



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:47 PM UTC

PDB ID : 4Q8H / pdb_00004q8h
Title : Structure of the *Saccharomyces cerevisiae* PAN2 pseudoubiquitin-hydrolase-R
Nase module
Authors : Schaefer, I.B.; Conti, E.
Deposited on : 2014-04-27
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

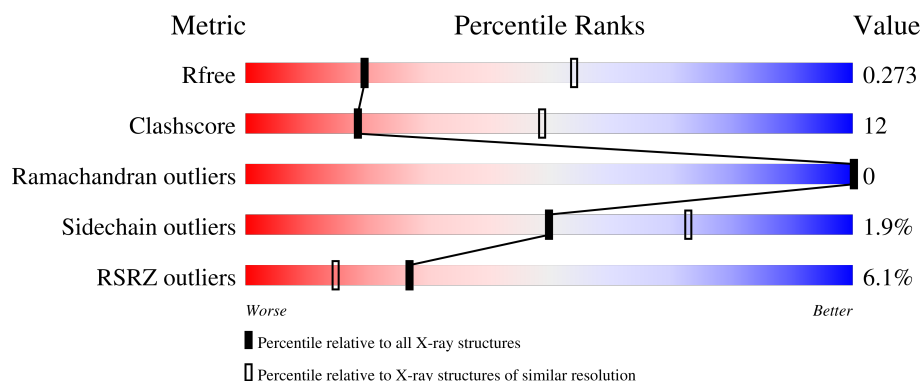
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	180053	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. 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	658	6% 69% 26% • 5%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4904 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 PAB-dependent poly(A)-specific ribonuclease subunit PAN2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	627	Total	C	N	O	S	0	0	0
			4902	3120	815	946	21			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	458	GLY	-	expression tag	UNP P53010
A	459	PRO	-	expression tag	UNP P53010

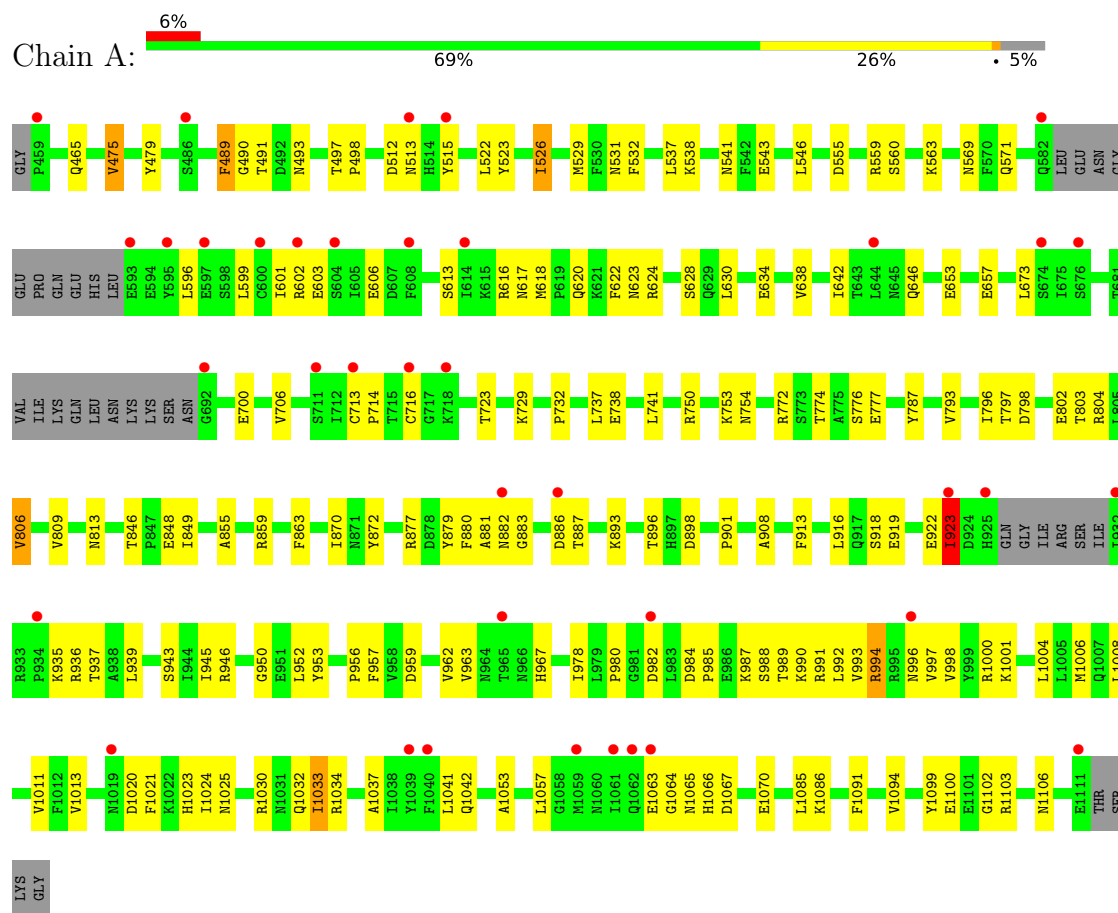
- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Mg	0	0
			2	2		

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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 geometry and 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: PAB-dependent poly(A)-specific ribonuclease subunit PAN2



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	91.71Å 115.50Å 257.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.01 – 3.10 48.01 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.01-3.10) 99.6 (48.01-3.10)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: dev_1647)	Depositor
R, R_{free}	0.239 , 0.275 0.240 , 0.273	Depositor DCC
R_{free} test set	1401 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	110.7	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 112.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4904	wwPDB-VP
Average B, all atoms (Å ²)	131.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.60% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.33	0/5005	0.80	14/6797 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	923	ILE	N-CA-C	7.58	120.53	112.96
1	A	497	THR	CA-C-N	-6.00	113.50	119.56
1	A	497	THR	C-N-CA	-6.00	113.50	119.56
1	A	526	ILE	CA-C-N	5.82	125.29	119.24
1	A	526	ILE	C-N-CA	5.82	125.29	119.24
1	A	813	ASN	CA-C-N	5.47	124.99	119.19
1	A	813	ASN	C-N-CA	5.47	124.99	119.19
1	A	918	SER	N-CA-C	5.38	122.26	110.80
1	A	923	ILE	CB-CA-C	-5.32	106.38	111.06
1	A	475	VAL	CA-C-N	5.28	123.51	119.66
1	A	475	VAL	C-N-CA	5.28	123.51	119.66
1	A	1033	ILE	CA-C-N	5.13	130.94	121.70
1	A	1033	ILE	C-N-CA	5.13	130.94	121.70
1	A	613	SER	N-CA-C	5.01	116.82	111.36

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	4902	0	4634	114	1
2	A	2	0	0	0	0
All	All	4904	0	4634	114	1

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 12.

All (114) 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:A:982:ASP:O	1:A:991:ARG:NH1	2.06	0.89
1:A:963:VAL:HG22	1:A:991:ARG:HE	1.43	0.84
1:A:569:ASN:H	1:A:1025:ASN:HD22	1.33	0.76
1:A:963:VAL:HG13	1:A:991:ARG:HH21	1.52	0.74
1:A:1013:VAL:HG12	1:A:1034:ARG:HB3	1.70	0.74
1:A:893:LYS:O	1:A:946:ARG:NH2	2.21	0.73
1:A:523:TYR:OH	1:A:623:ASN:OD1	2.05	0.73
1:A:750:ARG:NH2	1:A:846:THR:OG1	2.25	0.69
1:A:1053:ALA:O	1:A:1057:LEU:N	2.25	0.68
1:A:1021:PHE:HE2	1:A:1033:ILE:HD11	1.58	0.68
1:A:908:ALA:HB3	1:A:945:ILE:HG12	1.78	0.66
1:A:624:ARG:NH1	1:A:628:SER:OG	2.29	0.65
1:A:490:GLY:N	1:A:491:THR:HA	2.12	0.65
1:A:992:LEU:HD22	1:A:998:VAL:HG13	1.79	0.65
1:A:963:VAL:HB	1:A:993:VAL:HA	1.79	0.64
1:A:475:VAL:HG21	1:A:798:ASP:HA	1.80	0.63
1:A:1085:LEU:HB3	1:A:1091:PHE:HB3	1.81	0.63
1:A:996:ASN:O	1:A:1000:ARG:N	2.29	0.63
1:A:774:THR:HG23	1:A:776:SER:H	1.64	0.61
1:A:887:THR:OG1	1:A:988:SER:O	2.12	0.61
1:A:1102:GLY:O	1:A:1106:ASN:N	2.34	0.61
1:A:512:ASP:OD2	1:A:936:ARG:NH2	2.34	0.60
1:A:950:GLY:H	1:A:953:TYR:HB2	1.64	0.60
1:A:732:PRO:O	1:A:787:TYR:OH	2.17	0.60
1:A:978:ILE:HD13	1:A:980:PRO:HB3	1.83	0.59
1:A:538:LYS:HA	1:A:870:ILE:HG23	1.84	0.59
1:A:963:VAL:HG22	1:A:991:ARG:NE	2.15	0.58
1:A:1033:ILE:HA	1:A:1034:ARG:HB2	1.85	0.58
1:A:994:ARG:C	1:A:996:ASN:HA	2.30	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:657:GLU:HB3	1:A:723:THR:HG23	1.88	0.56
1:A:560:SER:HB3	1:A:563:LYS:HB3	1.88	0.56
1:A:653:GLU:HB3	1:A:729:LYS:HZ3	1.71	0.55
1:A:987:LYS:O	1:A:988:SER:OG	2.25	0.55
1:A:1099:TYR:O	1:A:1103:ARG:HG3	2.07	0.55
1:A:465:GLN:NE2	1:A:498:PRO:O	2.38	0.54
1:A:489:PHE:O	1:A:493:ASN:N	2.40	0.54
1:A:880:PHE:HE1	1:A:883:GLY:HA2	1.73	0.54
1:A:982:ASP:O	1:A:991:ARG:HD2	2.08	0.54
1:A:1085:LEU:HD23	1:A:1094:VAL:HG11	1.90	0.54
1:A:596:LEU:HA	1:A:599:LEU:HD12	1.90	0.53
1:A:916:LEU:HB2	1:A:936:ARG:HG3	1.91	0.53
1:A:601:ILE:HG12	1:A:618:MET:HE1	1.91	0.53
1:A:987:LYS:O	1:A:989:THR:N	2.38	0.53
1:A:526:ILE:HB	1:A:529:MET:HB3	1.92	0.52
1:A:569:ASN:H	1:A:1025:ASN:ND2	2.06	0.52
1:A:963:VAL:HG13	1:A:991:ARG:NH2	2.22	0.52
1:A:798:ASP:OD1	1:A:802:GLU:N	2.43	0.52
1:A:877:ARG:HH12	1:A:879:TYR:HD2	1.56	0.51
1:A:602:ARG:HH12	1:A:622:PHE:HA	1.76	0.51
1:A:989:THR:OG1	1:A:990:LYS:N	2.42	0.51
1:A:1042:GLN:HB3	1:A:1099:TYR:CZ	2.46	0.51
1:A:653:GLU:HB3	1:A:729:LYS:NZ	2.26	0.51
1:A:700:GLU:OE2	1:A:772:ARG:NH1	2.43	0.50
1:A:673:LEU:HD22	1:A:737:LEU:HD22	1.94	0.50
1:A:774:THR:HG22	1:A:777:GLU:HG3	1.92	0.50
1:A:855:ALA:O	1:A:859:ARG:NH1	2.39	0.50
1:A:602:ARG:O	1:A:606:GLU:N	2.42	0.50
1:A:797:THR:HG22	1:A:803:THR:HG22	1.94	0.50
1:A:531:ASN:OD1	1:A:863:PHE:N	2.45	0.50
1:A:896:THR:OG1	1:A:898:ASP:OD1	2.21	0.50
1:A:796:ILE:HD13	1:A:806:VAL:HB	1.93	0.49
1:A:1011:VAL:HA	1:A:1032:GLN:HB3	1.93	0.49
1:A:529:MET:HE1	1:A:630:LEU:HD13	1.93	0.49
1:A:537:LEU:O	1:A:1000:ARG:NH1	2.34	0.49
1:A:946:ARG:HD2	1:A:952:LEU:O	2.12	0.49
1:A:1091:PHE:HA	1:A:1094:VAL:HG12	1.95	0.49
1:A:479:TYR:O	1:A:804:ARG:NH1	2.46	0.48
1:A:620:GLN:NE2	1:A:848:GLU:OE1	2.47	0.48
1:A:945:ILE:HA	1:A:956:PRO:HA	1.94	0.48
1:A:913:PHE:HD1	1:A:939:LEU:HA	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1020:ASP:O	1:A:1024:ILE:HG13	2.14	0.48
1:A:886:ASP:O	1:A:989:THR:HA	2.14	0.47
1:A:1100:GLU:HG3	1:A:1103:ARG:NH2	2.30	0.47
1:A:1067:ASP:OD2	1:A:1070:GLU:N	2.47	0.47
1:A:922:GLU:OE1	1:A:923:ILE:HB	2.15	0.46
1:A:1065:ASN:HA	1:A:1066:HIS:HA	1.68	0.46
1:A:1063:GLU:HA	1:A:1064:GLY:HA2	1.62	0.45
1:A:916:LEU:HG	1:A:967:HIS:O	2.16	0.45
1:A:937:THR:HG21	1:A:1023:HIS:CE1	2.50	0.45
1:A:522:LEU:HD22	1:A:793:VAL:HG23	1.97	0.45
1:A:1037:ALA:O	1:A:1041:LEU:HB2	2.17	0.45
1:A:946:ARG:HG3	1:A:957:PHE:HD2	1.82	0.44
1:A:513:ASN:O	1:A:515:TYR:N	2.44	0.44
1:A:943:SER:OG	1:A:959:ASP:OD1	2.30	0.43
1:A:532:PHE:CZ	1:A:634:GLU:HG3	2.53	0.43
1:A:543:GLU:H	1:A:543:GLU:CD	2.25	0.43
1:A:555:ASP:O	1:A:559:ARG:HG2	2.19	0.43
1:A:616:ARG:HA	1:A:617:ASN:HA	1.72	0.43
1:A:935:LYS:HA	1:A:936:ARG:HA	1.86	0.43
1:A:713:CYS:HA	1:A:714:PRO:HD3	1.81	0.42
1:A:984:ASP:N	1:A:985:PRO:HD2	2.34	0.42
1:A:603:GLU:OE1	1:A:603:GLU:N	2.47	0.42
1:A:532:PHE:HZ	1:A:634:GLU:HG3	1.85	0.42
1:A:753:LYS:HD3	1:A:754:ASN:H	1.84	0.42
1:A:939:LEU:HD22	1:A:962:VAL:HG21	2.01	0.42
1:A:616:ARG:NH2	1:A:741:LEU:O	2.53	0.42
1:A:872:TYR:CD1	1:A:1004:LEU:HD22	2.55	0.41
1:A:541:ASN:ND2	1:A:638:VAL:HG13	2.36	0.41
1:A:880:PHE:CE1	1:A:883:GLY:HA2	2.53	0.41
1:A:543:GLU:OE1	1:A:543:GLU:N	2.48	0.41
1:A:620:GLN:HB3	1:A:738:GLU:HB3	2.02	0.41
1:A:642:ILE:O	1:A:646:GLN:N	2.49	0.41
1:A:1100:GLU:HG3	1:A:1103:ARG:HH21	1.86	0.41
1:A:978:ILE:H	1:A:978:ILE:HG13	1.69	0.41
1:A:623:ASN:HB2	1:A:849:ILE:HD13	2.03	0.41
1:A:997:VAL:O	1:A:1001:LYS:HG3	2.20	0.41
1:A:489:PHE:HD1	1:A:489:PHE:HA	1.78	0.40
1:A:1021:PHE:CE2	1:A:1033:ILE:HD11	2.48	0.40
1:A:1086:LYS:HA	1:A:1091:PHE:CD2	2.55	0.40
1:A:901:PRO:O	1:A:1008:LEU:HD13	2.21	0.40
1:A:945:ILE:HG22	1:A:956:PRO:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:ASN:HB3	1:A:571:GLN:OE1	2.22	0.40
1:A:602:ARG:NH1	1:A:622:PHE:HA	2.36	0.40
1:A:881:ALA:HA	1:A:882:ASN:HA	1.52	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:716:CYS:CB	1:A:716:CYS:SG[3_555]	1.79	0.41

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	619/658 (94%)	583 (94%)	36 (6%)	0	100	100

There are no Ramachandran outliers to report.

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	521/604 (86%)	511 (98%)	10 (2%)	50	73

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	489	PHE
1	A	546	LEU
1	A	706	VAL
1	A	806	VAL
1	A	809	VAL
1	A	919	GLU
1	A	923	ILE
1	A	994	ARG
1	A	1006	MET
1	A	1030	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	493	ASN
1	A	514	HIS
1	A	541	ASN
1	A	639	ASN
1	A	679	ASN
1	A	1025	ASN
1	A	1031	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95th 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	627/658 (95%)	0.38	38 (6%)	27 15	62, 124, 223, 307	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	600	CYS	6.4
1	A	674	SER	4.5
1	A	604	SER	4.5
1	A	934	PRO	4.1
1	A	582	GLN	3.8
1	A	982	ASP	3.8
1	A	1111	GLU	3.5
1	A	486	SER	3.5
1	A	882	ASN	3.4
1	A	716	CYS	3.3
1	A	1063	GLU	3.1
1	A	459	PRO	3.0
1	A	1040	PHE	2.9
1	A	711	SER	2.8
1	A	602	ARG	2.8
1	A	597	GLU	2.7
1	A	1062	GLN	2.6
1	A	718	LYS	2.6
1	A	713	CYS	2.5
1	A	932	ILE	2.5
1	A	676	SER	2.5
1	A	996	ASN	2.4
1	A	925	HIS	2.4
1	A	923	ILE	2.4
1	A	593	GLU	2.4
1	A	692	GLY	2.4
1	A	614	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1019	ASN	2.3
1	A	1059	MET	2.3
1	A	644	LEU	2.3
1	A	965	THR	2.3
1	A	1039	TYR	2.2
1	A	1061	ILE	2.2
1	A	595	TYR	2.1
1	A	513	ASN	2.1
1	A	608	PHE	2.1
1	A	886	ASP	2.1
1	A	515	TYR	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 oligosaccharides 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, 95th 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($\text{\AA}^2$)	Q<0.9
2	MG	A	1201	1/1	0.37	0.13	254,254,254,254	0
2	MG	A	1202	1/1	0.71	0.10	253,253,253,253	0

6.5 Other polymers [i](#)

There are no such residues in this entry.