Full wwPDB X-ray Structure Validation Report ⓘ

Sep 26, 2023 – 10:50 PM EDT

PDB ID	:	6CMQ
Title	:	Structure of human SHP2 without N-SH2 domain
Authors	:	Padua, R.A.P.; Sun, Y.; Marko, I.; Pitsawong, W.; Kern, D.
Deposited on	:	2018-03-06
Resolution	:	2.90 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:

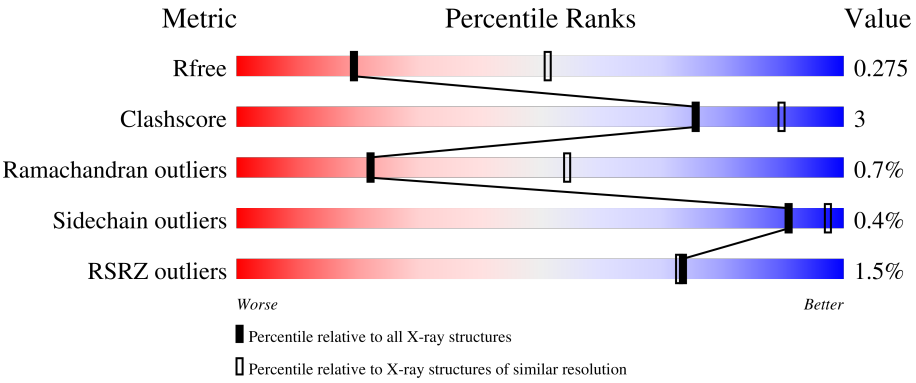
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 <=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	427	85% 9% 6%
1	B	427	% 82% 10% 8%
1	C	427	3% 84% 7% 9%
1	D	427	% 84% 7% 8%

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 24607 atoms, of which 12089 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 Tyrosine-protein phosphatase non-receptor type 11.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	400	Total	C	H	N	O	S	0	0	0
			6319	2013	3122	576	594	14			
1	B	394	Total	C	H	N	O	S	0	2	0
			6166	1975	3035	560	580	16			
1	C	388	Total	C	H	N	O	S	0	0	0
			6029	1936	2952	547	578	16			
1	D	392	Total	C	H	N	O	S	0	0	0
			6091	1956	2980	557	583	15			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	103	GLY	-	expression tag	UNP Q06124
A	104	SER	-	expression tag	UNP Q06124
A	105	GLY	-	expression tag	UNP Q06124
B	103	GLY	-	expression tag	UNP Q06124
B	104	SER	-	expression tag	UNP Q06124
B	105	GLY	-	expression tag	UNP Q06124
C	103	GLY	-	expression tag	UNP Q06124
C	104	SER	-	expression tag	UNP Q06124
C	105	GLY	-	expression tag	UNP Q06124
D	103	GLY	-	expression tag	UNP Q06124
D	104	SER	-	expression tag	UNP Q06124
D	105	GLY	-	expression tag	UNP Q06124

- Molecule 2 is water.

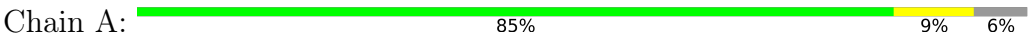
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	D	2	Total	O	0	0
			2	2		

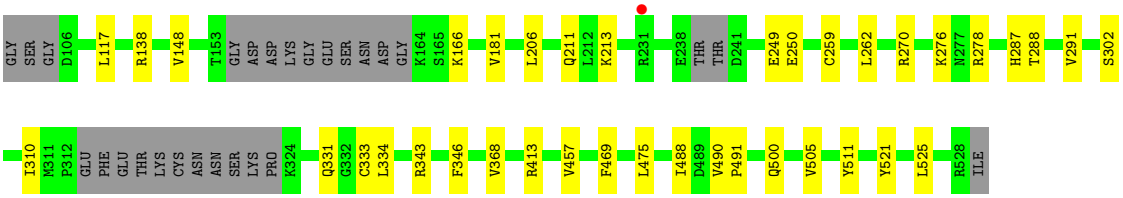
3 Residue-property plots (i)

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: Tyrosine-protein phosphatase non-receptor type 11

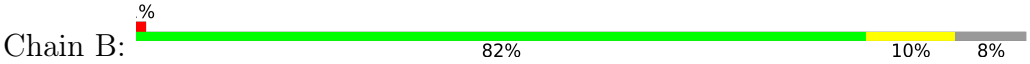
Chain A:

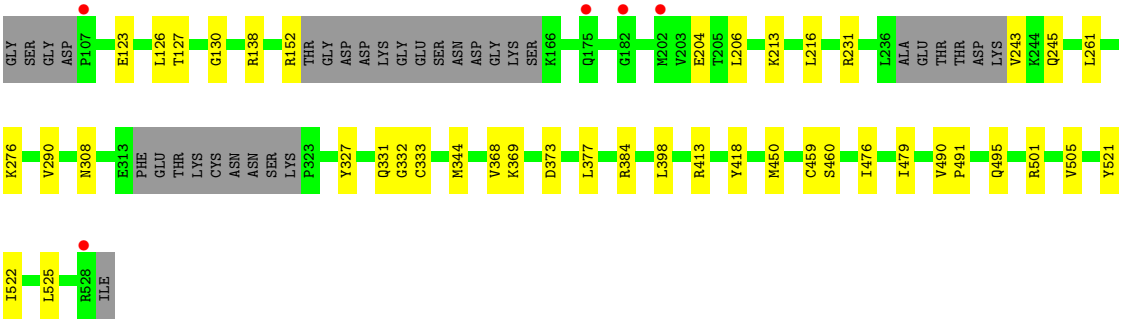




• Molecule 1: Tyrosine-protein phosphatase non-receptor type 11

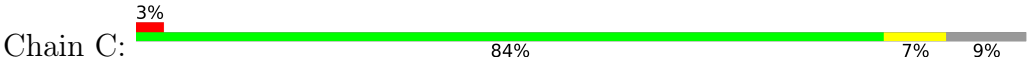
Chain B:

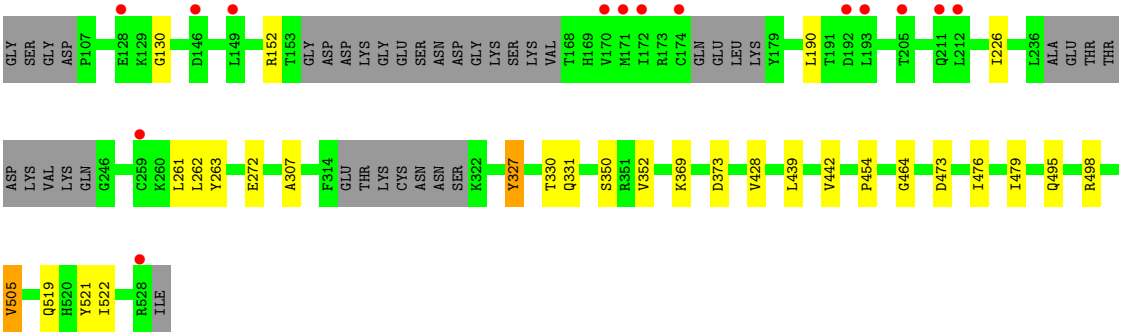




• Molecule 1: Tyrosine-protein phosphatase non-receptor type 11

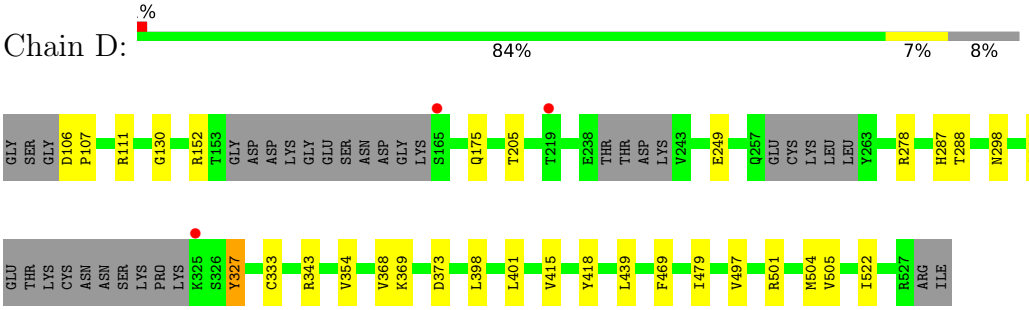
Chain C:





• Molecule 1: Tyrosine-protein phosphatase non-receptor type 11

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	69.55Å 56.20Å 247.46Å 90.00° 93.99° 90.00°	Depositor
Resolution (Å)	82.29 – 2.90 82.29 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.5 (82.29-2.90) 76.5 (82.29-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.47 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.249 , 0.276 0.249 , 0.275	Depositor DCC
R_{free} test set	1997 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å^2)	37.0	Xtriage
Anisotropy	0.408	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 7.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.26$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.75	EDS
Total number of atoms	24607	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.19% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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	0.24	0/3261	0.41	0/4403
1	B	0.24	0/3203	0.42	0/4332
1	C	0.24	0/3141	0.41	0/4250
1	D	0.24	0/3175	0.42	0/4294
All	All	0.24	0/12780	0.41	0/17279

There are no bond length outliers.

There are no bond angle outliers.

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	3197	3122	3122	20	0
1	B	3131	3035	3023	23	0
1	C	3077	2952	2952	18	0
1	D	3111	2980	2980	20	0
2	D	2	0	0	0	0
All	All	12518	12089	12077	77	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 (77) 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:B:130:GLY:O	1:B:152:ARG:NH1	2.15	0.79
1:D:369:LYS:NZ	1:D:373:ASP:OD1	2.17	0.77
1:A:346:PHE:O	1:A:413:ARG:NH1	2.19	0.75
1:A:250:GLU:OE1	1:A:511:TYR:OH	2.04	0.74
1:D:130:GLY:O	1:D:152:ARG:NH1	2.20	0.73
1:D:439:LEU:HD13	1:D:469:PHE:CE1	2.27	0.70
1:B:369:LYS:NZ	1:B:373:ASP:OD1	2.26	0.68
1:C:479:ILE:HD13	1:C:522:ILE:HD11	1.75	0.68
1:C:439:LEU:HD11	1:C:473:ASP:OD2	1.94	0.68
1:B:479:ILE:HD13	1:B:522:ILE:HD11	1.76	0.67
1:B:261:LEU:HD11	1:B:495:GLN:OE1	1.97	0.65
1:D:111:ARG:NH2	1:D:249:GLU:OE2	2.28	0.65
1:D:439:LEU:HD13	1:D:469:PHE:HE1	1.66	0.61
1:C:190:LEU:HD23	1:C:190:LEU:O	2.02	0.60
1:A:333:CYS:O	1:A:368:VAL:HG22	2.02	0.59
1:A:521:TYR:CE2	1:A:525:LEU:HD11	2.38	0.59
1:B:398:LEU:HD13	1:B:418:TYR:CE1	2.40	0.56
1:A:302:SER:O	1:A:343:ARG:NH2	2.39	0.55
1:C:498:ARG:NH2	1:C:505:VAL:O	2.40	0.55
1:A:181:VAL:O	1:A:181:VAL:HG23	2.07	0.55
1:D:287:HIS:ND1	1:D:288:THR:HG23	2.22	0.55
1:C:369:LYS:NZ	1:C:373:ASP:OD1	2.40	0.55
1:B:126:LEU:HD23	1:B:216:LEU:HD22	1.91	0.52
1:B:204:GLU:OE1	1:B:206:LEU:N	2.41	0.52
1:C:130:GLY:O	1:C:152:ARG:NH1	2.42	0.52
1:A:276:LYS:O	1:A:331:GLN:NE2	2.44	0.50
1:C:352:VAL:HG11	1:C:442:VAL:HG13	1.94	0.50
1:A:259:CYS:O	1:A:262:LEU:HD23	2.12	0.50
1:A:291:VAL:HG21	1:B:231:ARG:CZ	2.42	0.50
1:B:243:VAL:O	1:B:243:VAL:HG13	2.11	0.50
1:C:261:LEU:O	1:C:263:TYR:N	2.43	0.50
1:C:428:VAL:O	1:D:298:ASN:ND2	2.44	0.49
1:A:211:GLN:OE1	1:A:213:LYS:NZ	2.47	0.48
1:D:333:CYS:O	1:D:368:VAL:HG22	2.14	0.48
1:A:166:LYS:HE3	1:A:206:LEU:HD12	1.96	0.47
1:B:377:LEU:HD21	1:B:384:ARG:HH11	1.79	0.47
1:B:476:ILE:HD12	1:B:521:TYR:CG	2.49	0.47
1:A:475:LEU:HD22	1:A:488:ILE:HG23	1.96	0.47
1:C:261:LEU:HD11	1:C:495:GLN:OE1	2.15	0.47
1:B:123:GLU:O	1:B:127:THR:HG23	2.15	0.46
1:B:521:TYR:CE2	1:B:525:LEU:HD11	2.50	0.46
1:A:270:ARG:NH2	1:B:245:GLN:OE1	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:272:GLU:OE1	1:C:272:GLU:N	2.45	0.46
1:C:330:THR:HG22	1:C:331:GLN:N	2.32	0.45
1:A:117:LEU:O	1:A:138:ARG:NH1	2.46	0.45
1:D:278:ARG:NH2	1:D:333:CYS:O	2.50	0.45
1:C:307:ALA:HB2	1:C:330:THR:HG23	1.99	0.45
1:A:278:ARG:HG2	1:A:334:LEU:HD21	1.97	0.45
1:C:476:ILE:HD12	1:C:521:TYR:CG	2.52	0.44
1:D:327:TYR:CD1	1:D:327:TYR:N	2.86	0.44
1:C:439:LEU:HD11	1:C:473:ASP:CG	2.38	0.44
1:D:398:LEU:HD13	1:D:418:TYR:CE1	2.53	0.43
1:D:497:VAL:HG12	1:D:504:MET:HG3	2.00	0.43
1:B:459:CYS:SG	1:B:460:SER:N	2.88	0.43
1:B:333:CYS:O	1:B:368:VAL:HG22	2.18	0.43
1:C:327:TYR:OH	1:C:473:ASP:HB3	2.17	0.43
1:D:479:ILE:HD13	1:D:522:ILE:HD11	2.01	0.43
1:D:287:HIS:CE1	1:D:288:THR:HG23	2.54	0.43
1:D:354:VAL:HG11	1:D:469:PHE:CE2	2.54	0.42
1:A:310:ILE:HA	1:A:500:GLN:OE1	2.20	0.42
1:A:457:VAL:HG11	1:A:469:PHE:HD2	1.84	0.42
1:B:276:LYS:O	1:B:331:GLN:NE2	2.53	0.42
1:B:490:VAL:HB	1:B:491:PRO:HD3	2.01	0.42
1:A:138:ARG:NH2	1:A:148:VAL:HG11	2.35	0.42
1:A:287:HIS:CD2	1:A:288:THR:HG23	2.55	0.42
1:C:350:SER:OG	1:C:454:PRO:O	2.33	0.41
1:D:302:SER:O	1:D:343:ARG:NH2	2.54	0.41
1:D:401:LEU:O	1:D:415:VAL:N	2.42	0.41
1:B:290:VAL:HG11	1:B:344:MET:HG3	2.01	0.41
1:C:226:ILE:HG21	1:C:519:GLN:HA	2.02	0.41
1:B:204:GLU:OE2	1:D:205:THR:OG1	2.39	0.41
1:D:106:ASP:N	1:D:107:PRO:HD2	2.35	0.41
1:B:308:ASN:OD1	1:B:501:ARG:NH1	2.50	0.41
1:D:308:ASN:OD1	1:D:501:ARG:NH1	2.47	0.41
1:A:490:VAL:HB	1:A:491:PRO:HD3	2.02	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	392/427 (92%)	373 (95%)	18 (5%)	1 (0%)	41 71
1	B	388/427 (91%)	365 (94%)	19 (5%)	4 (1%)	15 45
1	C	378/427 (88%)	352 (93%)	23 (6%)	3 (1%)	19 51
1	D	382/427 (90%)	360 (94%)	20 (5%)	2 (0%)	29 61
All	All	1540/1708 (90%)	1450 (94%)	80 (5%)	10 (1%)	22 58

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	175	GLN
1	C	464	GLY
1	B	213	LYS
1	B	450	MET
1	B	505	VAL
1	C	262	LEU
1	A	505	VAL
1	C	505	VAL
1	D	505	VAL
1	B	332	GLY

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	344/383 (90%)	343 (100%)	1 (0%)	92 98

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	336/383 (88%)	334 (99%)	2 (1%)	86 96
1	C	330/383 (86%)	329 (100%)	1 (0%)	92 98
1	D	332/383 (87%)	331 (100%)	1 (0%)	92 98
All	All	1342/1532 (88%)	1337 (100%)	5 (0%)	91 97

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	249	GLU
1	B	138	ARG
1	B	413	ARG
1	C	327	TYR
1	D	327	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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, 95^{th} 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	400/427 (93%)	0.11	1 (0%)	94	94	18, 40, 70, 87	0
1	B	394/427 (92%)	0.09	5 (1%)	77	77	20, 42, 77, 103	0
1	C	388/427 (90%)	0.27	14 (3%)	42	37	22, 43, 91, 114	0
1	D	392/427 (91%)	0.06	4 (1%)	82	82	21, 41, 70, 84	0
All	All	1574/1708 (92%)	0.13	24 (1%)	73	73	18, 42, 78, 114	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	182	GLY	3.6
1	C	259	CYS	3.4
1	C	205	THR	3.2
1	C	170	VAL	3.2
1	C	149	LEU	3.2
1	C	211	GLN	3.1
1	B	107	PRO	2.8
1	C	212	LEU	2.7
1	D	219	THR	2.6
1	B	202	MET	2.6
1	D	314	PHE	2.5
1	D	325	LYS	2.5
1	C	174	CYS	2.5
1	C	528	ARG	2.4
1	C	128	GLU	2.3
1	C	172	ILE	2.3
1	C	171	MET	2.3
1	A	231	ARG	2.3
1	C	192	ASP	2.2
1	C	146	ASP	2.2
1	B	175	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	193	LEU	2.1
1	B	528	ARG	2.1
1	D	165	SER	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.