



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 7, 2026 – 01:03 AM UTC

PDB ID : 6H5N / pdb_00006h5n
Title : Plasmodium falciparum Pfs48/45 C-terminal domain bound to monoclonal antibody 85RF45.1
Authors : Lennartz, F.; Higgins, M.K.
Deposited on : 2018-07-25
Resolution : 3.23 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

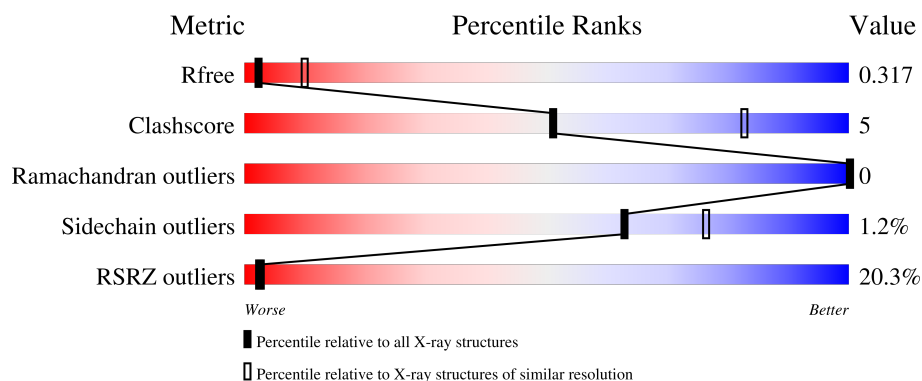
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.23 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	2153 (3.28-3.20)
Clashscore	190562	2275 (3.28-3.20)
Ramachandran outliers	187476	2233 (3.28-3.20)
Sidechain outliers	187428	2232 (3.28-3.20)
RSRZ outliers	180081	2153 (3.28-3.20)

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	136	18% 81% 13% 6%
1	D	136	14% 85% 9% 6%
2	B	212	14% 90% 10%
2	E	212	30% 77% 22% .
3	C	220	13% 79% 15% 6%

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Mol	Chain	Length	Quality of chain
3	F	220	25% 85% 8% 6%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8407 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 Gametocyte surface protein P45/48.

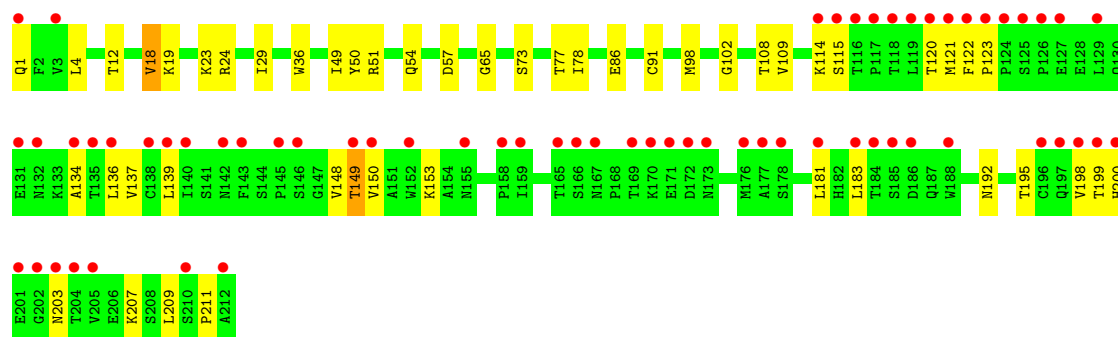
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	128	Total	C	N	O	S	0	0	0
			991	627	157	200	7			
1	D	128	Total	C	N	O	S	0	0	0
			996	630	158	201	7			

- Molecule 2 is a protein called Antibody 85RF45.1 light chain.

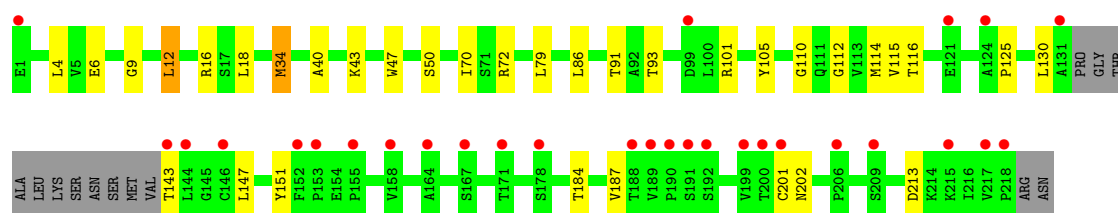
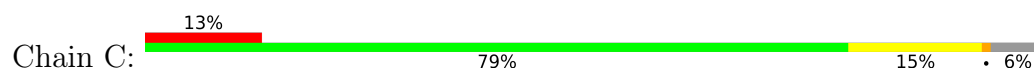
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	212	Total	C	N	O	S	0	0	0
			1628	1008	280	332	8			
2	E	212	Total	C	N	O	S	0	0	0
			1628	1008	280	332	8			

- Molecule 3 is a protein called Antibody 85RF45.1 heavy chain.

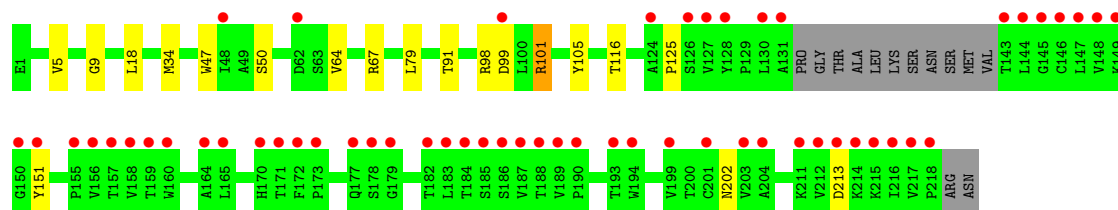
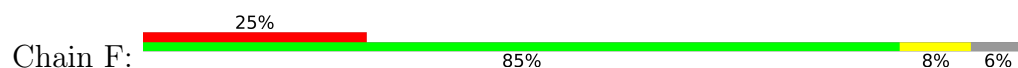
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	207	Total	C	N	O	S	0	0	0
			1582	1007	260	307	8			
3	F	207	Total	C	N	O	S	0	0	0
			1582	1007	260	307	8			



● Molecule 3: Antibody 85RF45.1 heavy chain



● Molecule 3: Antibody 85RF45.1 heavy chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	59.69Å 165.39Å 189.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.98 – 3.23 41.98 – 3.23	Depositor EDS
% Data completeness (in resolution range)	99.8 (41.98-3.23) 99.7 (41.98-3.23)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 3.25Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.261 , 0.282 0.285 , 0.317	Depositor DCC
R_{free} test set	1564 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	72.6	Xtriage
Anisotropy	0.451	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 75.5	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	0.87	EDS
Total number of atoms	8407	wwPDB-VP
Average B, all atoms (Å ²)	91.0	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 21.03 % 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 7.6464e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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](#)

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	0.10	0/1012	0.40	1/1372 (0.1%)
1	D	0.09	0/1016	0.29	0/1376
2	B	0.10	0/1667	0.30	0/2270
2	E	0.10	0/1667	0.30	0/2270
3	C	0.11	0/1623	0.30	0/2218
3	F	0.11	0/1623	0.31	0/2218
All	All	0.10	0/8608	0.31	1/11724 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	351	ASP	N-CA-C	-7.26	98.69	109.15

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	991	0	948	11	0
1	D	996	0	954	8	0
2	B	1628	0	1551	13	0
2	E	1628	0	1551	31	0
3	C	1582	0	1544	20	0
3	F	1582	0	1544	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	8407	0	8092	86	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 5.

All (86) 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)
2:E:1:GLN:HG2	2:E:98:MET:SD	2.07	0.92
3:C:12:LEU:HD11	3:C:86:LEU:HD12	1.69	0.75
2:B:99:TYR:OH	3:C:101:ARG:NH1	2.23	0.71
1:A:398:ILE:HD11	1:A:402:ILE:HD11	1.73	0.70
2:E:19:LYS:HG2	2:E:77:THR:HG22	1.75	0.69
1:A:405:THR:HG22	1:A:427:SER:H	1.59	0.66
2:E:148:VAL:HG22	2:E:200:HIS:HB2	1.79	0.65
2:B:149:THR:HG23	2:B:199:THR:HB	1.80	0.64
3:C:93:THR:HG22	3:C:114:MET:HG2	1.79	0.63
2:E:122:PHE:HB2	2:E:137:VAL:HB	1.81	0.62
2:E:1:GLN:CG	2:E:98:MET:SD	2.84	0.62
3:C:9:GLY:HA2	3:C:18:LEU:HD21	1.82	0.62
2:B:122:PHE:HB2	2:B:137:VAL:HB	1.80	0.61
2:B:148:VAL:HG22	2:B:200:HIS:HB2	1.82	0.61
3:F:125:PRO:HB3	3:F:151:TYR:HB3	1.82	0.61
2:E:149:THR:HG23	2:E:199:THR:HB	1.80	0.61
2:E:86:GLU:HB2	2:E:109:VAL:HG22	1.82	0.61
2:B:136:LEU:HD12	2:B:181:LEU:HD23	1.84	0.59
2:E:36:TRP:HD1	2:E:49:ILE:HD11	1.68	0.58
1:A:341:GLY:HA3	1:A:395:LEU:HD23	1.86	0.57
3:C:91:THR:HG23	3:C:116:THR:HA	1.86	0.57
1:A:376:ILE:HD11	1:A:402:ILE:HG12	1.86	0.56
2:E:136:LEU:HD12	2:E:181:LEU:HD23	1.87	0.55
3:F:99:ASP:OD2	3:F:101:ARG:NH2	2.40	0.55
2:E:4:LEU:HD23	2:E:24:ARG:HB3	1.87	0.55
2:E:134:ALA:HB3	2:E:183:LEU:O	2.08	0.54
1:D:349:ILE:HD11	3:F:101:ARG:HG2	1.90	0.53
1:A:413:LYS:NZ	3:C:101:ARG:O	2.42	0.53
3:C:34:MET:HE3	3:C:72:ARG:HH22	1.75	0.52
3:F:34:MET:HB3	3:F:79:LEU:HD22	1.91	0.52
2:B:134:ALA:HB3	2:B:183:LEU:O	2.11	0.51
2:E:120:THR:HB	2:E:139:LEU:HB2	1.92	0.51
3:C:202:ASN:ND2	3:C:213:ASP:OD1	2.44	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:E:18:VAL:HG22	2:E:78:ILE:HB	1.93	0.50
1:A:313:SER:HB3	1:D:328:ASN:HB2	1.93	0.50
2:E:12:THR:HG21	2:E:18:VAL:HG11	1.94	0.50
3:F:91:THR:HG23	3:F:116:THR:HA	1.93	0.50
3:C:6:GLU:OE2	3:C:112:GLY:N	2.44	0.49
2:E:36:TRP:HB2	2:E:49:ILE:HG12	1.95	0.49
1:A:336:TYR:OH	1:A:426:ASP:O	2.31	0.49
3:C:40:ALA:HB3	3:C:43:LYS:HB2	1.94	0.49
3:C:47:TRP:HE1	3:C:50:SER:HB2	1.78	0.48
2:B:197:GLN:HG2	2:B:206:GLU:HG3	1.95	0.48
1:D:341:GLY:HA3	1:D:395:LEU:HD23	1.96	0.48
3:F:202:ASN:ND2	3:F:213:ASP:OD1	2.45	0.48
3:F:47:TRP:HE1	3:F:50:SER:HB2	1.80	0.47
1:D:386:ASP:OD1	1:D:387:ALA:N	2.48	0.47
2:E:57:ASP:N	2:E:57:ASP:OD1	2.45	0.46
3:F:64:VAL:HG23	3:F:67:ARG:HB3	1.97	0.46
1:A:372:LEU:O	1:A:376:ILE:HG22	2.16	0.46
2:E:150:VAL:HG12	2:E:198:VAL:HG22	1.98	0.45
3:C:4:LEU:HB2	3:C:110:GLY:HA2	1.99	0.45
2:E:23:LYS:HG2	2:E:73:SER:HB3	1.99	0.45
2:E:49:ILE:O	2:E:49:ILE:HG13	2.16	0.45
1:D:352:CYS:HA	1:D:355:GLN:O	2.17	0.45
3:C:34:MET:HE3	3:C:72:ARG:NH2	2.32	0.45
2:B:60:PRO:HB2	2:B:62:ARG:HG2	1.98	0.45
3:C:125:PRO:HB3	3:C:151:TYR:HB3	1.98	0.45
2:B:155:ASN:HA	2:B:193:SER:HB3	1.97	0.45
2:E:49:ILE:HD13	2:E:65:GLY:HA3	1.99	0.45
2:E:114:LYS:HG2	2:E:115:SER:H	1.82	0.45
2:E:50:TYR:HB2	3:F:105:TYR:CD1	2.51	0.44
3:C:12:LEU:HD13	3:C:16:ARG:HB2	1.99	0.43
2:E:123:PRO:HA	2:E:136:LEU:HD23	1.99	0.43
2:B:123:PRO:HA	2:B:136:LEU:HD23	2.00	0.43
3:C:70:ILE:HD11	3:C:79:LEU:HD11	2.00	0.42
2:E:24:ARG:HH11	2:E:29:ILE:HA	1.83	0.42
2:E:86:GLU:HG3	2:E:108:THR:HA	2.01	0.42
1:A:319:VAL:HG11	1:A:325:ILE:HD11	2.01	0.42
2:B:50:TYR:HB2	3:C:105:TYR:CD1	2.54	0.42
3:F:9:GLY:HA2	3:F:18:LEU:HD21	2.01	0.42
2:E:51:ARG:HB2	2:E:54:GLN:HB2	2.02	0.42
1:A:357:TYR:CZ	1:A:367:SER:HB2	2.54	0.42
1:D:349:ILE:HA	1:D:350:PRO:HA	1.94	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:349:ILE:HB	1:D:411:ILE:HB	2.02	0.42
3:C:130:LEU:HD11	3:C:147:LEU:HB2	2.01	0.42
2:E:121:MET:HB3	2:E:209:LEU:HD11	2.01	0.42
2:E:91:CYS:O	2:E:102:GLY:N	2.52	0.41
3:C:143:THR:HA	3:C:187:VAL:O	2.21	0.41
1:A:328:ASN:N	1:D:311:THR:O	2.52	0.41
2:B:153:LYS:HB2	2:B:195:THR:OG1	2.21	0.41
2:E:207:LYS:HE2	2:E:207:LYS:HB3	1.87	0.41
2:E:153:LYS:HB2	2:E:195:THR:OG1	2.22	0.40
2:E:192:ASN:HA	2:E:211:PRO:HD2	2.03	0.40
2:B:207:LYS:HE2	2:B:207:LYS:HB3	1.89	0.40
3:C:91:THR:HA	3:C:115:VAL:O	2.20	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	124/136 (91%)	113 (91%)	11 (9%)	0	100	100
1	D	124/136 (91%)	115 (93%)	9 (7%)	0	100	100
2	B	210/212 (99%)	197 (94%)	13 (6%)	0	100	100
2	E	210/212 (99%)	196 (93%)	14 (7%)	0	100	100
3	C	203/220 (92%)	190 (94%)	13 (6%)	0	100	100
3	F	203/220 (92%)	192 (95%)	11 (5%)	0	100	100
All	All	1074/1136 (94%)	1003 (93%)	71 (7%)	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	118/125 (94%)	118 (100%)	0	100	100
1	D	118/125 (94%)	117 (99%)	1 (1%)	73	80
2	B	189/189 (100%)	188 (100%)	1 (0%)	81	84
2	E	189/189 (100%)	186 (98%)	3 (2%)	55	72
3	C	178/189 (94%)	174 (98%)	4 (2%)	45	68
3	F	178/189 (94%)	175 (98%)	3 (2%)	53	72
All	All	970/1006 (96%)	958 (99%)	12 (1%)	63	76

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	149	THR
3	C	12	LEU
3	C	34	MET
3	C	184	THR
3	C	201	CYS
1	D	296	HIS
2	E	18	VAL
2	E	149	THR
2	E	203	ASN
3	F	5	VAL
3	F	98	ARG
3	F	101	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	328	ASN
2	B	197	GLN
3	C	77	ASN
3	C	202	ASN
1	D	296	HIS

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Mol	Chain	Res	Type
1	D	299	ASN
1	D	355	GLN
2	E	13	ASN
2	E	197	GLN
2	E	203	ASN
3	F	53	ASN
3	F	202	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	128/136 (94%)	1.18	25 (19%) 3 2	35, 72, 144, 190	0
1	D	128/136 (94%)	1.05	19 (14%) 5 4	36, 72, 120, 186	0
2	B	212/212 (100%)	1.05	29 (13%) 6 5	35, 83, 139, 189	0
2	E	212/212 (100%)	1.56	64 (30%) 1 1	28, 100, 230, 288	0
3	C	207/220 (94%)	0.88	29 (14%) 6 5	30, 63, 164, 195	0
3	F	207/220 (94%)	1.30	56 (27%) 1 1	34, 64, 228, 278	0
All	All	1094/1136 (96%)	1.18	222 (20%) 3 2	28, 79, 197, 288	0

All (222) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	E	117	PRO	9.9
3	F	147	LEU	6.4
3	F	150	GLY	5.8
2	E	166	SER	5.7
3	F	99	ASP	5.4
1	A	366	PRO	5.1
3	F	156	VAL	5.0
1	A	420	TYR	5.0
2	E	140	ILE	4.9
1	A	323	ALA	4.7
1	A	378	ILE	4.7
3	C	189	VAL	4.6
1	D	378	ILE	4.6
3	F	186	SER	4.6
2	E	201	GLU	4.5
2	E	176	MET	4.5
1	D	379	GLY	4.5
2	E	118	THR	4.5
3	C	144	LEU	4.5

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Mol	Chain	Res	Type	RSRZ
2	B	98	MET	4.4
3	F	146	CYS	4.4
2	E	204	THR	4.3
3	F	130	LEU	4.2
2	E	121	MET	4.2
2	E	123	PRO	4.1
1	D	368	ASN	4.1
1	A	379	GLY	4.1
2	E	136	LEU	4.0
3	F	165	LEU	4.0
3	C	191	SER	3.9
2	E	150	VAL	3.8
3	F	171	THR	3.7
2	E	212	ALA	3.7
3	F	190	PRO	3.7
3	F	148	VAL	3.7
2	E	199	THR	3.6
2	E	171	GLU	3.6
3	C	121	GLU	3.6
1	A	321	ASP	3.6
3	C	153	PRO	3.6
2	E	205	VAL	3.6
2	E	114	LYS	3.6
2	E	129	LEU	3.6
2	E	134	ALA	3.6
3	F	187	VAL	3.6
3	F	128	TYR	3.6
2	E	172	ASP	3.6
2	E	152	TRP	3.5
3	F	179	GLY	3.5
2	E	188	TRP	3.5
2	E	202	GLY	3.5
3	F	127	VAL	3.4
3	F	131	ALA	3.4
2	B	121	MET	3.4
2	E	178	SER	3.4
2	E	167	ASN	3.4
2	E	183	LEU	3.4
3	C	158	VAL	3.4
2	B	133	LYS	3.4
2	E	169	THR	3.4
3	F	126	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	D	315	ASP	3.3
3	F	173	PRO	3.3
3	F	172	PHE	3.3
1	D	410	CYS	3.3
1	D	400	GLY	3.3
3	F	158	VAL	3.3
1	A	320	ASP	3.2
2	E	139	LEU	3.2
1	A	426	ASP	3.2
2	E	159	ILE	3.2
3	F	203	VAL	3.1
3	C	99	ASP	3.1
2	E	126	PRO	3.1
1	A	296	HIS	3.1
3	F	183	LEU	3.1
3	F	184	THR	3.1
3	C	190	PRO	3.1
1	D	325	ILE	3.1
2	B	176	MET	3.1
3	F	218	PRO	3.1
2	E	1	GLN	3.0
2	E	115	SER	3.0
2	E	120	THR	3.0
2	E	122	PHE	3.0
2	E	127	GLU	3.0
1	D	357	TYR	3.0
2	B	117	PRO	3.0
2	B	172	ASP	3.0
3	F	170	HIS	3.0
3	C	146	CYS	3.0
2	B	183	LEU	2.9
3	F	189	VAL	2.9
2	B	122	PHE	2.9
2	E	200	HIS	2.9
1	A	322	SER	2.9
2	B	131	GLU	2.9
3	F	164	ALA	2.9
3	F	211	LYS	2.9
3	F	160	TRP	2.8
3	F	212	VAL	2.8
3	F	177	GLN	2.8
2	B	212	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
2	E	185	SER	2.8
1	A	359	PRO	2.8
2	E	132	ASN	2.8
2	E	196	CYS	2.8
2	B	157	THR	2.8
2	E	116	THR	2.8
1	D	326	SER	2.7
2	E	135	THR	2.7
2	B	134	ALA	2.7
2	E	125	SER	2.7
1	A	336	TYR	2.7
3	C	124	ALA	2.7
3	C	217	VAL	2.7
3	C	152	PHE	2.7
2	B	156	GLY	2.7
2	B	110	LEU	2.7
3	C	188	THR	2.7
1	D	324	HIS	2.7
3	C	200	THR	2.6
2	E	181	LEU	2.6
3	F	124	ALA	2.6
2	B	136	LEU	2.6
3	F	213	ASP	2.6
3	F	145	GLY	2.6
3	F	214	LYS	2.6
3	F	151	TYR	2.6
3	C	167	SER	2.6
1	A	377	ASN	2.6
1	D	323	ALA	2.6
2	E	158	PRO	2.5
1	A	427	SER	2.5
1	D	427	SER	2.5
2	E	119	LEU	2.5
1	A	368	ASN	2.5
3	C	143	THR	2.5
1	A	357	TYR	2.5
3	F	155	PRO	2.5
1	A	352	CYS	2.5
2	B	125	SER	2.5
2	E	203	ASN	2.5
3	F	204	ALA	2.5
2	E	131	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
3	F	157	THR	2.5
3	F	193	THR	2.5
1	D	338	HIS	2.5
2	B	111	GLY	2.5
2	E	145	PRO	2.5
3	C	178	SER	2.4
1	D	380	ASP	2.4
2	E	184	THR	2.4
3	F	159	THR	2.4
1	D	359	PRO	2.4
2	E	3	VAL	2.4
2	B	145	PRO	2.4
3	F	143	THR	2.4
3	F	182	THR	2.4
3	C	164	ALA	2.4
2	B	14	LEU	2.4
3	F	217	VAL	2.4
2	B	11	SER	2.4
3	C	199	VAL	2.4
2	B	51	ARG	2.3
2	E	177	ALA	2.3
2	E	149	THR	2.3
3	F	62	ASP	2.3
2	E	198	VAL	2.3
2	E	124	PRO	2.3
2	B	188	TRP	2.3
2	B	148	VAL	2.3
2	E	170	LYS	2.3
3	F	199	VAL	2.3
3	C	218	PRO	2.3
3	C	131	ALA	2.3
2	E	146	SER	2.3
2	E	155	ASN	2.3
3	C	155	PRO	2.3
1	A	294	VAL	2.2
2	B	112	GLN	2.2
3	F	201	CYS	2.2
3	C	206	PRO	2.2
2	E	165	THR	2.2
1	A	410	CYS	2.2
1	D	334	PRO	2.2
3	F	215	LYS	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	405	THR	2.2
2	E	210	SER	2.2
3	F	178	SER	2.2
3	F	185	SER	2.2
1	D	318	LEU	2.2
2	E	138	CYS	2.2
1	D	301	SER	2.1
2	B	132	ASN	2.1
3	F	216	ILE	2.1
3	F	144	LEU	2.1
3	F	149	LYS	2.1
1	D	407	SER	2.1
3	C	192	SER	2.1
3	F	194	TRP	2.1
1	A	324	HIS	2.1
3	F	188	THR	2.1
2	E	197	GLN	2.1
3	C	1	GLU	2.1
2	E	143	PHE	2.1
2	E	142	ASN	2.1
1	A	330	HIS	2.1
2	E	186	ASP	2.1
2	B	96	THR	2.1
2	B	82	GLN	2.1
1	A	367	SER	2.1
1	A	380	ASP	2.1
3	C	171	THR	2.1
1	A	302	SER	2.0
2	E	173	ASN	2.0
3	C	201	CYS	2.0
3	C	209	SER	2.0
3	F	48	ILE	2.0
2	B	147	GLY	2.0
3	C	215	LYS	2.0
2	B	86	GLU	2.0

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

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.