



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 26, 2022 – 11:08 pm BST

PDB ID : 4C9A
Title : Mouse ZNRF3 ectodomain in complex with Xenopus RSPO2 Fu1-Fu2 (Seleno Met) crystal form I
Authors : Zebisch, M.; Jones, E.Y.
Deposited on : 2013-10-02
Resolution : 2.40 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.31.2
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

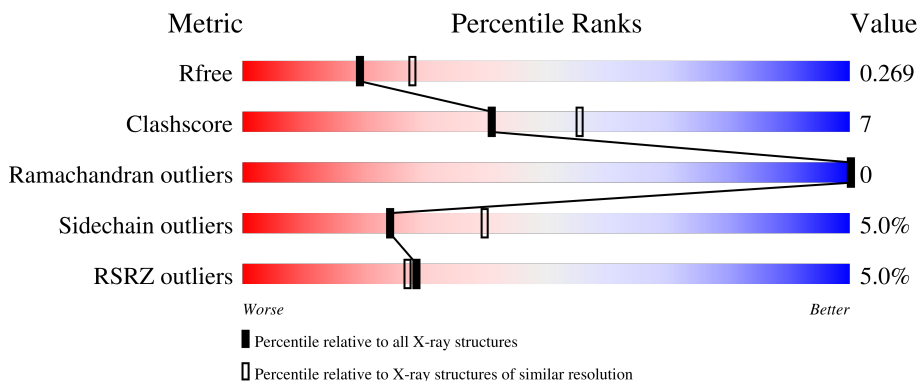
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	165	 78% 13% • 7%
1	C	165	 81% 12% 8%
2	B	121	 7% 63% 21% • 15%
2	D	121	 12% 71% 11% • 15%

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 3815 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 E3 UBIQUITIN-PROTEIN LIGASE ZNR3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	153	1170	735	204	226	5	0	0	0
1	C	152	1159	729	200	225	5	0	0	0

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	50	GLU	-	expression tag	UNP Q5SSZ7
A	51	THR	-	expression tag	UNP Q5SSZ7
A	52	GLY	-	expression tag	UNP Q5SSZ7
A	206	GLY	-	expression tag	UNP Q5SSZ7
A	207	THR	-	expression tag	UNP Q5SSZ7
A	208	LYS	-	expression tag	UNP Q5SSZ7
A	209	HIS	-	expression tag	UNP Q5SSZ7
A	210	HIS	-	expression tag	UNP Q5SSZ7
A	211	HIS	-	expression tag	UNP Q5SSZ7
A	212	HIS	-	expression tag	UNP Q5SSZ7
A	213	HIS	-	expression tag	UNP Q5SSZ7
A	214	HIS	-	expression tag	UNP Q5SSZ7
C	50	GLU	-	expression tag	UNP Q5SSZ7
C	51	THR	-	expression tag	UNP Q5SSZ7
C	52	GLY	-	expression tag	UNP Q5SSZ7
C	206	GLY	-	expression tag	UNP Q5SSZ7
C	207	THR	-	expression tag	UNP Q5SSZ7
C	208	LYS	-	expression tag	UNP Q5SSZ7
C	209	HIS	-	expression tag	UNP Q5SSZ7
C	210	HIS	-	expression tag	UNP Q5SSZ7
C	211	HIS	-	expression tag	UNP Q5SSZ7
C	212	HIS	-	expression tag	UNP Q5SSZ7
C	213	HIS	-	expression tag	UNP Q5SSZ7
C	214	HIS	-	expression tag	UNP Q5SSZ7

- Molecule 2 is a protein called R-SPONDIN-2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
2	B	103	717	436	134	129	16	2	0	0	0
2	D	103	769	472	142	137	16	2	0	0	0

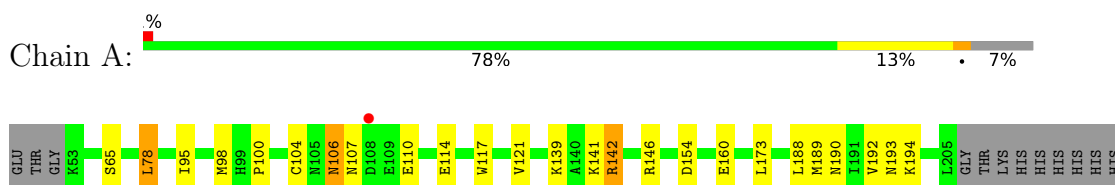
There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	32	GLU	-	expression tag	UNP Q5M7L6
B	33	THR	-	expression tag	UNP Q5M7L6
B	34	GLY	-	expression tag	UNP Q5M7L6
B	145	THR	-	expression tag	UNP Q5M7L6
B	146	LYS	-	expression tag	UNP Q5M7L6
B	147	HIS	-	expression tag	UNP Q5M7L6
B	148	HIS	-	expression tag	UNP Q5M7L6
B	149	HIS	-	expression tag	UNP Q5M7L6
B	150	HIS	-	expression tag	UNP Q5M7L6
B	151	HIS	-	expression tag	UNP Q5M7L6
B	152	HIS	-	expression tag	UNP Q5M7L6
D	32	GLU	-	expression tag	UNP Q5M7L6
D	33	THR	-	expression tag	UNP Q5M7L6
D	34	GLY	-	expression tag	UNP Q5M7L6
D	145	THR	-	expression tag	UNP Q5M7L6
D	146	LYS	-	expression tag	UNP Q5M7L6
D	147	HIS	-	expression tag	UNP Q5M7L6
D	148	HIS	-	expression tag	UNP Q5M7L6
D	149	HIS	-	expression tag	UNP Q5M7L6
D	150	HIS	-	expression tag	UNP Q5M7L6
D	151	HIS	-	expression tag	UNP Q5M7L6
D	152	HIS	-	expression tag	UNP Q5M7L6

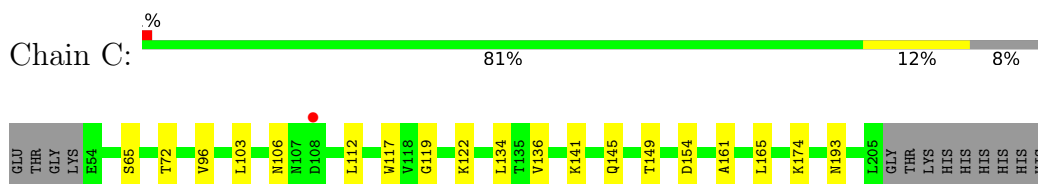
3 Residue-property plots [i](#)

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.

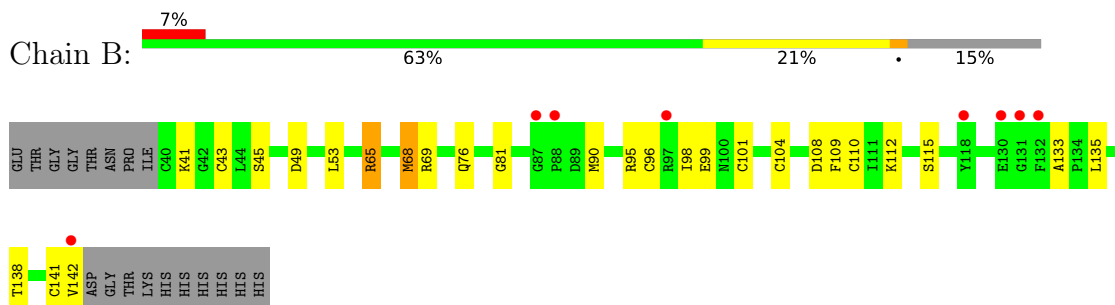
- Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE ZNRF3



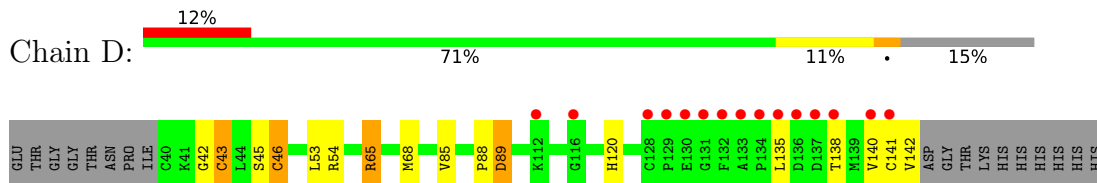
- Molecule 1: E3 UBIQUITIN-PROTEIN LIGASE ZNRF3



- Molecule 2: R-SPONDIN-2



- Molecule 2: R-SPONDIN-2



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	36.36Å 70.96Å 71.99Å 109.15° 101.71° 101.30°	Depositor
Resolution (Å)	38.92 – 2.40 34.94 – 2.40	Depositor EDS
% Data completeness (in resolution range)	78.2 (38.92-2.40) 78.2 (34.94-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.72 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.195 , 0.273 0.197 , 0.269	Depositor DCC
R_{free} test set	993 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	62.2	Xtrriage
Anisotropy	0.026	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.009 for -h,-l,-k	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3815	wwPDB-VP
Average B, all atoms (Å ²)	79.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.82% 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	0.89	0/1190	1.00	4/1614 (0.2%)
1	C	0.84	0/1179	0.97	1/1600 (0.1%)
2	B	0.63	0/727	0.89	1/973 (0.1%)
2	D	0.66	0/782	0.86	1/1042 (0.1%)
All	All	0.78	0/3878	0.94	7/5229 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	D	0	1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	142	ARG	NE-CZ-NH1	8.11	124.35	120.30
1	A	78	LEU	CA-CB-CG	7.63	132.84	115.30
2	B	65	ARG	CG-CD-NE	-6.85	97.41	111.80
2	D	65	ARG	NE-CZ-NH2	-6.57	117.01	120.30
1	A	142	ARG	NE-CZ-NH2	-6.48	117.06	120.30
1	A	189	MET	CG-SD-CE	-5.68	91.11	100.20
1	C	72	THR	N-CA-C	-5.05	97.38	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	D	42	GLY	Peptide

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	1170	0	1163	24	0
1	C	1159	0	1150	10	0
2	B	717	0	610	22	0
2	D	769	0	701	9	0
All	All	3815	0	3624	53	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 7.

All (53) 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:192:VAL:HG22	2:B:68:MSE:CE	1.98	0.94
1:A:192:VAL:HG22	2:B:68:MSE:HE2	1.67	0.77
2:B:101:CYS:SG	2:B:112:LYS:O	2.47	0.72
2:D:120:HIS:HB2	2:D:141:CYS:SG	2.29	0.72
2:B:133:ALA:H	2:B:142:VAL:HG22	1.56	0.71
1:C:141:LYS:HG2	1:C:145:GLN:HE21	1.56	0.69
1:C:136:VAL:HG12	1:C:165:LEU:HD13	1.80	0.64
1:A:107:ASN:CG	1:A:110:GLU:HG3	2.19	0.63
1:A:114:GLU:O	1:A:117:TRP:HD1	1.82	0.63
1:A:141:LYS:HG3	1:A:173:LEU:HD21	1.81	0.61
1:A:192:VAL:HA	2:B:68:MSE:HE2	1.84	0.58
2:B:98:ILE:HG23	2:B:101:CYS:HB3	1.85	0.58
2:B:98:ILE:HD12	2:B:108:ASP:HA	1.86	0.57
1:A:110:GLU:OE1	1:A:142:ARG:NH2	2.37	0.56
2:D:138:THR:OG1	2:D:140:VAL:HG22	2.05	0.56
1:C:161:ALA:O	1:C:165:LEU:HB2	2.09	0.53
2:B:133:ALA:N	2:B:142:VAL:HG22	2.23	0.52
1:C:96:VAL:O	1:C:119:GLY:HA2	2.11	0.51
2:B:104:CYS:HB2	2:B:109:PHE:O	2.11	0.50
1:C:122:LYS:HA	1:C:154:ASP:HB3	1.94	0.49
2:D:43:CYS:SG	2:D:46:CYS:HB2	2.52	0.49
1:A:95:ILE:HG21	2:B:68:MSE:HE3	1.94	0.49
2:D:53:LEU:O	2:D:54:ARG:HG3	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:117:TRP:O	1:C:149:THR:HG22	2.13	0.48
1:A:65:SER:HB3	1:C:112:LEU:HD21	1.96	0.48
1:A:100:PRO:O	1:A:139:LYS:HE3	2.15	0.47
1:A:106:ASN:OD1	1:A:106:ASN:N	2.46	0.47
2:B:133:ALA:O	2:B:141:CYS:HA	2.15	0.46
1:A:98:MET:HB2	1:A:121:VAL:HG22	1.98	0.46
2:B:81:GLY:O	2:B:96:CYS:HB2	2.15	0.46
1:A:193:ASN:OD1	2:B:69:ARG:NH1	2.48	0.46
2:B:81:GLY:O	2:B:96:CYS:CB	2.64	0.46
1:A:193:ASN:ND2	2:B:49:ASP:OD1	2.36	0.45
1:A:65:SER:CB	1:C:112:LEU:HD21	2.47	0.45
2:D:88:PRO:HG2	2:D:89:ASP:OD1	2.17	0.45
2:D:89:ASP:OD1	2:D:89:ASP:N	2.49	0.44
2:B:96:CYS:SG	2:B:104:CYS:N	2.91	0.44
1:A:78:LEU:HD21	1:A:188:LEU:HB2	1.99	0.44
1:A:95:ILE:CG2	2:B:68:MSE:HE3	2.48	0.43
1:A:192:VAL:HA	2:B:68:MSE:CE	2.47	0.43
1:C:103:LEU:O	1:C:134:LEU:HD12	2.19	0.43
1:A:192:VAL:CG2	2:B:68:MSE:HE2	2.44	0.43
1:A:142:ARG:O	1:A:146:ARG:HG3	2.19	0.43
2:B:45:SER:HB2	2:B:53:LEU:HB2	2.01	0.42
2:D:65:ARG:NH2	2:D:68:MSE:O	2.53	0.42
2:D:135:LEU:CD1	2:D:142:VAL:HG11	2.49	0.42
1:A:192:VAL:HG22	2:B:68:MSE:HE1	1.94	0.42
2:B:135:LEU:CB	2:B:138:THR:CB	2.97	0.42
2:D:85:VAL:O	2:D:85:VAL:HG12	2.19	0.42
1:C:136:VAL:CG1	1:C:165:LEU:HD13	2.47	0.41
1:A:190:ASN:HB3	1:A:194:LYS:CE	2.51	0.41
1:A:154:ASP:OD1	1:A:154:ASP:C	2.59	0.41
1:A:104:CYS:HB3	1:A:106:ASN:OD1	2.22	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	151/165 (92%)	145 (96%)	6 (4%)	0	100	100
1	C	150/165 (91%)	141 (94%)	9 (6%)	0	100	100
2	B	101/121 (84%)	92 (91%)	9 (9%)	0	100	100
2	D	101/121 (84%)	89 (88%)	12 (12%)	0	100	100
All	All	503/572 (88%)	467 (93%)	36 (7%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	126/138 (91%)	124 (98%)	2 (2%)	62	79
1	C	125/138 (91%)	121 (97%)	4 (3%)	39	59
2	B	69/104 (66%)	59 (86%)	10 (14%)	3	3
2	D	83/104 (80%)	79 (95%)	4 (5%)	25	41
All	All	403/484 (83%)	383 (95%)	20 (5%)	24	40

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	ASN
1	A	160	GLU
2	B	41	LYS
2	B	43	CYS
2	B	65	ARG
2	B	68	MSE
2	B	76	GLN
2	B	90	MSE
2	B	95	ARG
2	B	99	GLU

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Mol	Chain	Res	Type
2	B	110	CYS
2	B	115	SER
1	C	65	SER
1	C	106	ASN
1	C	174	LYS
1	C	193	ASN
2	D	43	CYS
2	D	45	SER
2	D	46	CYS
2	D	89	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	HIS
1	C	74	HIS
1	C	106	ASN
1	C	107	ASN
1	C	125	GLN
1	C	145	GLN
1	C	167	GLN
1	C	190	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 monosaccharides 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	153/165 (92%)	-0.12	1 (0%) 87 86	35, 58, 104, 136	0
1	C	152/165 (92%)	-0.15	1 (0%) 87 86	38, 62, 110, 130	0
2	B	100/121 (82%)	0.31	8 (8%) 12 11	53, 106, 153, 186	0
2	D	100/121 (82%)	0.40	15 (15%) 2 1	60, 93, 160, 168	0
All	All	505/572 (88%)	0.06	25 (4%) 28 27	35, 71, 142, 186	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	88	PRO	9.1
2	B	87	GLY	8.6
2	B	97	ARG	4.7
2	D	136	ASP	4.7
2	D	141	CYS	3.7
2	D	131	GLY	3.6
2	D	137	ASP	3.2
2	B	118	TYR	3.0
2	B	130	GLU	2.9
2	D	134	PRO	2.8
2	D	130	GLU	2.8
2	B	132	PHE	2.7
2	D	132	PHE	2.7
2	D	129	PRO	2.7
1	C	108	ASP	2.5
2	D	138	THR	2.4
2	D	128	CYS	2.4
2	D	135	LEU	2.4
2	B	131	GLY	2.4
2	D	133	ALA	2.2
2	D	140	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	108	ASP	2.2
2	D	112	LYS	2.2
2	B	142	VAL	2.0
2	D	116	GLY	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 monosaccharides 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.