



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 20, 2025 – 01:31 pm BST

PDB ID : 9EZE / pdb_00009eze
Title : Structure of subdomain 3 of the Plasmodium vivax Duffy binding protein (PvDBP) bound to human antibody DB9
Authors : Barber, N.M.; Higgins, M.K.
Deposited on : 2024-04-11
Resolution : 1.55 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	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
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)	:	2.46

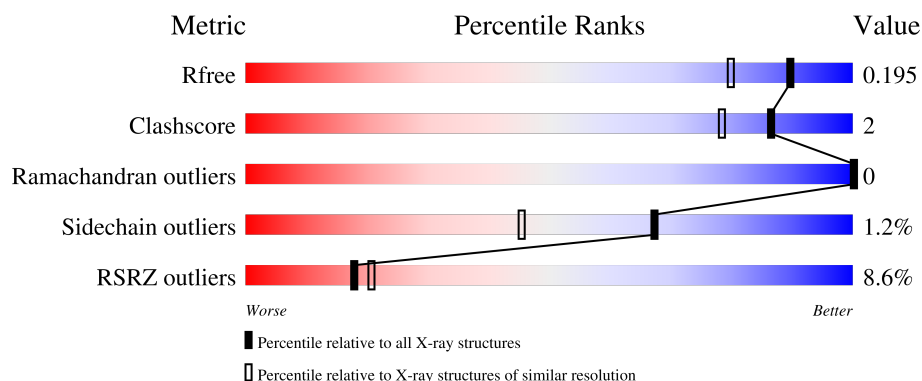
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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}	164625	1935 (1.56-1.56)
Clashscore	180529	2073 (1.56-1.56)
Ramachandran outliers	177936	2037 (1.56-1.56)
Sidechain outliers	177891	2034 (1.56-1.56)
RSRZ outliers	164620	1935 (1.56-1.56)

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	300	<div> <div>7%</div> <div>37%</div> <div>59%</div> </div>
1	D	300	<div> <div>5%</div> <div>37%</div> <div>60%</div> </div>
2	B	278	<div> <div>4%</div> <div>77%</div> <div>21%</div> </div>
2	E	278	<div> <div>3%</div> <div>78%</div> <div>21%</div> </div>
3	C	233	<div> <div>8%</div> <div>88%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
3	F	233	<div><div></div><div>9%</div><div>83%</div><div>7%</div><div>9%</div></div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 9514 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 Duffy receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	123	Total	C	N	O	S	0	0	0
			1017	645	172	194	6			
1	D	119	Total	C	N	O	S	0	0	0
			985	625	166	188	6			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	209	SER	-	expression tag	UNP P22290
A	210	GLY	-	expression tag	UNP P22290
D	209	SER	-	expression tag	UNP P22290
D	210	GLY	-	expression tag	UNP P22290

- Molecule 2 is a protein called Antibody DB9 heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	220	Total	C	N	O	S	0	2	0
			1635	1030	269	332	4			
2	E	220	Total	C	N	O	S	0	0	0
			1627	1027	268	328	4			

- Molecule 3 is a protein called Antibody DB9 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	213	Total	C	N	O	S	0	0	0
			1637	1028	280	324	5			
3	F	212	Total	C	N	O	S	0	0	0
			1635	1027	279	324	5			

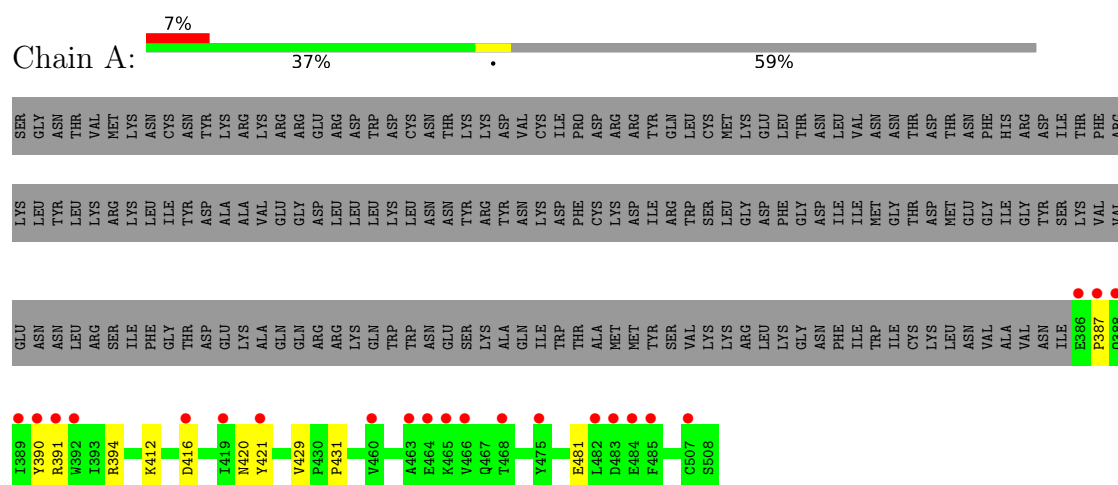
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	96	Total 96	O 96	0	0
4	B	227	Total 227	O 227	0	0
4	C	153	Total 153	O 153	0	0
4	D	96	Total 96	O 96	0	0
4	E	242	Total 242	O 242	0	0
4	F	164	Total 164	O 164	0	0

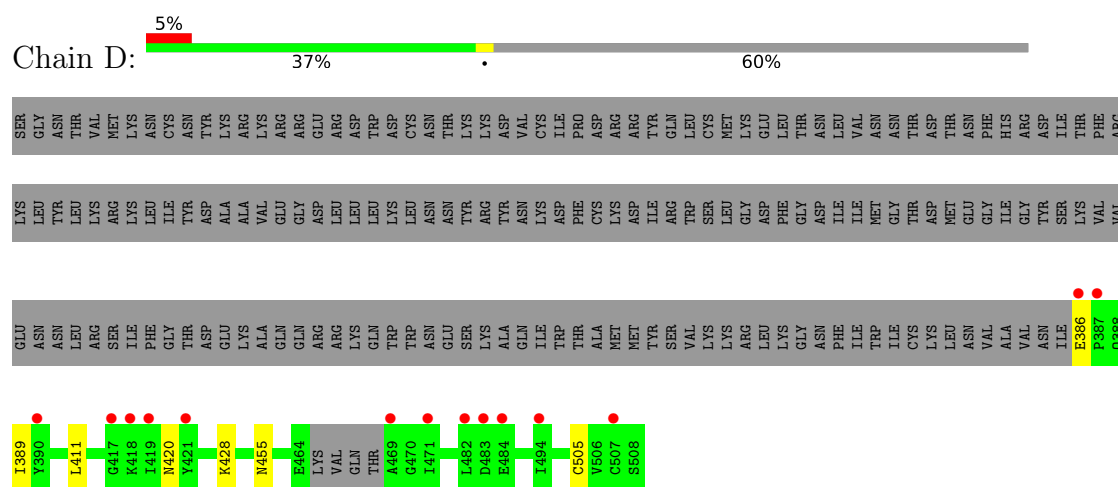
3 Residue-property plots

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.

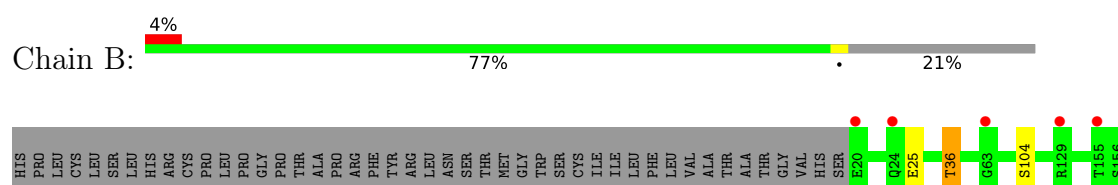
• Molecule 1: Duffy receptor

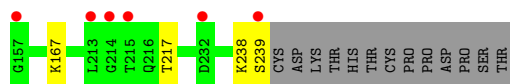


• Molecule 1: Duffy receptor

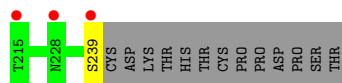
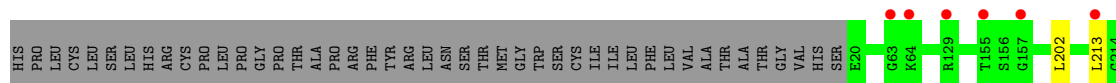
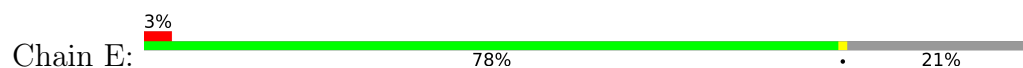


• Molecule 2: Antibody DB9 heavy chain

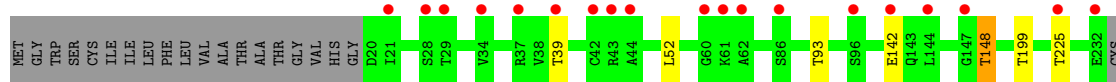
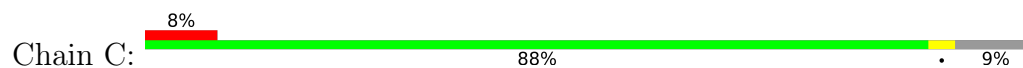




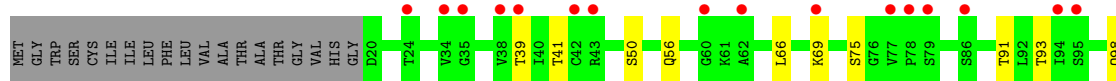
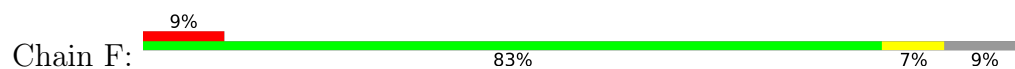
• Molecule 2: Antibody DB9 heavy chain



• Molecule 3: Antibody DB9 light chain



• Molecule 3: Antibody DB9 light chain



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.43Å 126.19Å 129.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	90.50 – 1.55 90.50 – 1.55	Depositor EDS
% Data completeness (in resolution range)	98.3 (90.50-1.55) 98.3 (90.50-1.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.79 (at 1.55Å)	Xtriage
Refinement program	BUSTER 2.10.4 (26-JUL-2023)	Depositor
R, R_{free}	0.204 , 0.223 0.199 , 0.195	Depositor DCC
R_{free} test set	9103 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	21.4	Xtriage
Anisotropy	0.273	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 37.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.016 for -h,l,k	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	9514	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.30% 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](#)

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	0.77	0/1038	0.98	0/1402
1	D	0.84	0/1005	1.00	3/1356 (0.2%)
2	B	0.82	0/1675	0.99	0/2291
2	E	0.84	0/1667	0.96	2/2279 (0.1%)
3	C	0.76	0/1676	0.96	0/2279
3	F	0.76	0/1674	0.97	0/2277
All	All	0.80	0/8735	0.98	5/11884 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	213	LEU	N-CA-C	6.83	118.38	111.07
1	D	455	ASN	CA-CB-CG	-6.44	106.16	112.60
1	D	420	ASN	CA-C-N	5.57	130.04	122.07
1	D	420	ASN	C-N-CA	5.57	130.04	122.07
2	E	213	LEU	CA-C-O	-5.50	115.04	120.82

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	1017	0	999	12	0
1	D	985	0	961	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1635	0	1601	3	0
2	E	1627	0	1604	1	0
3	C	1637	0	1588	3	0
3	F	1635	0	1586	12	0
4	A	96	0	0	0	0
4	B	227	0	0	1	0
4	C	153	0	0	2	0
4	D	96	0	0	0	0
4	E	242	0	0	0	0
4	F	164	0	0	1	0
All	All	9514	0	8339	33	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 2.

All (33) 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)
3:F:109:HIS:HD2	3:F:111:ASN:H	1.43	0.66
3:F:98:GLN:HG3	3:F:99:PRO:HD2	1.79	0.65
3:F:216:THR:HG21	4:F:433:HOH:O	1.96	0.65
3:F:216:THR:HG22	3:F:223:PRO:HG3	1.79	0.65
1:A:390:TYR:HD1	1:A:394:ARG:HH11	1.44	0.63
3:F:50:SER:HB2	3:F:69:LYS:NZ	2.14	0.63
1:A:390:TYR:HD1	1:A:394:ARG:NH1	1.99	0.60
2:B:36:THR:HB	2:B:104:SER:HA	1.83	0.59
3:F:50:SER:HB2	3:F:69:LYS:HZ2	1.67	0.58
3:F:164:LYS:HB3	3:F:216:THR:OG1	2.05	0.56
1:D:386:GLU:HG2	1:D:389:ILE:HG22	1.89	0.54
3:C:199:THR:HG23	4:C:320:HOH:O	2.11	0.51
3:C:39:THR:HG22	3:C:93:THR:HG22	1.92	0.51
3:F:216:THR:CG2	3:F:223:PRO:HG3	2.41	0.51
2:B:36:THR:HG22	4:B:419:HOH:O	2.11	0.50
3:F:41:THR:HG22	3:F:91:THR:HG22	1.95	0.49
2:B:238:LYS:O	2:B:239:SER:OG	2.30	0.49
3:F:56:GLN:HB2	3:F:66:LEU:HD11	1.95	0.48
1:A:391:ARG:HG2	1:A:394:ARG:NH2	2.29	0.47
3:F:168:LYS:HG2	3:F:173:LEU:HD23	1.98	0.46
1:A:387:PRO:O	1:A:391:ARG:HG3	2.15	0.46
3:F:39:THR:HG22	3:F:93:THR:HG22	1.97	0.46
1:A:390:TYR:CD1	1:A:394:ARG:NH1	2.79	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:390:TYR:CE1	1:A:394:ARG:HD3	2.55	0.42
1:A:394:ARG:HG2	1:A:481:GLU:HG3	2.02	0.42
1:A:390:TYR:HE1	1:A:394:ARG:HD3	1.84	0.42
1:A:429:VAL:HG12	1:A:431:PRO:HD2	2.02	0.42
1:A:420:ASN:O	1:A:421:TYR:HB2	2.19	0.41
2:E:202:LEU:C	2:E:202:LEU:HD12	2.45	0.41
1:D:411:LEU:HD11	1:D:505:CYS:SG	2.61	0.41
1:A:390:TYR:O	1:A:394:ARG:HG3	2.20	0.41
1:A:412:LYS:O	1:A:416:ASP:HB2	2.21	0.41
3:C:148:THR:HG23	4:C:304:HOH: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	121/300 (40%)	119 (98%)	2 (2%)	0	100	100
1	D	115/300 (38%)	113 (98%)	2 (2%)	0	100	100
2	B	220/278 (79%)	217 (99%)	3 (1%)	0	100	100
2	E	218/278 (78%)	215 (99%)	3 (1%)	0	100	100
3	C	211/233 (91%)	206 (98%)	5 (2%)	0	100	100
3	F	210/233 (90%)	204 (97%)	6 (3%)	0	100	100
All	All	1095/1622 (68%)	1074 (98%)	21 (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	114/276 (41%)	114 (100%)	0	100	100
1	D	110/276 (40%)	109 (99%)	1 (1%)	75	58
2	B	189/240 (79%)	185 (98%)	4 (2%)	48	20
2	E	188/240 (78%)	187 (100%)	1 (0%)	86	76
3	C	185/202 (92%)	181 (98%)	4 (2%)	47	19
3	F	185/202 (92%)	183 (99%)	2 (1%)	70	49
All	All	971/1436 (68%)	959 (99%)	12 (1%)	67	45

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

Mol	Chain	Res	Type
2	B	25	GLU
2	B	36	THR
2	B	167	LYS
2	B	217	THR
3	C	52	LEU
3	C	142	GLU
3	C	148	THR
3	C	225	THR
1	D	428	LYS
2	E	239	SER
3	F	75	SER
3	F	216	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	409	GLN
1	A	495	ASN
2	B	24	GLN
3	C	111	ASN
1	D	455	ASN

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Mol	Chain	Res	Type
1	D	495	ASN
2	E	24	GLN
3	F	109	HIS
3	F	179	GLN
3	F	218	GLN

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	123/300 (41%)	0.80	22 (17%) 4 5	18, 30, 55, 67	0
1	D	119/300 (39%)	0.62	14 (11%) 10 12	18, 28, 52, 61	0
2	B	220/278 (79%)	0.11	11 (5%) 35 42	9, 22, 41, 58	2 (0%)
2	E	220/278 (79%)	0.11	9 (4%) 42 49	15, 22, 40, 51	0
3	C	213/233 (91%)	0.72	19 (8%) 17 20	20, 35, 47, 58	0
3	F	212/233 (90%)	0.61	20 (9%) 15 18	18, 33, 53, 62	0
All	All	1107/1622 (68%)	0.45	95 (8%) 18 21	9, 28, 49, 67	2 (0%)

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	466	VAL	6.5
1	A	390	TYR	4.3
1	A	419	ILE	4.3
1	D	419	ILE	4.2
3	F	231	GLY	3.9
2	E	155	THR	3.6
1	A	386	GLU	3.6
2	E	228	ASN	3.6
1	A	475	TYR	3.5
2	B	214	GLY	3.5
1	A	387	PRO	3.5
3	C	62	ALA	3.3
1	A	465	LYS	3.3
3	F	35	GLY	3.3
1	D	387	PRO	3.3
1	D	390	TYR	3.2
3	F	94	ILE	3.2
3	F	60	GLY	3.2
2	B	63	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
3	C	60	GLY	3.1
1	A	507	CYS	3.1
1	D	469	ALA	3.0
1	A	483	ASP	3.0
1	D	386	GLU	3.0
1	D	418	LYS	3.0
1	D	471	ILE	2.9
1	A	421	TYR	2.9
2	E	63	GLY	2.8
2	B	239	SER	2.8
3	F	42	CYS	2.8
1	D	482	LEU	2.8
3	C	61	LYS	2.8
3	F	100	ASP	2.8
1	A	484	GLU	2.8
1	D	421	TYR	2.7
3	C	42	CYS	2.7
3	F	34	VAL	2.7
3	C	225	THR	2.7
3	F	38	VAL	2.7
1	A	482	LEU	2.6
2	B	213	LEU	2.6
2	B	215	THR	2.6
2	B	129	ARG	2.6
3	C	232	GLU	2.6
1	A	464	GLU	2.6
1	D	417	GLY	2.5
3	C	147	GLY	2.5
3	C	21	ILE	2.5
1	A	485	PHE	2.5
3	C	86	SER	2.4
2	E	215	THR	2.4
1	D	494	ILE	2.4
3	F	189	ASP	2.4
3	F	77	VAL	2.4
3	F	79	SER	2.4
1	A	468	THR	2.4
1	A	392	TRP	2.4
2	E	129	ARG	2.4
3	C	144	LEU	2.3
2	E	239	SER	2.3
2	B	24	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
3	F	39	THR	2.3
1	A	463	ALA	2.3
1	A	388	GLN	2.3
1	A	416	ASP	2.3
3	F	216	THR	2.2
3	C	44	ALA	2.2
1	A	389	ILE	2.2
1	D	483	ASP	2.2
2	E	157	GLY	2.2
3	C	142	GLU	2.2
3	C	39	THR	2.2
3	F	69	LYS	2.2
1	A	460	VAL	2.2
3	C	28	SER	2.2
2	B	155	THR	2.2
3	F	62	ALA	2.2
1	D	507	CYS	2.2
3	C	37	ARG	2.1
2	E	213	LEU	2.1
1	D	484	GLU	2.1
2	B	20	GLU	2.1
3	F	24	THR	2.1
2	B	157	GLY	2.1
3	C	96	SER	2.1
3	F	78	PRO	2.1
3	C	43	ARG	2.1
3	F	43	ARG	2.1
3	C	29	THR	2.1
3	F	86	SER	2.1
3	F	95	SER	2.1
2	B	232	ASP	2.0
1	A	391	ARG	2.0
2	E	64	LYS	2.0
3	C	34	VAL	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.