



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 10:37 AM UTC

PDB ID : 6S5Y / pdb_00006s5y
Title : Structure of tandemly arrayed consecutive Rib domains (Rib2R) from Group B Streptococcal species Streptococcus agalactiae
Authors : Whelan, F.; Griffiths, S.C.; Bateman, A.; Potts, J.R.
Deposited on : 2019-07-02
Resolution : 2.30 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:

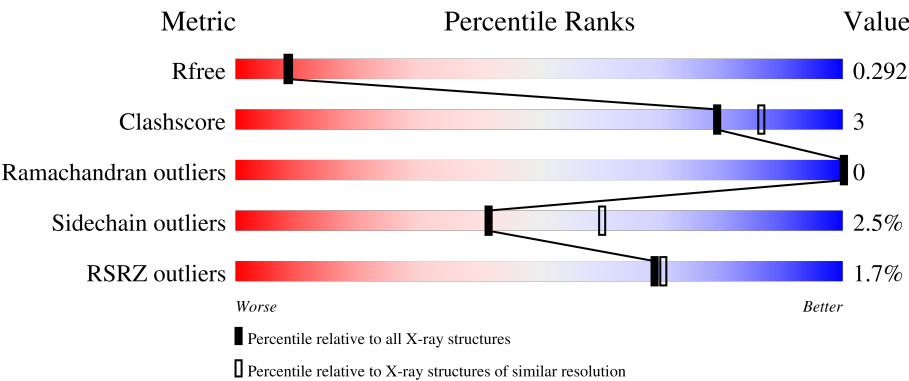
MolProbity : 4-5-2 with Phenix2.0
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)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

1 Overall quality at a glance 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}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (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 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	163	2% 91% 9%
1	B	163	% 87% 12% ..
1	C	163	2% 89% 10% .
1	D	163	% 91% 7% .
1	E	163	89% 9% ..

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Mol	Chain	Length	Quality of chain
1	F	163	5% 88% 10%
1	G	163	% 87% 11%
1	H	163	2% 91% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 9423 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 Group B streptococcal R4 surface protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	163	Total	C	N	O	0	0	0
			1185	730	195	260			
1	B	161	Total	C	N	O	0	0	0
			1173	723	193	257			
1	C	161	Total	C	N	O	0	0	0
			1174	724	193	257			
1	D	161	Total	C	N	O	0	0	0
			1174	724	193	257			
1	E	161	Total	C	N	O	0	0	0
			1174	724	193	257			
1	F	161	Total	C	N	O	0	0	0
			1174	724	193	257			
1	G	161	Total	C	N	O	0	0	0
			1174	724	193	257			
1	H	160	Total	C	N	O	0	0	0
			1163	718	189	256			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	225	GLY	-	expression tag	UNP P72362
A	226	PRO	-	expression tag	UNP P72362
A	227	LEU	-	expression tag	UNP P72362
A	228	GLY	-	expression tag	UNP P72362
A	229	SER	-	expression tag	UNP P72362
B	225	GLY	-	expression tag	UNP P72362
B	226	PRO	-	expression tag	UNP P72362
B	227	LEU	-	expression tag	UNP P72362
B	228	GLY	-	expression tag	UNP P72362
B	229	SER	-	expression tag	UNP P72362
C	225	GLY	-	expression tag	UNP P72362
C	226	PRO	-	expression tag	UNP P72362
C	227	LEU	-	expression tag	UNP P72362

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Chain	Residue	Modelled	Actual	Comment	Reference
C	228	GLY	-	expression tag	UNP P72362
C	229	SER	-	expression tag	UNP P72362
D	225	GLY	-	expression tag	UNP P72362
D	226	PRO	-	expression tag	UNP P72362
D	227	LEU	-	expression tag	UNP P72362
D	228	GLY	-	expression tag	UNP P72362
D	229	SER	-	expression tag	UNP P72362
E	225	GLY	-	expression tag	UNP P72362
E	226	PRO	-	expression tag	UNP P72362
E	227	LEU	-	expression tag	UNP P72362
E	228	GLY	-	expression tag	UNP P72362
E	229	SER	-	expression tag	UNP P72362
F	225	GLY	-	expression tag	UNP P72362
F	226	PRO	-	expression tag	UNP P72362
F	227	LEU	-	expression tag	UNP P72362
F	228	GLY	-	expression tag	UNP P72362
F	229	SER	-	expression tag	UNP P72362
G	225	GLY	-	expression tag	UNP P72362
G	226	PRO	-	expression tag	UNP P72362
G	227	LEU	-	expression tag	UNP P72362
G	228	GLY	-	expression tag	UNP P72362
G	229	SER	-	expression tag	UNP P72362
H	225	GLY	-	expression tag	UNP P72362
H	226	PRO	-	expression tag	UNP P72362
H	227	LEU	-	expression tag	UNP P72362
H	228	GLY	-	expression tag	UNP P72362
H	229	SER	-	expression tag	UNP P72362

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	5	Total O 5 5	0	0
2	B	8	Total O 8 8	0	0
2	C	1	Total O 1 1	0	0
2	D	2	Total O 2 2	0	0
2	F	3	Total O 3 3	0	0
2	G	8	Total O 8 8	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	H	5	Total	O	0	0
			5	5		

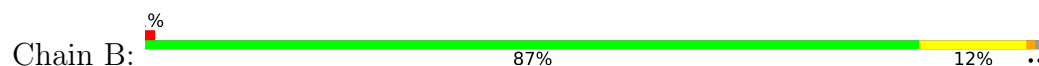
3 Residue-property plots [i](#)

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.

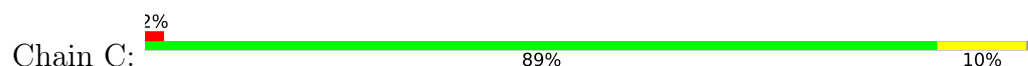
- Molecule 1: Group B streptococcal R4 surface protein



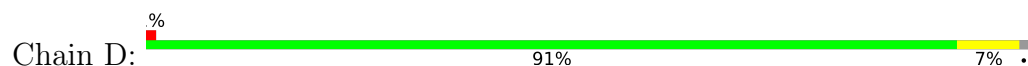
- Molecule 1: Group B streptococcal R4 surface protein



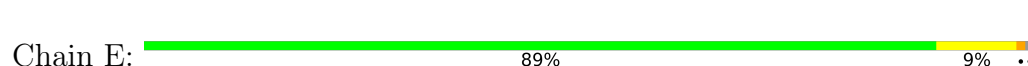
- Molecule 1: Group B streptococcal R4 surface protein



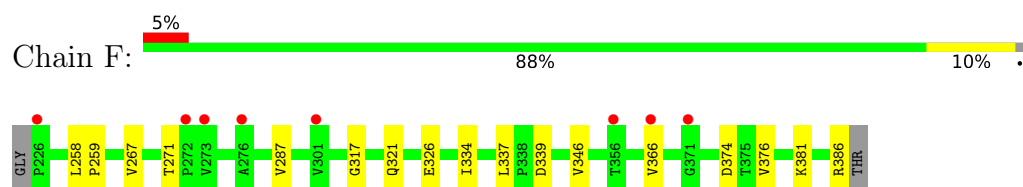
- Molecule 1: Group B streptococcal R4 surface protein



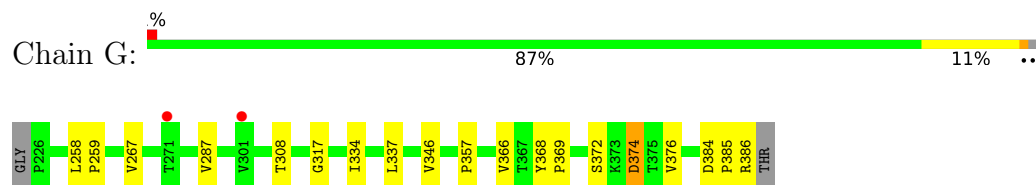
- Molecule 1: Group B streptococcal R4 surface protein



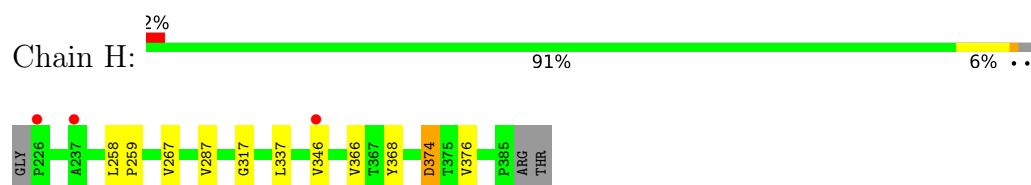
- Molecule 1: Group B streptococcal R4 surface protein



- Molecule 1: Group B streptococcal R4 surface protein



- Molecule 1: Group B streptococcal R4 surface protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	37.83Å 380.85Å 37.85Å 90.00° 91.60° 90.00°	Depositor
Resolution (Å)	38.09 – 2.30 38.09 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.8 (38.09-2.30) 99.8 (38.09-2.30)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.75 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.234 , 0.274 0.255 , 0.292	Depositor DCC
R_{free} test set	2349 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	48.3	Xtriage
Anisotropy	0.689	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 97.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.003 for l,k,-h 0.096 for h,-k,-l 0.056 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9423	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 9.87% 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

5.1 Standard geometry

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	0.80	0/1207	1.13	3/1658 (0.2%)
1	B	0.92	2/1195 (0.2%)	1.21	4/1641 (0.2%)
1	C	0.81	0/1196	1.14	0/1642
1	D	0.79	0/1196	1.15	0/1642
1	E	0.74	0/1196	1.11	0/1642
1	F	0.75	0/1196	1.08	0/1642
1	G	0.76	0/1196	1.13	2/1642 (0.1%)
1	H	0.76	0/1185	1.12	0/1628
All	All	0.79	2/9567 (0.0%)	1.13	9/13137 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	236	PRO	C-O	5.26	1.29	1.23
1	B	251	ALA	C-O	5.00	1.30	1.24

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	255	ILE	CA-C-N	7.59	129.90	120.34
1	B	255	ILE	C-N-CA	7.59	129.90	120.34
1	G	385	PRO	CA-C-N	6.02	132.54	121.70
1	G	385	PRO	C-N-CA	6.02	132.54	121.70
1	B	253	ASP	CA-CB-CG	5.97	118.57	112.60
1	A	232	ASP	CA-CB-CG	5.77	118.37	112.60
1	A	248	THR	CB-CA-C	5.20	115.78	109.85
1	B	238	GLY	N-CA-C	5.11	118.74	112.14
1	A	339	ASP	CA-CB-CG	5.05	117.65	112.60

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	1185	0	1162	7	0
1	B	1173	0	1148	7	0
1	C	1174	0	1153	7	0
1	D	1174	0	1153	7	0
1	E	1174	0	1153	7	0
1	F	1174	0	1153	7	0
1	G	1174	0	1153	10	0
1	H	1163	0	1140	6	0
2	A	5	0	0	0	0
2	B	8	0	0	0	0
2	C	1	0	0	0	0
2	D	2	0	0	0	0
2	F	3	0	0	0	0
2	G	8	0	0	0	0
2	H	5	0	0	0	0
All	All	9423	0	9215	51	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 3.

All (51) 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:E:357:PRO:HG3	1:E:384:ASP:HB2	1.68	0.74
1:B:239:LYS:O	1:B:254:SER:HA	1.91	0.69
1:C:227:LEU:HB3	1:D:327:THR:HB	1.75	0.69
1:F:321:GLN:HG2	1:F:381:LYS:HB3	1.77	0.66
1:E:284:LYS:HZ3	1:E:296:THR:HG21	1.65	0.61
1:A:292:GLY:HA2	1:D:351:PRO:HG2	1.84	0.59
1:G:317:GLY:HA3	1:G:376:VAL:HG11	1.85	0.57
1:C:321:GLN:HG3	1:C:381:LYS:HB3	1.88	0.55
1:E:317:GLY:HA3	1:E:376:VAL:HG11	1.86	0.55
1:H:317:GLY:HA3	1:H:376:VAL:HG11	1.90	0.53
1:C:317:GLY:HA3	1:C:376:VAL:HG11	1.90	0.53
1:B:317:GLY:HA3	1:B:376:VAL:HG11	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:317:GLY:HA3	1:F:376:VAL:HG11	1.92	0.52
1:B:252:GLU:HG3	1:B:267:VAL:CG2	2.40	0.51
1:C:277:THR:HG21	1:F:271:THR:HG23	1.93	0.50
1:G:384:ASP:C	1:G:386:ARG:H	2.19	0.49
1:H:267:VAL:HG12	1:H:287:VAL:HG22	1.95	0.49
1:D:247:GLU:O	1:D:275:THR:HG21	2.13	0.48
1:H:346:VAL:HG12	1:H:366:VAL:HG22	1.96	0.47
1:H:368:TYR:HE2	1:H:374:ASP:HB2	1.79	0.47
1:B:267:VAL:HG12	1:B:287:VAL:HG22	1.98	0.46
1:G:308:THR:OG1	1:G:372:SER:HB3	2.16	0.46
1:F:346:VAL:HG12	1:F:366:VAL:HG22	1.99	0.45
1:G:267:VAL:HG12	1:G:287:VAL:HG22	1.99	0.44
1:E:267:VAL:HG12	1:E:287:VAL:HG22	2.00	0.44
1:F:267:VAL:HG12	1:F:287:VAL:HG22	2.00	0.44
1:A:317:GLY:O	1:D:235:ASP:HB3	2.18	0.43
1:B:334:ILE:HG13	1:B:346:VAL:HG11	2.00	0.43
1:E:368:TYR:HE2	1:E:374:ASP:HB2	1.83	0.43
1:F:334:ILE:HG13	1:F:346:VAL:HG11	2.00	0.43
1:G:258:LEU:N	1:G:259:PRO:HD2	2.34	0.43
1:G:368:TYR:HE2	1:G:374:ASP:HB2	1.84	0.43
1:E:346:VAL:HG12	1:E:366:VAL:HG22	2.01	0.43
1:G:334:ILE:HG13	1:G:346:VAL:HG11	2.01	0.43
1:F:258:LEU:N	1:F:259:PRO:HD2	2.34	0.42
1:G:346:VAL:HG12	1:G:366:VAL:HG22	2.01	0.42
1:A:267:VAL:HG12	1:A:287:VAL:HG22	1.99	0.42
1:C:346:VAL:HG12	1:C:366:VAL:HG22	2.01	0.42
1:A:258:LEU:N	1:A:259:PRO:HD2	2.35	0.42
1:B:252:GLU:HG3	1:B:267:VAL:HG21	2.02	0.41
1:D:267:VAL:HG12	1:D:287:VAL:HG22	2.02	0.41
1:H:258:LEU:N	1:H:259:PRO:HD2	2.35	0.41
1:A:338:PRO:HG2	1:G:357:PRO:HB2	2.02	0.41
1:C:258:LEU:N	1:C:259:PRO:HD2	2.36	0.41
1:B:258:LEU:N	1:B:259:PRO:HD2	2.35	0.41
1:E:258:LEU:N	1:E:259:PRO:HD2	2.36	0.41
1:A:317:GLY:HA2	1:A:334:ILE:HD13	2.03	0.41
1:D:258:LEU:N	1:D:259:PRO:HD2	2.36	0.40
1:A:316:ALA:HB2	1:D:237:ALA:HB2	2.04	0.40
1:G:369:PRO:O	1:H:259:PRO:HD3	2.21	0.40
1:C:334:ILE:HG13	1:C:346:VAL:HG11	2.04	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	161/163 (99%)	158 (98%)	3 (2%)	0	100	100
1	B	159/163 (98%)	156 (98%)	3 (2%)	0	100	100
1	C	159/163 (98%)	155 (98%)	4 (2%)	0	100	100
1	D	159/163 (98%)	157 (99%)	2 (1%)	0	100	100
1	E	159/163 (98%)	157 (99%)	2 (1%)	0	100	100
1	F	159/163 (98%)	157 (99%)	2 (1%)	0	100	100
1	G	159/163 (98%)	156 (98%)	3 (2%)	0	100	100
1	H	158/163 (97%)	157 (99%)	1 (1%)	0	100	100
All	All	1273/1304 (98%)	1253 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	137/137 (100%)	134 (98%)	3 (2%)	45	65
1	B	135/137 (98%)	130 (96%)	5 (4%)	30	45
1	C	136/137 (99%)	131 (96%)	5 (4%)	30	45
1	D	136/137 (99%)	134 (98%)	2 (2%)	57	75
1	E	136/137 (99%)	133 (98%)	3 (2%)	45	65
1	F	136/137 (99%)	131 (96%)	5 (4%)	30	45

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	G	136/137 (99%)	134 (98%)	2 (2%)	57	75
1	H	135/137 (98%)	133 (98%)	2 (2%)	57	75
All	All	1087/1096 (99%)	1060 (98%)	27 (2%)	42	60

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	333	SER
1	A	337	LEU
1	A	386	ARG
1	B	243	VAL
1	B	250	LYS
1	B	253	ASP
1	B	326	GLU
1	B	337	LEU
1	C	270	GLU
1	C	271	THR
1	C	286	VAL
1	C	337	LEU
1	C	374	ASP
1	D	244	ASN
1	D	337	LEU
1	E	326	GLU
1	E	337	LEU
1	E	374	ASP
1	F	326	GLU
1	F	337	LEU
1	F	339	ASP
1	F	374	ASP
1	F	386	ARG
1	G	337	LEU
1	G	374	ASP
1	H	337	LEU
1	H	374	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	242	GLN
1	C	241	GLN

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Mol	Chain	Res	Type
1	C	242	GLN
1	C	320	GLN
1	C	321	GLN
1	C	323	ASN
1	D	241	GLN
1	D	320	GLN
1	D	323	ASN
1	E	241	GLN
1	E	242	GLN
1	E	244	ASN
1	F	241	GLN
1	F	320	GLN
1	H	241	GLN
1	H	242	GLN
1	H	323	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](#)

There are no ligands in this entry.

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	163/163 (100%)	0.36	4 (2%) 58 60	61, 86, 112, 118	0
1	B	161/163 (98%)	0.45	1 (0%) 85 86	33, 83, 112, 138	0
1	C	161/163 (98%)	0.36	3 (1%) 66 68	46, 93, 134, 164	0
1	D	161/163 (98%)	0.15	1 (0%) 85 86	59, 81, 99, 117	0
1	E	161/163 (98%)	0.37	0 100 100	73, 91, 114, 124	0
1	F	161/163 (98%)	0.59	8 (4%) 34 35	60, 99, 130, 165	0
1	G	161/163 (98%)	0.51	2 (1%) 76 77	76, 94, 126, 139	0
1	H	160/163 (98%)	0.34	3 (1%) 66 68	71, 90, 109, 118	0
All	All	1289/1304 (98%)	0.39	22 (1%) 69 70	33, 89, 121, 165	0

All (22) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	237	ALA	3.1
1	F	226	PRO	3.0
1	H	226	PRO	2.7
1	A	366	VAL	2.7
1	F	356	THR	2.6
1	F	272	PRO	2.5
1	H	346	VAL	2.5
1	A	283	ALA	2.4
1	C	386	ARG	2.4
1	C	380	VAL	2.4
1	F	301	VAL	2.3
1	G	301	VAL	2.3
1	A	273	VAL	2.2
1	C	317	GLY	2.2
1	F	273	VAL	2.2
1	F	366	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	F	276	ALA	2.1
1	A	339	ASP	2.1
1	B	352	VAL	2.1
1	D	238	GLY	2.0
1	F	371	GLY	2.0
1	G	271	THR	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.