



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 04:34 PM UTC

PDB ID : 3VU1 / pdb_00003vu1
Title : Crystal structure of the C-terminal globular domain of oligosaccharyltransferase (PhAglB-L, O74088_PYRHO) from *Pyrococcus horikoshii*
Authors : Nyirenda, J.; Matsumoto, S.; Saitoh, T.; Maita, N.; Noda, N.N.; Inagaki, F.; Kohda, D.
Deposited on : 2012-06-13
Resolution : 2.70 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

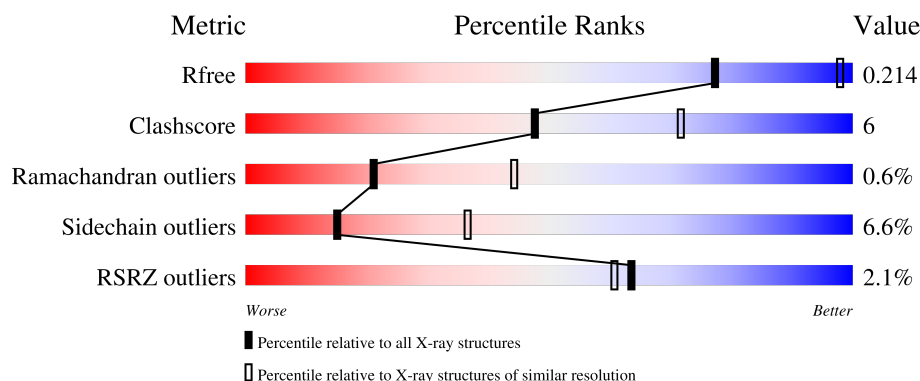
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

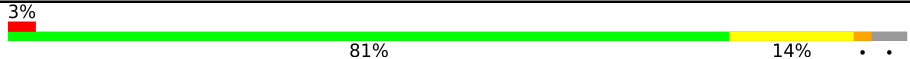
The reported resolution of this entry is 2.70 Å.

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	3538 (2.70-2.70)
Clashscore	190562	3843 (2.70-2.70)
Ramachandran outliers	187476	3778 (2.70-2.70)
Sidechain outliers	187428	3778 (2.70-2.70)
RSRZ outliers	180081	3538 (2.70-2.70)

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	506	
1	B	506	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7936 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 Putative uncharacterized protein PH0242.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	488	Total	C	N	O	S	0	1	0
			3942	2553	671	711	7			
1	B	490	Total	C	N	O	S	0	0	0
			3910	2528	659	716	7			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	481	MET	-	expression tag	UNP O74088
A	977	HIS	-	expression tag	UNP O74088
A	978	HIS	-	expression tag	UNP O74088
A	979	HIS	-	expression tag	UNP O74088
A	980	HIS	-	expression tag	UNP O74088
A	981	HIS	-	expression tag	UNP O74088
A	982	HIS	-	expression tag	UNP O74088
A	983	HIS	-	expression tag	UNP O74088
A	984	HIS	-	expression tag	UNP O74088
A	985	HIS	-	expression tag	UNP O74088
A	986	HIS	-	expression tag	UNP O74088
B	481	MET	-	expression tag	UNP O74088
B	977	HIS	-	expression tag	UNP O74088
B	978	HIS	-	expression tag	UNP O74088
B	979	HIS	-	expression tag	UNP O74088
B	980	HIS	-	expression tag	UNP O74088
B	981	HIS	-	expression tag	UNP O74088
B	982	HIS	-	expression tag	UNP O74088
B	983	HIS	-	expression tag	UNP O74088
B	984	HIS	-	expression tag	UNP O74088
B	985	HIS	-	expression tag	UNP O74088
B	986	HIS	-	expression tag	UNP O74088

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 1	Ca 1	0	0
2	B	1	Total 1	Ca 1	0	0

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total 1	Cl 1	0	0
3	B	1	Total 1	Cl 1	0	0

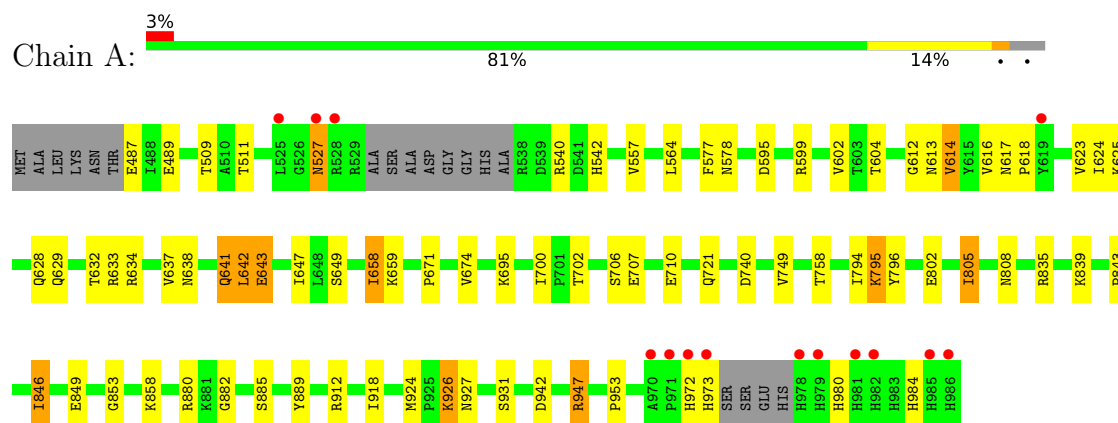
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	46	Total 46	O 46	0	0
4	B	34	Total 34	O 34	0	0

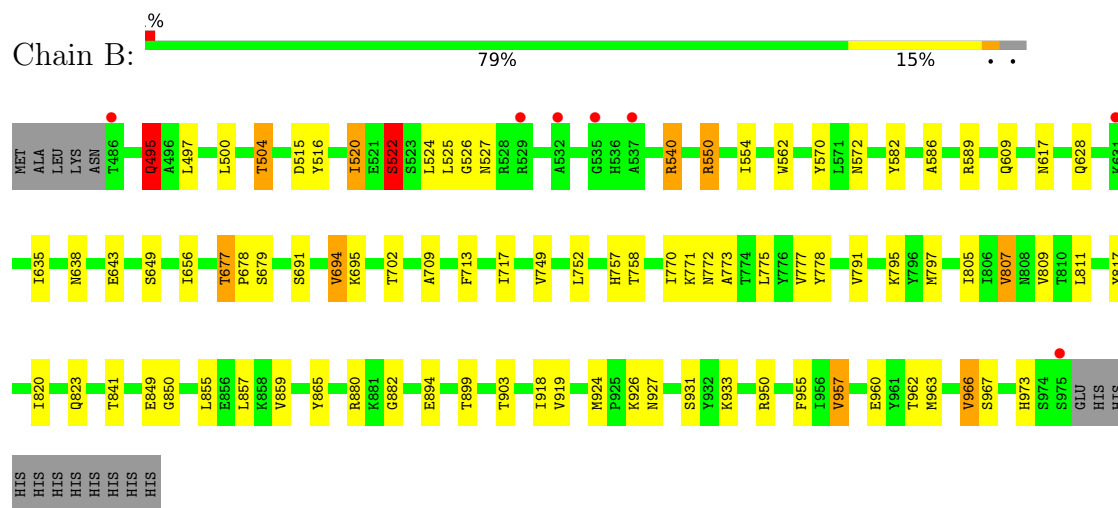
3 Residue-property plots [i](#)

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: Putative uncharacterized protein PH0242



• Molecule 1: Putative uncharacterized protein PH0242



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	83.47Å 94.84Å 186.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.70 30.00 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.3 (30.00-2.70) 99.3 (30.00-2.70)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.68Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.171 , 0.215 0.171 , 0.214	Depositor DCC
R_{free} test set	2081 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	52.0	Xtriage
Anisotropy	0.129	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 38.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7936	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.58% 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: CL, CA

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	0.85	0/4045	0.96	4/5477 (0.1%)
1	B	0.84	1/4004 (0.0%)	0.96	1/5425 (0.0%)
All	All	0.85	1/8049 (0.0%)	0.96	5/10902 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	757	HIS	CG-CD2	5.30	1.41	1.35

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	853	GLY	N-CA-C	9.66	123.69	110.56
1	A	700	ILE	CA-C-N	-6.37	115.22	121.65
1	A	700	ILE	C-N-CA	-6.37	115.22	121.65
1	A	577	PHE	N-CA-C	5.23	117.89	111.82
1	B	495	GLN	N-CA-C	5.18	117.00	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	3942	0	3932	39	0
1	B	3910	0	3914	50	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	46	0	0	0	0
4	B	34	0	0	2	0
All	All	7936	0	7846	88	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 (88) 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:972:HIS:HB2	1:A:973:HIS:CB	1.72	1.19
1:B:865:TYR:HB3	1:B:957:VAL:HG21	1.52	0.92
1:A:509:THR:HG23	1:A:527:ASN:HB2	1.53	0.90
1:A:846:ILE:HG12	1:A:953:PRO:HD3	1.64	0.78
1:B:497:LEU:HD21	1:B:520:ILE:HD11	1.67	0.75
1:B:771:LYS:H	1:B:823:GLN:HE22	1.36	0.72
1:B:850:GLY:HA2	1:B:926:LYS:HD3	1.69	0.72
1:A:927:ASN:O	1:A:931:SER:HB3	1.91	0.71
1:B:849:GLU:HA	1:B:924:MET:HE2	1.72	0.71
1:A:972:HIS:CB	1:A:973:HIS:CB	2.62	0.70
1:B:677:THR:HG22	1:B:679:SER:H	1.58	0.69
1:B:540:ARG:HG2	1:B:562:TRP:CZ2	2.32	0.65
1:B:500:LEU:O	1:B:504:THR:HB	1.97	0.65
1:A:578:ASN:HD21	1:A:604:THR:H	1.45	0.64
1:B:772:ASN:OD1	1:B:795:LYS:HE2	1.98	0.63
1:A:641:GLN:H	1:A:641:GLN:NE2	1.96	0.63
1:A:758:THR:OG1	1:A:808:ASN:ND2	2.32	0.63
1:B:771:LYS:H	1:B:823:GLN:NE2	1.96	0.63
1:B:927:ASN:O	1:B:931:SER:HB2	1.99	0.62
1:A:641:GLN:H	1:A:641:GLN:HE21	1.46	0.62
1:A:795:LYS:HD2	1:A:796:TYR:H	1.63	0.62
1:B:497:LEU:HD21	1:B:520:ILE:CD1	2.30	0.62
1:A:629:GLN:O	1:A:632:THR:HG22	2.00	0.61
1:B:522:SER:O	4:B:1134:HOH:O	2.16	0.60
1:B:773:ALA:HB2	1:B:823:GLN:HE21	1.67	0.60
1:A:595:ASP:HA	1:A:889:TYR:CD2	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:927:ASN:O	1:A:931:SER:CB	2.51	0.59
1:A:706:SER:O	1:A:707:GLU:HB2	2.02	0.59
1:A:880:ARG:HD2	1:A:882:GLY:O	2.04	0.58
1:A:740:ASP:HB2	1:A:749:VAL:HG11	1.86	0.57
1:B:752:LEU:HD12	1:B:966:VAL:HG21	1.86	0.57
1:B:791:VAL:O	1:B:807:VAL:HG22	2.04	0.57
1:B:797:MET:HE1	1:B:805:ILE:HD11	1.85	0.57
1:A:695:LYS:HE3	1:A:702:THR:O	2.04	0.56
1:A:509:THR:CG2	1:A:527:ASN:HB2	2.32	0.55
1:B:495:GLN:H	1:B:495:GLN:CD	2.15	0.55
1:B:849:GLU:OE2	1:B:927:ASN:HA	2.07	0.54
1:A:634:ARG:HA	1:A:658:ILE:HD11	1.89	0.54
1:B:865:TYR:CB	1:B:957:VAL:HG21	2.30	0.54
1:B:865:TYR:HB3	1:B:957:VAL:CG2	2.31	0.53
1:B:880:ARG:HD2	1:B:882:GLY:O	2.09	0.52
1:B:497:LEU:HD11	1:B:525:LEU:HD12	1.91	0.52
1:B:695:LYS:HE3	1:B:702:THR:O	2.10	0.52
1:B:540:ARG:HD3	1:B:950:ARG:NH2	2.25	0.51
1:B:582:TYR:OH	1:B:589:ARG:HD2	2.11	0.50
1:B:778:TYR:OH	1:B:960:GLU:OE2	2.26	0.50
1:B:927:ASN:O	1:B:931:SER:CB	2.59	0.49
1:B:635:ILE:HG13	1:B:649:SER:CB	2.42	0.49
1:A:642:LEU:HD23	1:A:642:LEU:H	1.78	0.49
1:A:511:THR:HG22	1:A:564:LEU:HD11	1.94	0.49
1:B:677:THR:HG23	1:B:678:PRO:HD2	1.95	0.48
1:B:850:GLY:CA	1:B:926:LYS:HD3	2.42	0.48
1:A:638:ASN:ND2	1:A:643:GLU:HB2	2.29	0.48
1:B:691:SER:OG	1:B:694:VAL:HG13	2.13	0.48
1:A:846:ILE:HD12	1:A:846:ILE:HA	1.63	0.47
1:A:647:ILE:HD11	1:A:671:PRO:HA	1.97	0.47
1:A:794:ILE:HG12	1:A:805:ILE:HD11	1.96	0.47
1:A:843:PRO:HA	1:A:846:ILE:CD1	2.45	0.46
1:B:550:ARG:HD3	1:B:586:ALA:HB2	1.98	0.46
1:A:835:ARG:HA	1:A:839:LYS:O	2.16	0.46
1:A:849:GLU:HA	1:A:924:MET:HB3	1.99	0.45
1:B:859:VAL:HG21	1:B:955:PHE:CE1	2.52	0.45
1:A:614:VAL:HG22	1:A:625:LYS:HB3	1.99	0.44
1:A:624:ILE:HG12	1:A:637:VAL:HG22	1.99	0.44
1:B:865:TYR:CG	1:B:957:VAL:HG21	2.52	0.44
1:B:855:LEU:O	1:B:919:VAL:HA	2.18	0.44
1:A:599:ARG:HG2	1:B:841:THR:HG22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:770:ILE:HA	1:B:823:GLN:HE22	1.81	0.44
1:B:709:ALA:O	1:B:713:PHE:CD2	2.71	0.44
1:A:617:ASN:HA	1:A:618:PRO:HD2	1.85	0.44
1:A:527:ASN:ND2	1:A:540:ARG:HH12	2.15	0.44
1:B:638:ASN:OD1	1:B:643:GLU:HG3	2.18	0.43
1:B:811:LEU:HD13	1:B:817:TYR:CE2	2.53	0.43
1:A:649:SER:HA	1:A:674:VAL:O	2.19	0.43
1:B:570:TYR:CZ	1:B:572:ASN:HB2	2.53	0.43
1:B:495:GLN:CD	1:B:495:GLN:N	2.77	0.43
1:B:526:GLY:N	4:B:1134:HOH:O	2.50	0.43
1:A:926:LYS:O	1:A:927:ASN:HB2	2.19	0.42
1:B:775:LEU:HD22	1:B:963:MET:HE1	2.02	0.42
1:B:777:VAL:HG11	1:B:809:VAL:HG21	2.01	0.42
1:A:616:VAL:HG12	1:A:623:VAL:HG22	2.02	0.42
1:A:527:ASN:HD21	1:A:540:ARG:HH12	1.67	0.41
1:A:542:HIS:NE2	1:A:947:ARG:HD2	2.35	0.41
1:B:797:MET:CE	1:B:805:ILE:HD11	2.49	0.41
1:B:515:ASP:O	1:B:516:TYR:C	2.64	0.41
1:B:540:ARG:HG2	1:B:562:TRP:CH2	2.56	0.41
1:B:617:ASN:C	1:B:617:ASN:OD1	2.63	0.41
1:A:794:ILE:HG12	1:A:805:ILE:CD1	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	483/506 (96%)	460 (95%)	21 (4%)	2 (0%)	30	54
1	B	488/506 (96%)	460 (94%)	24 (5%)	4 (1%)	16	37
All	All	971/1012 (96%)	920 (95%)	45 (5%)	6 (1%)	21	44

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	612	GLY
1	B	524	LEU
1	B	522	SER
1	B	527	ASN
1	A	613	ASN
1	B	973	HIS

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	418/432 (97%)	390 (93%)	28 (7%)	15	36
1	B	414/432 (96%)	387 (94%)	27 (6%)	15	37
All	All	832/864 (96%)	777 (93%)	55 (7%)	15	36

All (55) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	487	GLU
1	A	489	GLU
1	A	527	ASN
1	A	557	VAL
1	A	602	VAL
1	A	614	VAL
1	A	628	GLN
1	A	633	ARG
1	A	641	GLN
1	A	642	LEU
1	A	643	GLU
1	A	658	ILE
1	A	659	LYS
1	A	710	GLU
1	A	721	GLN
1	A	795	LYS
1	A	802	GLU

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Mol	Chain	Res	Type
1	A	805	ILE
1	A	846	ILE
1	A	858	LYS
1	A	885	SER
1	A	912	ARG
1	A	918	ILE
1	A	926	LYS
1	A	942	ASP
1	A	947	ARG
1	A	980	HIS
1	A	984	HIS
1	B	495	GLN
1	B	504	THR
1	B	520	ILE
1	B	522	SER
1	B	540	ARG
1	B	550	ARG
1	B	554	ILE
1	B	609	GLN
1	B	628	GLN
1	B	656	ILE
1	B	677	THR
1	B	694	VAL
1	B	717	ILE
1	B	749	VAL
1	B	758	THR
1	B	807	VAL
1	B	820	ILE
1	B	857	LEU
1	B	894	GLU
1	B	899	THR
1	B	903	THR
1	B	918	ILE
1	B	933	LYS
1	B	957	VAL
1	B	962	THR
1	B	966	VAL
1	B	967	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	503	ASN
1	A	578	ASN
1	A	597	ASN
1	A	628	GLN
1	A	641	GLN
1	A	655	ASN
1	A	808	ASN
1	A	815	GLN
1	A	940	HIS
1	A	978	HIS
1	B	503	ASN
1	B	715	ASN
1	B	781	ASN
1	B	808	ASN
1	B	815	GLN
1	B	823	GLN
1	B	896	HIS
1	B	940	HIS

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 4 ligands modelled in this entry, 4 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 [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, 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	488/506 (96%)	-0.55	14 (2%)	53	50	26, 44, 82, 131	1 (0%)
1	B	490/506 (96%)	-0.48	7 (1%)	73	72	26, 46, 85, 129	0
All	All	978/1012 (96%)	-0.51	21 (2%)	63	61	26, 45, 85, 131	1 (0%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	979	HIS	4.5
1	A	973	HIS	4.4
1	B	532	ALA	4.1
1	A	972	HIS	3.6
1	A	971	PRO	3.5
1	A	619[A]	TYR	3.3
1	B	486	THR	3.3
1	A	525	LEU	3.2
1	B	529	ARG	3.0
1	A	981	HIS	3.0
1	B	537	ALA	2.8
1	A	527	ASN	2.7
1	A	986	HIS	2.7
1	B	535	GLY	2.6
1	A	978	HIS	2.4
1	B	631	LYS	2.4
1	A	970	ALA	2.3
1	A	982	HIS	2.2
1	A	528	ARG	2.1
1	B	975	SER	2.1
1	A	985	HIS	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
3	CL	B	1002	1/1	0.96	0.06	53,53,53,53	0
2	CA	B	1001	1/1	0.97	0.04	65,65,65,65	0
2	CA	A	1001	1/1	0.98	0.03	49,49,49,49	0
3	CL	A	1002	1/1	0.99	0.05	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.