Full wwPDB X-ray Structure Validation Report (i)

Sep 25, 2023 – 10:53 AM EDT

PDB ID	:	5WAK
Title	:	Crystal Structure of a Suz12-Rbbp4 Binary Complex
Authors	:	Chen, S.; Jiao, L.; Liu, X.
Deposited on	:	2017-06-26
Resolution	:	3.20 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 (i) 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 (1)) were used in the production of this report:

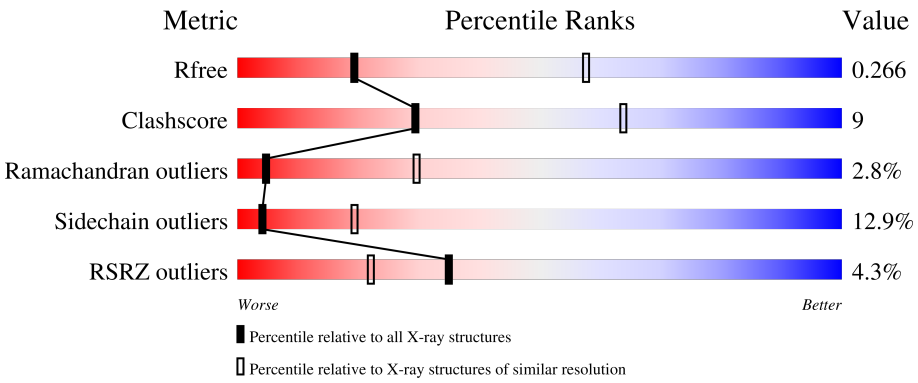
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation 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 3.20 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	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 <=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	439	4%, 64%, 23%, •, 11%
2	B	478	2%, 27%, 12%, •, 59%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4766 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 Histone-binding protein RBBP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	392	3128	1971	533	614	10	0	0	0

There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-13	MET	-	initiating methionine	UNP Q09028
A	-12	SER	-	expression tag	UNP Q09028
A	-11	HIS	-	expression tag	UNP Q09028
A	-10	HIS	-	expression tag	UNP Q09028
A	-9	HIS	-	expression tag	UNP Q09028
A	-8	HIS	-	expression tag	UNP Q09028
A	-7	HIS	-	expression tag	UNP Q09028
A	-6	HIS	-	expression tag	UNP Q09028
A	-5	LEU	-	expression tag	UNP Q09028
A	-4	VAL	-	expression tag	UNP Q09028
A	-3	PRO	-	expression tag	UNP Q09028
A	-2	ARG	-	expression tag	UNP Q09028
A	-1	GLY	-	expression tag	UNP Q09028
A	0	SER	-	expression tag	UNP Q09028

- Molecule 2 is a protein called Polycomb protein SUZ12.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	196	1637	1047	305	274	11	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	546	TRP	-	expression tag	UNP Q15022
B	547	SER	-	expression tag	UNP Q15022

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Chain	Residue	Modelled	Actual	Comment	Reference
B	548	HIS	-	expression tag	UNP Q15022
B	549	PRO	-	expression tag	UNP Q15022
B	550	GLN	-	expression tag	UNP Q15022
B	551	PHE	-	expression tag	UNP Q15022
B	552	GLU	-	expression tag	UNP Q15022
B	553	LYS	-	expression tag	UNP Q15022

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

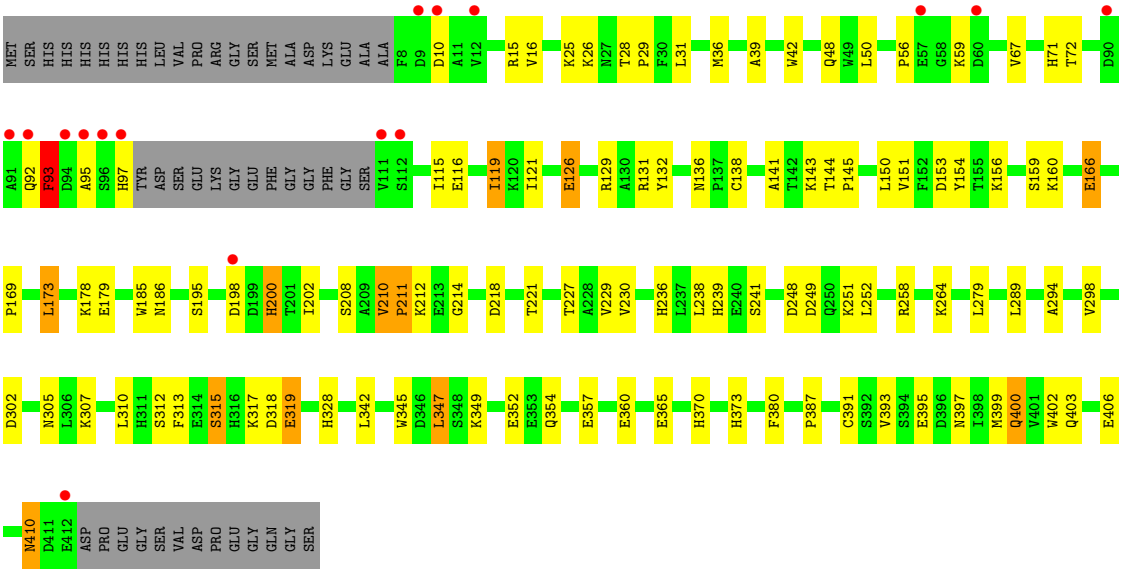
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	B	1	1	1	0	0

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.

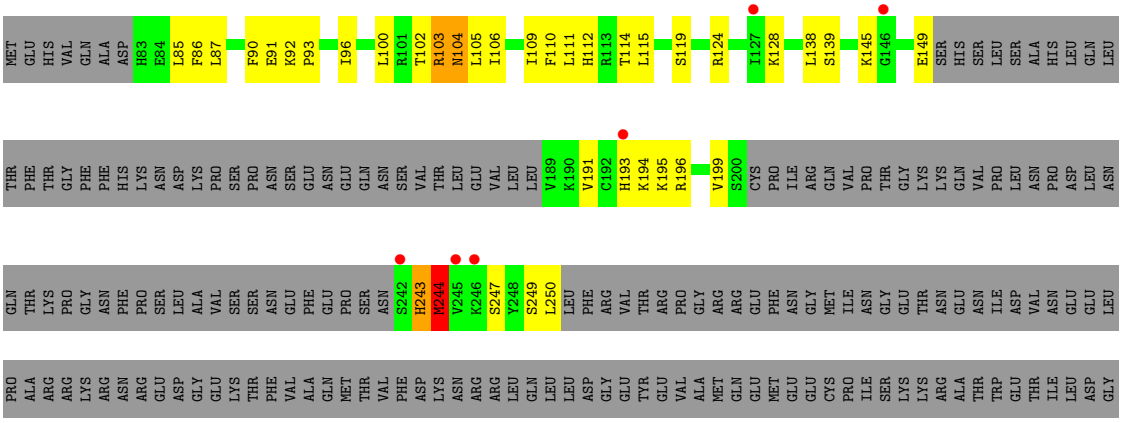
- Molecule 1: Histone-binding protein RBBP4

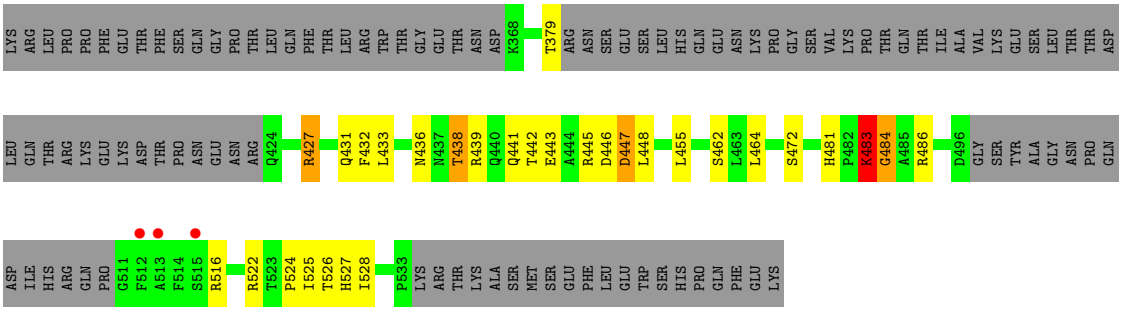
Chain A: 4% 64% 23% • 11%



- Molecule 2: Polycomb protein SUZ12

Chain B: 2% 27% 12% • 59%




LYS ARG LEU PRO PRO PHE GLU THR PHE SER GLN GLY PRO THR LEU GLN PHE THR LEU ARG TRP THR GLY GLU THR ASN ASP K368 T379 ARG ASN SER GLU SER LEU HIS GLN GLU ASN LYS PRO GLY SER VAL LYS PRO THR GLN THR ILE ALA VAL LYS GLU SER LEU THR THR ASP
LEU GLN THR ARG LYS GLU LYS ASP THR PRO ASN GLU ASN ARG Q424 R427 Q431 F432 L433 N436 N437 T438 R439 Q440 Q441 T442 E443 A444 R445 D446 D447 L448 L455 S462 L463 L464 S472 H481 P482 K483 G484 A485 R486 D496 GLY SER TYR ALA GLY ASN PRO GLN
ASP ILE HIS ARG GLN PRO G511 F512 A513 F514 S515 R516 R522 T523 P524 I525 T526 H527 I528 P533 LYS ARG THR LYS ALA SER MET SER GLU PHE LEU GLU TRP SER HIS PRO GLN PHE GLU LYS

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	105.98Å 107.70Å 107.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.76 – 3.20 28.76 – 3.20	Depositor EDS
% Data completeness (in resolution range)	73.6 (28.76-3.20) 73.6 (28.76-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.98 (at 3.17Å)	Xtriage
Refinement program	BUSTER 2.10.2	Depositor
R, R_{free}	0.178 , 0.251 0.193 , 0.266	Depositor DCC
R_{free} test set	797 reflections (5.18%)	wwPDB-VP
Wilson B-factor (Å^2)	56.4	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 80.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.015 for -h,l,k 0.027 for -l,-k,-h 0.019 for k,h,-l 0.000 for k,l,h 0.000 for l,h,k	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	4766	wwPDB-VP
Average B, all atoms (Å^2)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

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	0.50	0/3214	0.75	0/4382
2	B	0.56	0/1672	0.78	0/2240
All	All	0.52	0/4886	0.76	0/6622

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 (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	3128	0	2965	65	0
2	B	1637	0	1676	38	0
3	B	1	0	0	0	0
All	All	4766	0	4641	89	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 9.

All (89) 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:239:HIS:HD2	1:A:241:SER:H	1.34	0.75
1:A:119:ILE:HG23	1:A:159:SER:HA	1.69	0.71
1:A:198:ASP:HA	1:A:229:VAL:HG13	1.71	0.71
1:A:97:HIS:HD2	2:B:526:THR:H	1.37	0.71
2:B:431:GLN:HG2	2:B:441:GLN:CG	2.24	0.68
1:A:229:VAL:HB	1:A:248:ASP:OD2	1.94	0.67
1:A:298:VAL:HB	1:A:313:PHE:HB2	1.77	0.67
1:A:210:VAL:HG13	1:A:212:LYS:HE2	1.77	0.67
1:A:36:MET:HG2	2:B:528:ILE:HG13	1.81	0.63
1:A:95:ALA:HB3	2:B:528:ILE:HD13	1.81	0.63
2:B:483:LYS:H	2:B:484:GLY:HA3	1.65	0.62
2:B:431:GLN:HG2	2:B:441:GLN:HG2	1.81	0.62
2:B:481:HIS:O	2:B:484:GLY:HA3	2.00	0.60
2:B:427:ARG:HA	2:B:445:ARG:HA	1.84	0.60
1:A:380:PHE:HA	1:A:391:CYS:O	2.02	0.59
1:A:315:SER:HB2	1:A:345:TRP:HH2	1.68	0.58
1:A:305:ASN:HB3	2:B:138:LEU:HD21	1.84	0.58
1:A:48:GLN:NE2	1:A:131:ARG:HA	2.19	0.58
2:B:431:GLN:HG2	2:B:441:GLN:HG3	1.86	0.57
1:A:210:VAL:N	1:A:211:PRO:HD3	2.19	0.57
1:A:357:GLU:O	1:A:360:GLU:HB2	2.06	0.56
1:A:50:LEU:HG	1:A:67:VAL:HG23	1.89	0.54
1:A:315:SER:HB2	1:A:345:TRP:CH2	2.42	0.54
1:A:16:VAL:HG12	2:B:103:ARG:HH21	1.72	0.54
1:A:328:HIS:CD2	1:A:387:PRO:HA	2.44	0.53
1:A:354:GLN:HG2	2:B:124:ARG:HD3	1.90	0.53
2:B:427:ARG:HB3	2:B:445:ARG:HG3	1.89	0.53
1:A:48:GLN:HE22	1:A:131:ARG:HA	1.73	0.52
2:B:112:HIS:HA	2:B:115:LEU:HD12	1.92	0.52
1:A:92:GLN:HG2	1:A:93:PHE:H	1.75	0.51
1:A:153:ASP:HB3	1:A:156:LYS:HB2	1.94	0.50
2:B:194:LYS:HG2	2:B:244:MET:SD	2.52	0.50
2:B:483:LYS:N	2:B:484:GLY:HA3	2.27	0.50
1:A:28:THR:N	1:A:29:PRO:HD2	2.26	0.50
1:A:210:VAL:HG12	1:A:210:VAL:O	2.13	0.49
1:A:406:GLU:HG2	1:A:410:ASN:HB2	1.94	0.49
2:B:445:ARG:C	2:B:447:ASP:H	2.15	0.49
1:A:294:ALA:HA	1:A:319:GLU:HG2	1.95	0.48
1:A:71:HIS:HA	1:A:126:GLU:HB3	1.95	0.48
1:A:236:HIS:HE1	1:A:238:LEU:HB3	1.79	0.48
1:A:249:ASP:HB3	1:A:251:LYS:HB2	1.96	0.47
1:A:144:THR:HG22	1:A:145:PRO:HD2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:317:LYS:HD2	2:B:106:ILE:O	2.14	0.47
1:A:352:GLU:HB3	2:B:124:ARG:HD2	1.96	0.47
1:A:393:VAL:HG12	1:A:399:MET:HG3	1.96	0.47
1:A:313:PHE:CZ	1:A:347:LEU:HD22	2.50	0.46
1:A:92:GLN:HG2	1:A:93:PHE:N	2.31	0.46
2:B:191:VAL:HG13	2:B:247:SER:HB3	1.98	0.46
1:A:115:ILE:HD12	2:B:526:THR:HG23	1.98	0.46
1:A:302:ASP:HB2	1:A:310:LEU:HD11	1.98	0.45
2:B:100:LEU:O	2:B:104:ASN:HB2	2.16	0.45
1:A:126:GLU:O	1:A:145:PRO:HD3	2.15	0.45
2:B:92:LYS:HB3	2:B:93:PRO:HD3	1.98	0.45
2:B:110:PHE:CE1	2:B:115:LEU:HD11	2.52	0.45
1:A:178:LYS:HD3	1:A:198:ASP:HB2	1.99	0.45
1:A:313:PHE:HZ	1:A:347:LEU:HD22	1.82	0.45
1:A:144:THR:CG2	1:A:145:PRO:HD2	2.47	0.44
1:A:239:HIS:CD2	1:A:241:SER:H	2.24	0.44
1:A:31:LEU:HD21	2:B:115:LEU:HG	1.99	0.44
1:A:150:LEU:HB3	1:A:169:PRO:HB3	1.99	0.44
2:B:87:LEU:HD12	2:B:87:LEU:H	1.82	0.44
1:A:195:SER:O	1:A:202:ILE:HA	2.18	0.44
2:B:93:PRO:HA	2:B:96:ILE:HD12	1.98	0.44
1:A:42:TRP:CD2	1:A:72:THR:HG22	2.53	0.43
1:A:342:LEU:HB3	1:A:370:HIS:HB3	2.00	0.43
1:A:200:HIS:HA	1:A:230:VAL:HG23	2.01	0.43
2:B:193:HIS:HE1	2:B:247:SER:HB2	1.84	0.43
2:B:447:ASP:CG	2:B:448:LEU:H	2.22	0.43
1:A:16:VAL:HG11	2:B:103:ARG:HD3	2.01	0.43
1:A:39:ALA:O	2:B:524:PRO:HA	2.19	0.43
1:A:138:CYS:HA	1:A:154:TYR:CE2	2.54	0.43
1:A:210:VAL:HG22	1:A:212:LYS:HZ1	1.84	0.43
1:A:241:SER:HB3	1:A:258:ARG:HG3	2.01	0.43
1:A:397:ASN:HB2	2:B:522:ARG:HD3	2.00	0.43
2:B:111:LEU:HB2	2:B:114:THR:HG23	2.00	0.43
1:A:373:HIS:NE2	1:A:400:GLN:HG3	2.34	0.42
1:A:48:GLN:HE22	1:A:132:TYR:H	1.66	0.42
1:A:16:VAL:CG1	2:B:103:ARG:HH21	2.31	0.42
1:A:151:VAL:HG23	1:A:173:LEU:HD11	2.01	0.42
2:B:90:PHE:CE2	2:B:432:PHE:HD2	2.38	0.42
1:A:141:ALA:HB2	1:A:185:TRP:CZ2	2.55	0.42
1:A:92:GLN:CG	1:A:93:PHE:H	2.31	0.42
2:B:483:LYS:N	2:B:484:GLY:CA	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:56:PRO:HG2	1:A:59:LYS:HB2	2.01	0.41
1:A:393:VAL:CG1	1:A:399:MET:HG3	2.51	0.41
2:B:102:THR:O	2:B:106:ILE:HD12	2.20	0.41
1:A:129:ARG:HH11	1:A:131:ARG:HH11	1.69	0.40
1:A:342:LEU:HD13	1:A:402:TRP:HZ2	1.86	0.40
2:B:92:LYS:O	2:B:96:ILE:HG13	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	388/439 (88%)	359 (92%)	21 (5%)	8 (2%)	7 37
2	B	184/478 (38%)	154 (84%)	22 (12%)	8 (4%)	2 20
All	All	572/917 (62%)	513 (90%)	43 (8%)	16 (3%)	5 29

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	93	PHE
1	A	315	SER
1	A	214	GLY
2	B	438	THR
2	B	446	ASP
1	A	208	SER
2	B	119	SER
2	B	436	ASN
2	B	483	LYS
1	A	166	GLU
2	B	244	MET
1	A	319	GLU

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Mol	Chain	Res	Type
2	B	243	HIS
2	B	484	GLY
1	A	211	PRO
1	A	210	VAL

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	352/388 (91%)	318 (90%)	34 (10%)	8 31
2	B	184/442 (42%)	149 (81%)	35 (19%)	1 8
All	All	536/830 (65%)	467 (87%)	69 (13%)	4 19

All (69) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	ASP
1	A	15	ARG
1	A	25	LYS
1	A	26	LYS
1	A	93	PHE
1	A	116	GLU
1	A	119	ILE
1	A	121	ILE
1	A	126	GLU
1	A	136	ASN
1	A	143	LYS
1	A	160	LYS
1	A	166	GLU
1	A	173	LEU
1	A	179	GLU
1	A	186	ASN
1	A	200	HIS
1	A	218	ASP
1	A	221	THR

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Mol	Chain	Res	Type
1	A	227	THR
1	A	252	LEU
1	A	264	LYS
1	A	279	LEU
1	A	289	LEU
1	A	307	LYS
1	A	312	SER
1	A	318	ASP
1	A	347	LEU
1	A	349	LYS
1	A	365	GLU
1	A	395	GLU
1	A	400	GLN
1	A	403	GLN
1	A	410	ASN
2	B	85	LEU
2	B	86	PHE
2	B	91	GLU
2	B	103	ARG
2	B	104	ASN
2	B	105	LEU
2	B	109	ILE
2	B	128	LYS
2	B	139	SER
2	B	145	LYS
2	B	149	GLU
2	B	195	LYS
2	B	196	ARG
2	B	199	VAL
2	B	243	HIS
2	B	244	MET
2	B	249	SER
2	B	250	LEU
2	B	379	THR
2	B	427	ARG
2	B	433	LEU
2	B	438	THR
2	B	439	ARG
2	B	442	THR
2	B	443	GLU
2	B	447	ASP
2	B	455	LEU

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Mol	Chain	Res	Type
2	B	462	SER
2	B	464	LEU
2	B	472	SER
2	B	483	LYS
2	B	486	ARG
2	B	516	ARG
2	B	525	ILE
2	B	527	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	HIS
1	A	48	GLN
1	A	77	ASN
1	A	88	ASN
1	A	97	HIS
1	A	122	ASN
1	A	136	ASN
1	A	186	ASN
1	A	239	HIS
1	A	267	HIS
1	A	311	HIS
1	A	328	HIS
2	B	95	GLN
2	B	193	HIS
2	B	431	GLN
2	B	435	ASN
2	B	456	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)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	392/439 (89%)	-0.31	16 (4%)	37	24	23, 64, 134, 176	0
2	B	196/478 (41%)	0.03	9 (4%)	32	20	29, 79, 141, 170	0
All	All	588/917 (64%)	-0.20	25 (4%)	35	22	23, 69, 136, 176	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	95	ALA	4.5
1	A	96	SER	3.7
1	A	111	VAL	3.6
2	B	515	SER	3.2
1	A	97	HIS	3.2
1	A	9	ASP	2.7
1	A	12	VAL	2.7
2	B	245	VAL	2.6
2	B	193	HIS	2.6
2	B	513	ALA	2.6
2	B	512	PHE	2.6
2	B	146	GLY	2.5
2	B	246	LYS	2.5
1	A	198	ASP	2.5
1	A	92	GLN	2.4
1	A	90	ASP	2.4
1	A	112	SER	2.4
2	B	127	ILE	2.3
1	A	10	ASP	2.2
1	A	94	ASP	2.2
2	B	242	SER	2.2
1	A	91	ALA	2.2
1	A	57	GLU	2.0
1	A	412	GLU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	60	ASP	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)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ZN	B	1001	1/1	1.00	0.13	52,52,52,52	0

6.5 Other polymers (i)

There are no such residues in this entry.