E	588	ILE	2.2
1	D	949	PHE	2.1
1	B	941	MET	2.1
1	A	958	THR	2.1
1	G	633	ILE	2.1
1	G	659	HIS	2.0
1	A	968	ASP	2.0
1	B	626	ALA	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands (i)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	INH	I	5	34/?	0.91	0.17	33,46,65,67	0
2	INH	I	4	34/?	0.92	0.13	29,34,40,42	0
2	INH	I	2	34/?	0.93	0.13	28,33,47,49	0
2	INH	I	3	34/?	0.93	0.15	32,45,70,71	0
3	DMS	K	1	4/?	0.93	0.21	76,79,80,81	0
3	DMS	K	2	4/?	0.94	0.20	78,81,81,83	0
2	INH	I	8	34/?	0.96	0.12	21,28,40,43	0
2	INH	I	7	34/?	0.96	0.11	25,36,42,43	0
2	INH	I	1	34/?	0.97	0.12	20,28,44,47	0
2	INH	I	6	34/?	0.97	0.12	24,32,43,43	0

6.5 Other polymers (i)

There are no such residues in this entry.

Preliminary Full wwPDB X-ray Structure Validation Report (i)

Feb 20, 2019 – 12:59 pm GMT

Deposition ID : D_1292100769
PDB ID : *(not yet assigned)*

This is a Preliminary Full wwPDB X-ray Structure Validation Report.

This report is produced by the wwPDB Deposition System during initial deposition but before annotation of the structure.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

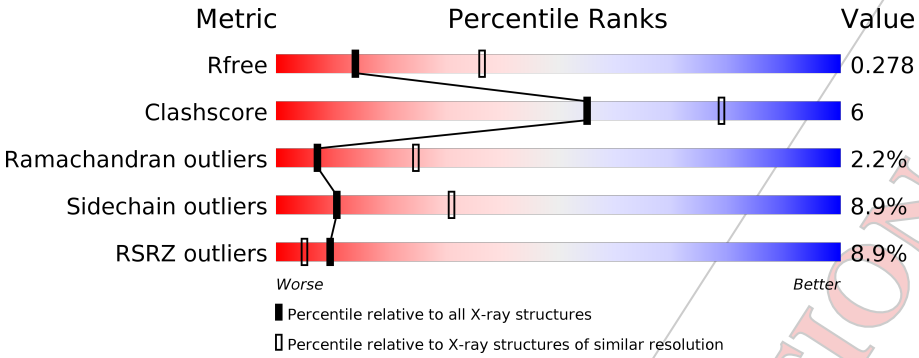
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.1
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	111664	2792 (2.80-2.80)
Clashscore	122126	3209 (2.80-2.80)
Ramachandran outliers	120053	3158 (2.80-2.80)
Sidechain outliers	120020	3160 (2.80-2.80)
RSRZ outliers	108989	2726 (2.80-2.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	320	6% 66% 17% • 16%
1	B	320	9% 67% 18% • 14%
1	C	320	8% 63% 19% • 17%
1	D	320	7% 67% 14% • 19%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8692 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called GCN2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	269	Total	C	N	O	S	0	0	0
			2124	1365	363	388	8			
1	B	275	Total	C	N	O	S	0	0	0
			2188	1405	376	398	9			
1	C	267	Total	C	N	O	S	0	0	0
			2133	1364	368	393	8			
1	D	260	Total	C	N	O	S	0	0	0
			2086	1341	361	376	8			

- Molecule 2 is a ligand with the chemical component id INH but its atom names do not match the existing wwPDB Chemical Component Dictionary definition for INH. Consequently no firm identification of ligand chemistry can be made. Once the structure is annotated then an identification and diagram will be given here.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	I	1	Total	C	F	N	O	0	0
			29	21	1	6	1		
2	I	1	Total	C	F	N	O	0	0
			29	21	1	6	1		
2	I	1	Total	C	F	N	O	0	0
			29	21	1	6	1		
2	I	1	Total	C	F	N	O	0	0
			29	21	1	6	1		

- Molecule 3 is water.

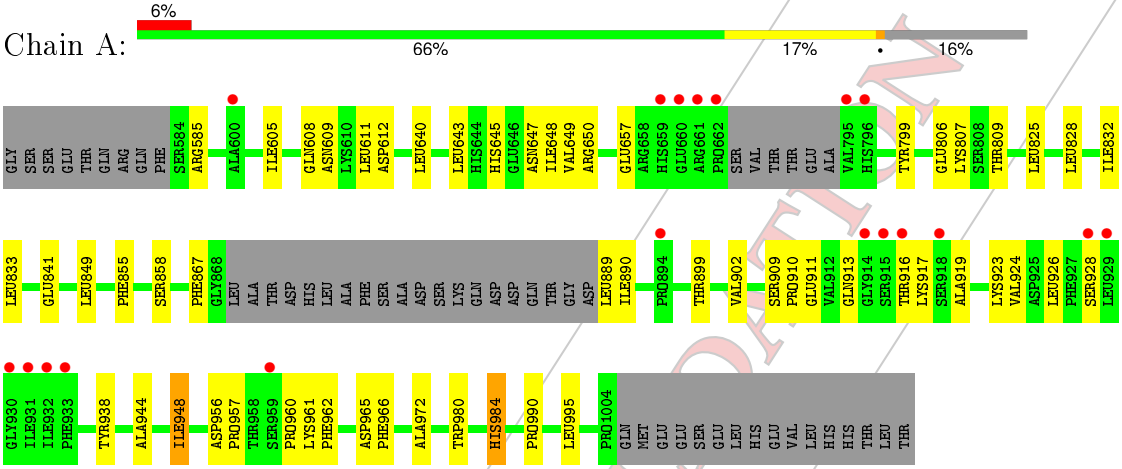
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	W	45	Total	O	0	0
			45	45		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometryand electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

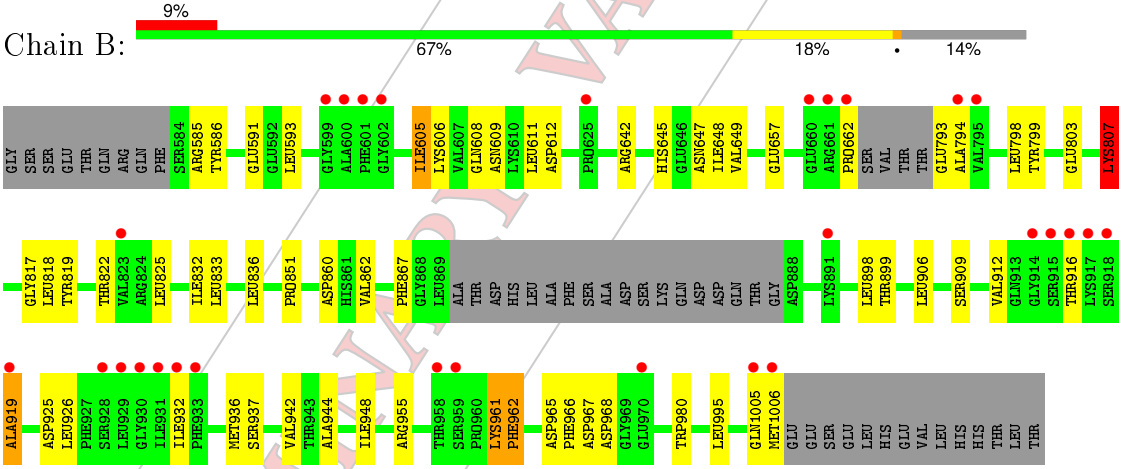
- Molecule 1: GCN2

Chain A:



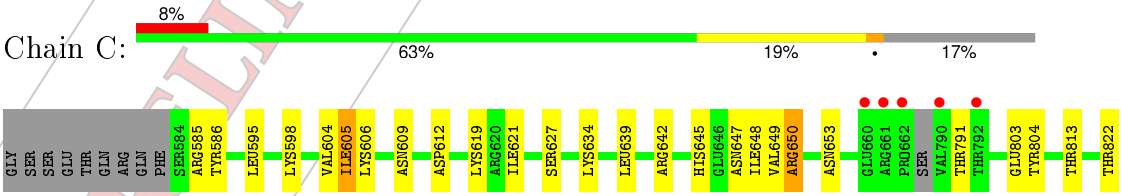
- Molecule 1: GCN2

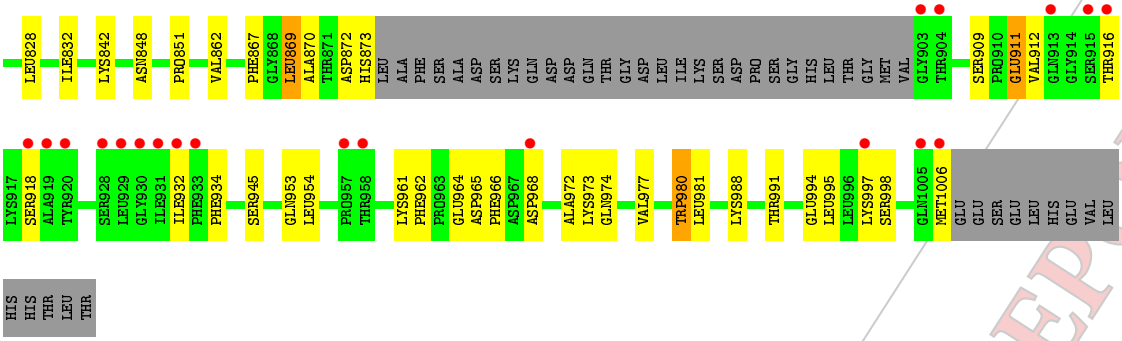
Chain B:



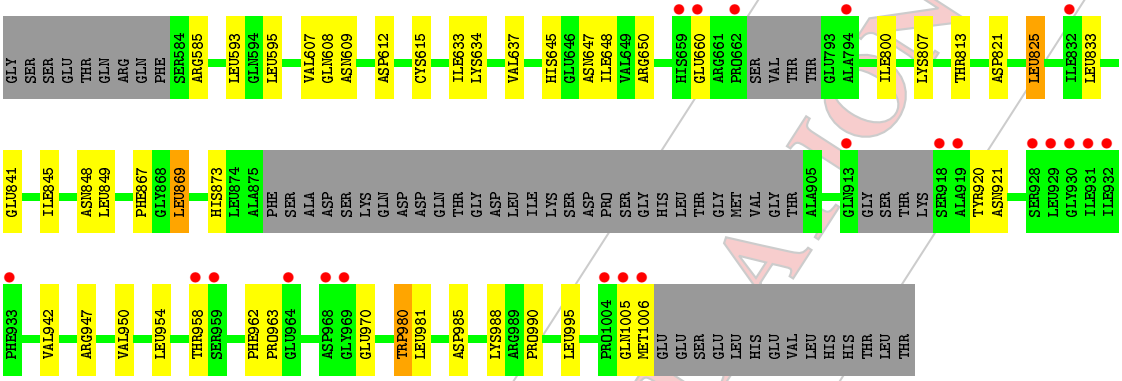
- Molecule 1: GCN2

Chain C:





- Molecule 1: GCN2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α, β, γ	155.42Å 162.60Å 123.89Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.64 – 2.80 24.64 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (24.64-2.80) 99.7 (24.64-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.36 (at 2.80Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.211 , 0.258 0.224 , 0.278	Depositor DCC
R_{free} test set	1946 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	92.5	Xtriage
Anisotropy	0.204	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 70.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.062 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	8692	wwPDB-VP
Average B, all atoms (Å^2)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: INH

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	A	0.51	0/2175	0.76	0/2950
1	B	0.50	0/2240	0.74	0/3034
1	C	0.50	0/2183	0.75	0/2960
1	D	0.54	0/2136	0.76	0/2893
All	All	0.51	0/8734	0.75	0/11837

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2124	0	2052	23	0
1	B	2188	0	2147	24	0
1	C	2133	0	2073	32	0
1	D	2086	0	2028	17	0
2	I	116	0	4	4	0
3	W	45	0	0	1	0
All	All	8692	0	8304	95	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (95) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:650:ARG:HG2	1:C:650:ARG:HH11	1.32	0.92
1:A:645:HIS:HB3	1:A:648:ILE:HG12	1.55	0.89
1:C:645:HIS:HB3	1:C:648:ILE:HG12	1.64	0.80
1:B:645:HIS:HB3	1:B:648:ILE:HG12	1.62	0.79
1:B:645:HIS:HD2	1:B:647:ASN:H	1.31	0.76
1:A:645:HIS:HD2	1:A:647:ASN:H	1.33	0.76
1:A:944:ALA:O	1:A:948:ILE:HG12	1.90	0.71
1:A:645:HIS:CD2	1:A:647:ASN:H	2.11	0.69
1:C:609:ASN:HD22	1:C:612:ASP:H	1.41	0.68
1:C:650:ARG:HG2	1:C:650:ARG:NH1	2.09	0.68
1:D:609:ASN:HD22	1:D:612:ASP:H	1.43	0.65
1:A:650:ARG:NH2	1:D:650:ARG:HB3	2.12	0.64
1:B:944:ALA:O	1:B:948:ILE:HG12	1.98	0.63
1:C:595:LEU:HD21	1:C:598:LYS:HB2	1.82	0.62
1:C:645:HIS:CD2	1:C:647:ASN:H	2.18	0.62
1:C:645:HIS:HD2	1:C:647:ASN:H	1.48	0.61
1:D:645:HIS:HB3	1:D:648:ILE:HG12	1.83	0.61
1:A:609:ASN:HD22	1:A:612:ASP:H	1.50	0.60
1:C:980:TRP:HZ3	1:C:988:LYS:O	1.86	0.58
1:D:821:ASP:O	1:D:825:LEU:HB2	2.03	0.58
1:A:923:LYS:HA	1:A:926:LEU:HD12	1.86	0.58
1:B:609:ASN:HD22	1:B:612:ASP:H	1.50	0.58
1:B:916:THR:HG23	1:B:919:ALA:HB3	1.87	0.56
1:B:609:ASN:HB3	1:B:612:ASP:OD1	2.06	0.55
1:A:890:ILE:HD13	1:A:948:ILE:HG21	1.88	0.55
1:D:593:LEU:HD11	1:D:608:GLN:HB2	1.88	0.55
1:C:828:LEU:O	1:C:832:ILE:HG13	2.07	0.55
1:D:607:VAL:O	1:D:615:CYS:HA	2.07	0.54
1:D:645:HIS:HD2	1:D:647:ASN:H	1.54	0.54
1:B:818:LEU:HD23	1:B:936:MET:HG2	1.89	0.54
1:C:595:LEU:HD12	1:C:605:ILE:HG23	1.89	0.54
1:B:657:GLU:HB2	1:B:799:TYR:HE1	1.73	0.53
1:C:848:ASN:HB2	1:C:869:LEU:HD11	1.90	0.53
1:B:662:PRO:HG3	1:B:793:GLU:HA	1.90	0.53
1:C:851:PRO:HD3	1:C:932:ILE:HG12	1.91	0.52
1:B:825:LEU:HD11	1:B:937:SER:HA	1.90	0.52
1:B:585:ARG:HD2	1:C:585:ARG:HD2	1.91	0.52
1:A:609:ASN:HB3	1:A:612:ASP:OD1	2.10	0.52
1:A:640:LEU:HA	1:A:643:LEU:HD12	1.92	0.52
1:A:833:LEU:HD11	1:A:995:LEU:HD23	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:586:TYR:OH	1:C:605:ILE:HG13	2.11	0.51
1:D:980:TRP:CE3	1:D:990:PRO:HD3	2.45	0.50
1:C:977:VAL:HG13	1:C:995:LEU:HD11	1.94	0.50
1:A:910:PRO:HA	1:A:913:GLN:HE21	1.77	0.50
1:A:980:TRP:CD1	1:A:990:PRO:HD3	2.46	0.50
1:B:645:HIS:CD2	1:B:647:ASN:H	2.20	0.50
1:C:909:SER:HB2	1:C:912:VAL:HG23	1.94	0.49
1:D:981:LEU:HD21	1:D:995:LEU:HD22	1.94	0.48
1:B:833:LEU:HD11	1:B:995:LEU:HD23	1.96	0.48
1:C:980:TRP:CZ3	1:C:988:LYS:O	2.67	0.47
1:C:981:LEU:HD21	1:C:995:LEU:HD22	1.96	0.47
1:B:961:LYS:O	1:B:962:PHE:HB2	2.15	0.47
1:D:833:LEU:HD11	1:D:995:LEU:HD23	1.97	0.47
1:C:619:LYS:HG2	1:C:621:ILE:HD11	1.97	0.47
1:C:828:LEU:HD22	1:C:862:VAL:HG23	1.97	0.47
1:A:828:LEU:O	1:A:832:ILE:HG13	2.16	0.45
1:A:611:LEU:HD12	1:D:634:LYS:HE2	1.97	0.45
2:I:1:INH:N5	2:I:1:INH:N2	2.64	0.45
1:C:911:GLU:HB3	1:C:918:SER:HB2	1.97	0.45
1:D:950:VAL:HG13	1:D:963:PRO:HG3	1.98	0.45
1:B:593:LEU:HD12	1:B:606:LYS:HE2	1.99	0.45
1:B:611:LEU:HD12	1:C:634:LYS:HE2	1.99	0.45
1:A:957:PRO:HB3	1:A:984:HIS:CD2	2.52	0.44
1:C:973:LYS:O	1:C:977:VAL:HG23	2.16	0.44
1:C:639:LEU:HB2	1:C:867:PHE:HE2	1.81	0.44
2:I:4:INH:N5	2:I:4:INH:N2	2.64	0.44
1:C:649:VAL:HG13	1:C:803:GLU:HG2	2.00	0.44
1:D:645:HIS:CD2	1:D:647:ASN:H	2.34	0.43
1:C:968:ASP:O	1:C:972:ALA:HB2	2.18	0.43
1:B:836:LEU:HD11	1:B:925:ASP:HB3	2.01	0.43
1:C:645:HIS:HB3	1:C:648:ILE:CG1	2.42	0.43
1:C:991:THR:H	1:C:994:GLU:HB3	1.83	0.43
2:I:2:INH:N5	2:I:2:INH:N2	2.66	0.43
1:A:960:PRO:HB2	3:W:27:HOH:O	2.18	0.43
1:A:909:SER:HB2	1:A:924:VAL:HG13	2.02	0.42
1:B:912:VAL:HA	1:B:919:ALA:HB1	2.02	0.42
1:B:906:LEU:O	1:B:955:ARG:HD2	2.18	0.42
1:B:898:LEU:HD13	1:B:948:ILE:HB	2.01	0.42
1:C:604:VAL:HG22	1:C:619:LYS:HG3	2.01	0.42
1:D:833:LEU:HD21	1:D:995:LEU:HD23	2.01	0.42
1:B:851:PRO:HD3	1:B:932:ILE:HG12	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:609:ASN:ND2	1:C:612:ASP:H	2.11	0.41
1:D:633:ILE:O	1:D:637:VAL:HG23	2.21	0.41
1:B:832:ILE:HG12	1:B:862:VAL:HG11	2.03	0.41
1:A:657:GLU:HB2	1:A:799:TYR:HE1	1.85	0.41
1:D:985:ASP:HB3	1:D:988:LYS:HG2	2.02	0.41
1:C:934:PHE:CG	1:C:954:LEU:HD21	2.56	0.41
1:A:809:THR:HG22	1:A:855:PHE:CD1	2.55	0.41
1:A:938:TYR:HD1	1:A:966:PHE:HD1	1.67	0.40
1:B:807:LYS:HE2	1:B:860:ASP:HB2	2.03	0.40
1:C:606:LYS:HD2	1:C:804:TYR:CZ	2.56	0.40
1:A:585:ARG:HD2	1:D:585:ARG:HD2	2.04	0.40
1:A:902:VAL:HG23	1:A:948:ILE:HD12	2.02	0.40
2:I:3:INH:N2	2:I:3:INH:N5	2.65	0.40
1:B:586:TYR:OH	1:B:605:ILE:HG13	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	263/320 (82%)	240 (91%)	19 (7%)	4 (2%)	11 36
1	B	269/320 (84%)	237 (88%)	24 (9%)	8 (3%)	5 16
1	C	261/320 (82%)	229 (88%)	27 (10%)	5 (2%)	9 28
1	D	252/320 (79%)	229 (91%)	17 (7%)	6 (2%)	6 22
All	All	1045/1280 (82%)	935 (90%)	87 (8%)	23 (2%)	7 25

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	919	ALA

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Mol	Chain	Res	Type
1	A	961	LYS
1	A	972	ALA
1	C	870	ALA
1	D	869	LEU
1	B	807	LYS
1	B	819	TYR
1	C	872	ASP
1	D	660	GLU
1	A	962	PHE
1	B	794	ALA
1	B	961	LYS
1	B	919	ALA
1	C	627	SER
1	C	962	PHE
1	D	867	PHE
1	D	920	TYR
1	D	954	LEU
1	B	817	GLY
1	B	967	ASP
1	C	961	LYS
1	B	962	PHE
1	D	962	PHE

5.3.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	224/286 (78%)	204 (91%)	20 (9%)	11 31
1	B	235/286 (82%)	215 (92%)	20 (8%)	12 33
1	C	228/286 (80%)	206 (90%)	22 (10%)	9 27
1	D	221/286 (77%)	202 (91%)	19 (9%)	11 33
All	All	908/1144 (79%)	827 (91%)	81 (9%)	11 31

All (81) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	605	ILE
1	A	608	GLN
1	A	649	VAL
1	A	806	GLU
1	A	807	LYS
1	A	825	LEU
1	A	841	GLU
1	A	849	LEU
1	A	858	SER
1	A	867	PHE
1	A	889	LEU
1	A	899	THR
1	A	911	GLU
1	A	916	THR
1	A	917	LYS
1	A	928	SER
1	A	948	ILE
1	A	956	ASP
1	A	965	ASP
1	A	984	HIS
1	B	591	GLU
1	B	605	ILE
1	B	608	GLN
1	B	642	ARG
1	B	649	VAL
1	B	798	LEU
1	B	803	GLU
1	B	807	LYS
1	B	822	THR
1	B	867	PHE
1	B	899	THR
1	B	909	SER
1	B	926	LEU
1	B	942	VAL
1	B	965	ASP
1	B	966	PHE
1	B	968	ASP
1	B	980	TRP
1	B	1005	GLN
1	B	1006	MET
1	C	605	ILE
1	C	642	ARG
1	C	650	ARG

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Mol	Chain	Res	Type
1	C	653	ASN
1	C	791	THR
1	C	813	THR
1	C	822	THR
1	C	842	LYS
1	C	869	LEU
1	C	873	HIS
1	C	911	GLU
1	C	916	THR
1	C	945	SER
1	C	953	GLN
1	C	964	GLU
1	C	965	ASP
1	C	966	PHE
1	C	974	GLN
1	C	980	TRP
1	C	997	LYS
1	C	998	SER
1	C	1006	MET
1	D	595	LEU
1	D	800	ILE
1	D	807	LYS
1	D	813	THR
1	D	825	LEU
1	D	841	GLU
1	D	845	ILE
1	D	848	ASN
1	D	849	LEU
1	D	869	LEU
1	D	873	HIS
1	D	921	ASN
1	D	942	VAL
1	D	947	ARG
1	D	958	THR
1	D	970	GLU
1	D	980	TRP
1	D	1005	GLN
1	D	1006	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	609	ASN
1	A	645	HIS
1	A	913	GLN
1	A	984	HIS
1	B	609	ASN
1	B	645	HIS
1	C	609	ASN
1	C	645	HIS
1	D	609	ASN
1	D	645	HIS
1	D	659	HIS
1	D	848	ASN
1	D	921	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 4 ligands modelled in this entry, 4 could not be matched to an existing wwPDB Chemical Component Dictionary definition at this stage - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95^{th} percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å^2)	Q<0.9
1	A	269/320 (84%)	0.19	19 (7%) 16 9	57, 82, 115, 145	0
1	B	275/320 (85%)	0.35	29 (10%) 6 3	62, 88, 125, 150	0
1	C	267/320 (83%)	0.45	25 (9%) 8 4	65, 89, 132, 175	0
1	D	260/320 (81%)	0.40	22 (8%) 11 5	62, 92, 139, 167	0
All	All	1071/1280 (83%)	0.35	95 (8%) 9 5	57, 88, 130, 175	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	916	THR	9.1
1	A	662	PRO	7.7
1	C	1006	MET	7.4
1	C	1005	GLN	7.1
1	B	1006	MET	6.7
1	D	1005	GLN	6.1
1	D	1006	MET	5.9
1	B	1005	GLN	5.1
1	D	958	THR	4.7
1	D	930	GLY	4.5
1	B	917	LYS	4.5
1	D	919	ALA	4.4
1	B	600	ALA	4.2
1	A	659	HIS	4.1
1	D	1004	PRO	4.0
1	D	959	SER	4.0
1	C	932	ILE	4.0
1	A	795	VAL	4.0
1	C	919	ALA	4.0
1	D	932	ILE	3.9
1	A	600	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
1	A	660	GLU	3.7
1	A	929	LEU	3.7
1	B	959	SER	3.7
1	B	929	LEU	3.7
1	B	919	ALA	3.7
1	A	915	SER	3.6
1	B	794	ALA	3.5
1	B	662	PRO	3.5
1	A	918	SER	3.4
1	B	958	THR	3.4
1	C	903	GLY	3.4
1	B	970	GLU	3.3
1	D	929	LEU	3.3
1	B	823	VAL	3.2
1	A	661	ARG	3.1
1	C	968	ASP	3.1
1	B	661	ARG	3.0
1	B	914	GLY	2.9
1	C	958	THR	2.9
1	C	928	SER	2.8
1	D	660	GLU	2.8
1	B	932	ILE	2.8
1	B	601	PHE	2.8
1	A	928	SER	2.8
1	A	959	SER	2.8
1	B	931	ILE	2.8
1	B	625	PRO	2.7
1	B	891	LYS	2.7
1	C	929	LEU	2.7
1	C	790	VAL	2.6
1	D	794	ALA	2.6
1	D	969	GLY	2.6
1	A	932	ILE	2.6
1	A	930	GLY	2.5
1	C	913	GLN	2.5
1	D	918	SER	2.5
1	B	915	SER	2.5
1	B	660	GLU	2.5
1	B	930	GLY	2.5
1	A	931	ILE	2.4
1	A	914	GLY	2.4
1	D	913	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	599	GLY	2.4
1	B	928	SER	2.4
1	D	662	PRO	2.3
1	D	968	ASP	2.3
1	C	920	TYR	2.3
1	C	957	PRO	2.3
1	B	918	SER	2.3
1	D	928	SER	2.3
1	C	997	LYS	2.3
1	D	964	GLU	2.3
1	D	832	ILE	2.3
1	C	792	THR	2.3
1	C	930	GLY	2.3
1	B	916	THR	2.2
1	D	659	HIS	2.2
1	C	915	SER	2.2
1	D	933	PHE	2.2
1	C	661	ARG	2.2
1	C	918	SER	2.1
1	A	933	PHE	2.1
1	C	660	GLU	2.1
1	D	931	ILE	2.1
1	A	894	PRO	2.1
1	B	602	GLY	2.1
1	C	662	PRO	2.1
1	A	916	THR	2.1
1	C	904	THR	2.1
1	A	796	HIS	2.0
1	B	795	VAL	2.0
1	C	931	ILE	2.0
1	B	933	PHE	2.0
1	C	933	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates (i)

There are no carbohydrates in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	INH	I	1	29/?	0.87	0.22	66,80,109,109	0
2	INH	I	4	29/?	0.87	0.22	66,79,115,117	0
2	INH	I	2	29/?	0.92	0.19	58,69,102,102	0
2	INH	I	3	29/?	0.93	0.19	72,83,117,119	0

6.5 Other polymers

There are no such residues in this entry.