



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 07:32 AM UTC

PDB ID : 3D1N / pdb_00003d1n
Title : Structure of human Brn-5 transcription factor in complex with corticotrophin
-releasing hormone gene promoter
Authors : Pereira, J.H.; Ha, S.C.; Kim, S.-H.
Deposited on : 2008-05-06
Resolution : 2.51 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

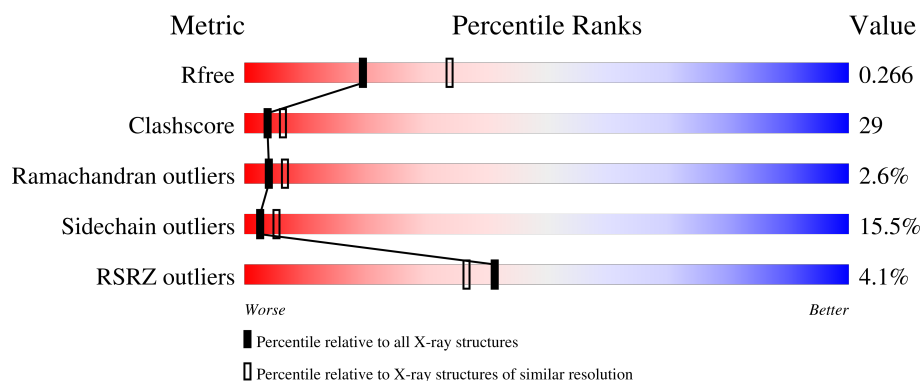
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.51 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	14	
1	C	14	
1	E	14	
1	G	14	
2	B	14	

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Mol	Chain	Length	Quality of chain
2	D	14	
2	F	14	
2	H	14	
3	I	151	
3	J	151	
3	K	151	
3	L	151	
3	M	151	
3	N	151	
3	O	151	
3	P	151	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10089 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 DNA chain called 5'-D(*DAP*DGP*DCP*DAP*DTP*DAP*DAP*DTP*DAP*DAP*DTP*DAP*DAP*DTP*DAP*DA)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	14	Total	C	N	O	P	0	0	0
			287	139	59	76	13			
1	C	14	Total	C	N	O	P	0	0	0
			287	139	59	76	13			
1	E	14	Total	C	N	O	P	0	0	0
			287	139	59	76	13			
1	G	14	Total	C	N	O	P	0	0	0
			287	139	59	76	13			

- Molecule 2 is a DNA chain called 5'-D(*DTP*DTP*DAP*DTP*DTP*DAP*DTP*DTP*DTP*DAP*DTP*DGP*DCP*DT)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	14	Total	C	N	O	P	0	0	0
			281	139	41	88	13			
2	D	14	Total	C	N	O	P	0	0	0
			281	139	41	88	13			
2	F	14	Total	C	N	O	P	0	0	0
			281	139	41	88	13			
2	H	14	Total	C	N	O	P	0	0	0
			281	139	41	88	13			

- Molecule 3 is a protein called POU domain, class 6, transcription factor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	I	150	Total	C	N	O	Se	0	0	0
			1192	746	216	226	4			
3	J	86	Total	C	N	O	Se	0	0	0
			666	420	114	129	3			
3	K	150	Total	C	N	O	Se	0	0	0
			1100	689	194	213	4			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	145	Total	C	N	O	Se	0	0	0
			1130	708	203	215	4			
3	M	150	Total	C	N	O	Se	0	0	0
			1188	742	215	227	4			
3	N	85	Total	C	N	O	Se	0	0	0
			658	414	113	128	3			
3	O	150	Total	C	N	O	Se	0	0	0
			1166	730	209	223	4			
3	P	82	Total	C	N	O	Se	0	0	0
			620	390	108	119	3			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	144	MSE	LEU	conflict	UNP Q14863
I	172	MSE	LEU	conflict	UNP Q14863
I	186	SER	CYS	engineered mutation	UNP Q14863
I	267	MSE	ILE	conflict	UNP Q14863
I	283	SER	CYS	engineered mutation	UNP Q14863
J	144	MSE	LEU	conflict	UNP Q14863
J	172	MSE	LEU	conflict	UNP Q14863
J	186	SER	CYS	engineered mutation	UNP Q14863
J	267	MSE	ILE	conflict	UNP Q14863
J	283	SER	CYS	engineered mutation	UNP Q14863
K	144	MSE	LEU	conflict	UNP Q14863
K	172	MSE	LEU	conflict	UNP Q14863
K	186	SER	CYS	engineered mutation	UNP Q14863
K	267	MSE	ILE	conflict	UNP Q14863
K	283	SER	CYS	engineered mutation	UNP Q14863
L	144	MSE	LEU	conflict	UNP Q14863
L	172	MSE	LEU	conflict	UNP Q14863
L	186	SER	CYS	engineered mutation	UNP Q14863
L	267	MSE	ILE	conflict	UNP Q14863
L	283	SER	CYS	engineered mutation	UNP Q14863
M	144	MSE	LEU	conflict	UNP Q14863
M	172	MSE	LEU	conflict	UNP Q14863
M	186	SER	CYS	engineered mutation	UNP Q14863
M	267	MSE	ILE	conflict	UNP Q14863
M	283	SER	CYS	engineered mutation	UNP Q14863
N	144	MSE	LEU	conflict	UNP Q14863
N	172	MSE	LEU	conflict	UNP Q14863
N	186	SER	CYS	engineered mutation	UNP Q14863
N	267	MSE	ILE	conflict	UNP Q14863

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Chain	Residue	Modelled	Actual	Comment	Reference
N	283	SER	CYS	engineered mutation	UNP Q14863
O	144	MSE	LEU	conflict	UNP Q14863
O	172	MSE	LEU	conflict	UNP Q14863
O	186	SER	CYS	engineered mutation	UNP Q14863
O	267	MSE	ILE	conflict	UNP Q14863
O	283	SER	CYS	engineered mutation	UNP Q14863
P	144	MSE	LEU	conflict	UNP Q14863
P	172	MSE	LEU	conflict	UNP Q14863
P	186	SER	CYS	engineered mutation	UNP Q14863
P	267	MSE	ILE	conflict	UNP Q14863
P	283	SER	CYS	engineered mutation	UNP Q14863

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	9	Total O 9 9	0	0
4	B	10	Total O 10 10	0	0
4	C	5	Total O 5 5	0	0
4	D	1	Total O 1 1	0	0
4	E	9	Total O 9 9	0	0
4	F	10	Total O 10 10	0	0
4	G	4	Total O 4 4	0	0
4	H	5	Total O 5 5	0	0
4	I	8	Total O 8 8	0	0
4	J	6	Total O 6 6	0	0
4	L	1	Total O 1 1	0	0
4	M	10	Total O 10 10	0	0
4	N	6	Total O 6 6	0	0
4	O	10	Total O 10 10	0	0

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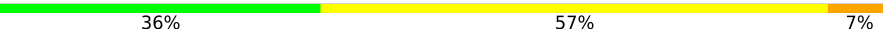
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	3	Total	O	0	0
			3	3		

3 Residue-property plots

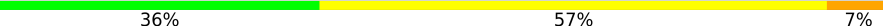
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: 5'-D(*DAP*DGP*DCP*DAP*DTP*DAP*DAP*DAP*DTP*DAP*DAP*DTP*DAP*DA)-3'

Chain A: 



- Molecule 1: 5'-D(*DAP*DGP*DCP*DAP*DTP*DAP*DAP*DAP*DTP*DAP*DAP*DTP*DAP*DA)-3'

Chain C: 



- Molecule 1: 5'-D(*DAP*DGP*DCP*DAP*DTP*DAP*DAP*DAP*DTP*DAP*DAP*DTP*DAP*DA)-3'

Chain E: 



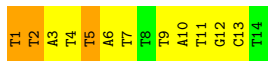
- Molecule 1: 5'-D(*DAP*DGP*DCP*DAP*DTP*DAP*DAP*DAP*DTP*DAP*DAP*DTP*DAP*DA)-3'

Chain G: 

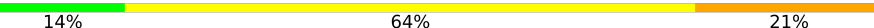


- Molecule 2: 5'-D(*DTP*DTP*DAP*DTP*DTP*DAP*DTP*DTP*DTP*DAP*DTP*DGP*DCP*DT)-3'

Chain B: 



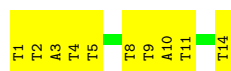
- Molecule 2: 5'-D(*DTP*DTP*DAP*DTP*DTP*DAP*DTP*DTP*DTP*DAP*DTP*DGP*DCP*DT)-3'

Chain D: 



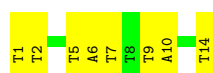
- Molecule 2: 5'-D(*DTP*DTP*DAP*DTP*DTP*DAP*DTP*DTP*DTP*DAP*DTP*DGP*DCP*DT)-3'

Chain F: 

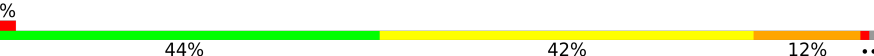


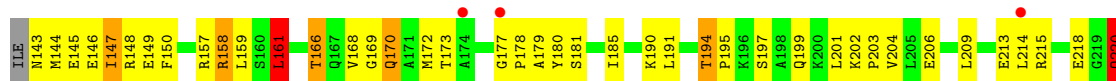
- Molecule 2: 5'-D(*DTP*DTP*DAP*DTP*DTP*DAP*DTP*DTP*DTP*DAP*DTP*DGP*DCP*DT)-3'

Chain H: 



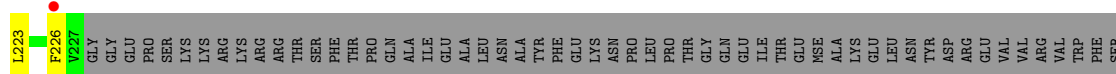
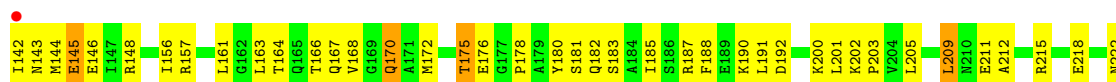
- Molecule 3: POU domain, class 6, transcription factor 1

Chain I: 

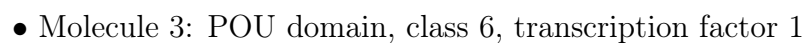


- Molecule 3: POU domain, class 6, transcription factor 1

Chain J: 



- Molecule 3: POU domain, class 6, transcription factor 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	100.30Å 112.06Å 181.50Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.91 – 2.51 48.91 – 2.51	Depositor EDS
% Data completeness (in resolution range)	91.0 (48.91-2.51) 74.7 (48.91-2.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	65.06 (at 2.51Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.212 , 0.270 0.209 , 0.266	Depositor DCC
R_{free} test set	2690 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å ²)	39.8	Xtriage
Anisotropy	0.886	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 76.9	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	0.95	EDS
Total number of atoms	10089	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.17% 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	0.35	0/324	1.30	1/498 (0.2%)
1	C	0.35	0/324	1.32	1/498 (0.2%)
1	E	0.39	0/324	1.32	0/498
1	G	0.38	0/324	1.28	2/498 (0.4%)
2	B	0.39	0/312	1.38	3/480 (0.6%)
2	D	0.39	0/312	1.43	4/480 (0.8%)
2	F	0.39	0/312	1.44	2/480 (0.4%)
2	H	0.45	0/312	1.43	1/480 (0.2%)
3	I	0.50	0/1208	0.94	4/1622 (0.2%)
3	J	0.49	0/672	0.91	1/900 (0.1%)
3	K	0.37	0/1114	0.87	0/1507
3	L	0.45	0/1146	0.90	2/1540 (0.1%)
3	M	0.53	0/1204	0.95	2/1620 (0.1%)
3	N	0.50	0/664	1.03	4/889 (0.4%)
3	O	0.45	0/1182	0.85	2/1593 (0.1%)
3	P	0.46	0/625	0.87	0/836
All	All	0.45	0/10359	1.05	29/14419 (0.2%)

There are no bond length outliers.

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	I	220	GLN	N-CA-C	-9.69	102.55	114.75
3	N	177	GLY	CA-C-N	8.51	128.16	119.82
3	N	177	GLY	C-N-CA	8.51	128.16	119.82
2	F	5	DT	O4'-C1'-N1	-6.36	98.87	108.40
2	D	9	DT	O4'-C1'-N1	5.82	117.13	108.40

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	287	0	159	13	0
1	C	287	0	159	7	0
1	E	287	0	159	8	0
1	G	287	0	159	8	0
2	B	281	0	165	14	0
2	D	281	0	165	18	0
2	F	281	0	165	21	0
2	H	281	0	165	11	0
3	I	1192	0	1174	70	0
3	J	666	0	654	31	0
3	K	1100	0	1017	69	0
3	L	1130	0	1090	66	0
3	M	1188	0	1157	82	0
3	N	658	0	643	40	0
3	O	1166	0	1120	83	0
3	P	620	0	606	23	0
4	A	9	0	0	5	0
4	B	10	0	0	2	0
4	C	5	0	0	0	0
4	D	1	0	0	0	0
4	E	9	0	0	2	0
4	F	10	0	0	3	0
4	G	4	0	0	0	0
4	H	5	0	0	0	0
4	I	8	0	0	2	0
4	J	6	0	0	1	0
4	L	1	0	0	0	0
4	M	10	0	0	1	0
4	N	6	0	0	2	0
4	O	10	0	0	0	0
4	P	3	0	0	1	0
All	All	10089	0	8757	531	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 29.

The worst 5 of 531 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:L:265:THR:HG22	3:L:275:ARG:HE	1.09	1.15
3:L:238:ARG:HG2	3:L:238:ARG:HH11	1.03	1.15
3:M:238:ARG:HH11	3:M:238:ARG:HG2	1.18	1.06
3:K:250:ASN:HA	3:K:253:PHE:HB3	1.38	1.03
2:F:9:DT:OP2	3:N:166:THR:HG23	1.59	1.03

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	
3	I	148/151 (98%)	123 (83%)	17 (12%)	8 (5%)	1	1
3	J	84/151 (56%)	78 (93%)	6 (7%)	0	100	100
3	K	148/151 (98%)	119 (80%)	22 (15%)	7 (5%)	2	2
3	L	143/151 (95%)	122 (85%)	16 (11%)	5 (4%)	3	4
3	M	148/151 (98%)	136 (92%)	10 (7%)	2 (1%)	9	17
3	N	83/151 (55%)	79 (95%)	3 (4%)	1 (1%)	10	20
3	O	148/151 (98%)	127 (86%)	19 (13%)	2 (1%)	9	17
3	P	80/151 (53%)	70 (88%)	9 (11%)	1 (1%)	9	18
All	All	982/1208 (81%)	854 (87%)	102 (10%)	26 (3%)	4	7

5 of 26 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	I	230	GLU
3	I	231	PRO
3	I	232	SER
3	K	218	GLU
3	N	218	GLU

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	
3	I	125/129 (97%)	100 (80%)	25 (20%)	1	2
3	J	69/129 (54%)	60 (87%)	9 (13%)	4	8
3	K	105/129 (81%)	89 (85%)	16 (15%)	3	5
3	L	115/129 (89%)	105 (91%)	10 (9%)	9	21
3	M	124/129 (96%)	97 (78%)	27 (22%)	1	2
3	N	68/129 (53%)	62 (91%)	6 (9%)	9	20
3	O	119/129 (92%)	96 (81%)	23 (19%)	1	2
3	P	62/129 (48%)	56 (90%)	6 (10%)	8	17
All	All	787/1032 (76%)	665 (84%)	122 (16%)	2	5

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	279	ARG
3	O	258	LEU
3	M	211	GLU
3	O	250	ASN
3	P	209	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
3	M	244	GLN
3	P	170	GLN
3	N	210	ASN
3	P	210	ASN
3	O	250	ASN

5.3.3 RNA ⓘ

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	14/14 (100%)	-0.66	0 100 100	36, 43, 52, 53	0
1	C	14/14 (100%)	-0.54	0 100 100	42, 48, 57, 58	0
1	E	14/14 (100%)	-0.93	0 100 100	33, 37, 49, 53	0
1	G	14/14 (100%)	-0.77	0 100 100	35, 41, 59, 59	0
2	B	14/14 (100%)	-0.74	0 100 100	34, 46, 58, 59	0
2	D	14/14 (100%)	-0.55	0 100 100	43, 50, 54, 55	0
2	F	14/14 (100%)	-0.89	0 100 100	33, 41, 45, 55	0
2	H	14/14 (100%)	-0.72	0 100 100	37, 44, 48, 52	0
3	I	146/151 (96%)	0.21	4 (2%) 56 51	34, 67, 102, 131	0
3	J	83/151 (54%)	0.15	2 (2%) 59 55	37, 60, 91, 103	0
3	K	146/151 (96%)	1.15	16 (10%) 10 8	51, 107, 136, 146	0
3	L	141/151 (93%)	0.30	2 (1%) 73 70	46, 67, 114, 142	0
3	M	146/151 (96%)	0.03	4 (2%) 56 51	33, 57, 91, 123	0
3	N	82/151 (54%)	0.14	2 (2%) 59 55	38, 58, 88, 106	0
3	O	146/151 (96%)	0.62	10 (6%) 23 20	40, 79, 122, 136	0
3	P	79/151 (52%)	0.45	4 (5%) 33 29	43, 73, 107, 119	0
All	All	1081/1320 (81%)	0.29	44 (4%) 41 37	33, 67, 121, 146	0

The worst 5 of 44 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	L	143	ASN	5.8
3	M	174	ALA	4.4
3	L	231	PRO	4.2
3	O	287	GLN	4.2
3	K	174	ALA	4.1

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.