



# Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 07:59 PM UTC

PDB ID : 3EAP / pdb\_00003eap  
Title : Crystal structure of the RhoGAP domain of ARHGAP11A  
Authors : Shen, Y.; Shen, L.; Tong, Y.; Tempel, W.; MacKenzie, F.; Arrowsmith, C.H.;  
Edwards, A.M.; Bountra, C.; Weigelt, J.; Bochkarev, A.; Park, H.; Structural  
Genomics Consortium (SGC)  
Deposited on : 2008-08-26  
Resolution : 2.30 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](mailto:validation@mail.wwpdb.org)

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<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>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0  
Xtrriage (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

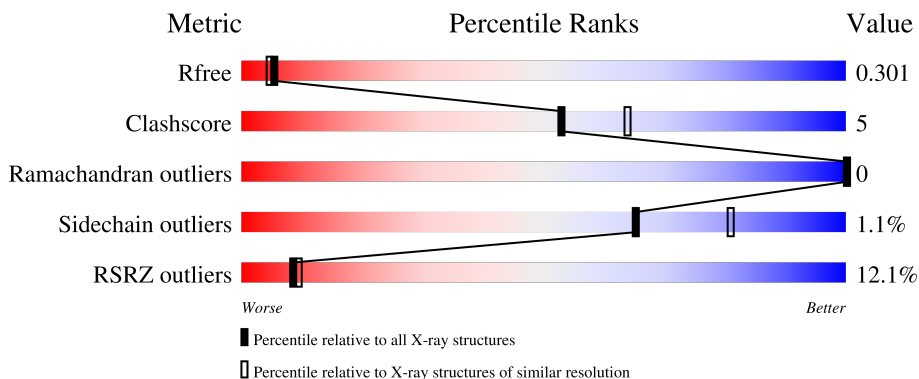
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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  $\geq 3$ , 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	271	 10% 75% 8% 17%
1	B	271	 9% 71% 7% 21%
1	C	271	 11% 69% 10% 20%
1	D	271	 9% 66% 12% 22%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	UNX	A	254	-	-	-	X
2	UNX	B	254	-	-	-	X
2	UNX	B	255	-	-	-	X
2	UNX	B	256	-	-	-	X
2	UNX	B	257	-	-	-	X
2	UNX	C	254	-	-	-	X

## 2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 6525 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 Rho GTPase-activating protein 11A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	225	Total 1665	C 1079	N 281	O 299	S 6	0	0	0
1	B	213	Total 1606	C 1041	N 275	O 286	S 4	0	0	0
1	C	216	Total 1613	C 1049	N 273	O 285	S 6	0	0	0
1	D	212	Total 1577	C 1026	N 266	O 280	S 5	0	0	0

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-17	MET	-	expression tag	UNP Q6P4F7
A	-16	HIS	-	expression tag	UNP Q6P4F7
A	-15	HIS	-	expression tag	UNP Q6P4F7
A	-14	HIS	-	expression tag	UNP Q6P4F7
A	-13	HIS	-	expression tag	UNP Q6P4F7
A	-12	HIS	-	expression tag	UNP Q6P4F7
A	-11	HIS	-	expression tag	UNP Q6P4F7
A	-10	SER	-	expression tag	UNP Q6P4F7
A	-9	SER	-	expression tag	UNP Q6P4F7
A	-8	GLY	-	expression tag	UNP Q6P4F7
A	-7	ARG	-	expression tag	UNP Q6P4F7
A	-6	GLU	-	expression tag	UNP Q6P4F7
A	-5	ASN	-	expression tag	UNP Q6P4F7
A	-4	LEU	-	expression tag	UNP Q6P4F7
A	-3	TYR	-	expression tag	UNP Q6P4F7
A	-2	PHE	-	expression tag	UNP Q6P4F7
A	-1	GLN	-	expression tag	UNP Q6P4F7
A	0	GLY	-	expression tag	UNP Q6P4F7
B	-17	MET	-	expression tag	UNP Q6P4F7
B	-16	HIS	-	expression tag	UNP Q6P4F7
B	-15	HIS	-	expression tag	UNP Q6P4F7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	HIS	-	expression tag	UNP Q6P4F7
B	-13	HIS	-	expression tag	UNP Q6P4F7
B	-12	HIS	-	expression tag	UNP Q6P4F7
B	-11	HIS	-	expression tag	UNP Q6P4F7
B	-10	SER	-	expression tag	UNP Q6P4F7
B	-9	SER	-	expression tag	UNP Q6P4F7
B	-8	GLY	-	expression tag	UNP Q6P4F7
B	-7	ARG	-	expression tag	UNP Q6P4F7
B	-6	GLU	-	expression tag	UNP Q6P4F7
B	-5	ASN	-	expression tag	UNP Q6P4F7
B	-4	LEU	-	expression tag	UNP Q6P4F7
B	-3	TYR	-	expression tag	UNP Q6P4F7
B	-2	PHE	-	expression tag	UNP Q6P4F7
B	-1	GLN	-	expression tag	UNP Q6P4F7
B	0	GLY	-	expression tag	UNP Q6P4F7
C	-17	MET	-	expression tag	UNP Q6P4F7
C	-16	HIS	-	expression tag	UNP Q6P4F7
C	-15	HIS	-	expression tag	UNP Q6P4F7
C	-14	HIS	-	expression tag	UNP Q6P4F7
C	-13	HIS	-	expression tag	UNP Q6P4F7
C	-12	HIS	-	expression tag	UNP Q6P4F7
C	-11	HIS	-	expression tag	UNP Q6P4F7
C	-10	SER	-	expression tag	UNP Q6P4F7
C	-9	SER	-	expression tag	UNP Q6P4F7
C	-8	GLY	-	expression tag	UNP Q6P4F7
C	-7	ARG	-	expression tag	UNP Q6P4F7
C	-6	GLU	-	expression tag	UNP Q6P4F7
C	-5	ASN	-	expression tag	UNP Q6P4F7
C	-4	LEU	-	expression tag	UNP Q6P4F7
C	-3	TYR	-	expression tag	UNP Q6P4F7
C	-2	PHE	-	expression tag	UNP Q6P4F7
C	-1	GLN	-	expression tag	UNP Q6P4F7
C	0	GLY	-	expression tag	UNP Q6P4F7
D	-17	MET	-	expression tag	UNP Q6P4F7
D	-16	HIS	-	expression tag	UNP Q6P4F7
D	-15	HIS	-	expression tag	UNP Q6P4F7
D	-14	HIS	-	expression tag	UNP Q6P4F7
D	-13	HIS	-	expression tag	UNP Q6P4F7
D	-12	HIS	-	expression tag	UNP Q6P4F7
D	-11	HIS	-	expression tag	UNP Q6P4F7
D	-10	SER	-	expression tag	UNP Q6P4F7
D	-9	SER	-	expression tag	UNP Q6P4F7

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-8	GLY	-	expression tag	UNP Q6P4F7
D	-7	ARG	-	expression tag	UNP Q6P4F7
D	-6	GLU	-	expression tag	UNP Q6P4F7
D	-5	ASN	-	expression tag	UNP Q6P4F7
D	-4	LEU	-	expression tag	UNP Q6P4F7
D	-3	TYR	-	expression tag	UNP Q6P4F7
D	-2	PHE	-	expression tag	UNP Q6P4F7
D	-1	GLN	-	expression tag	UNP Q6P4F7
D	0	GLY	-	expression tag	UNP Q6P4F7

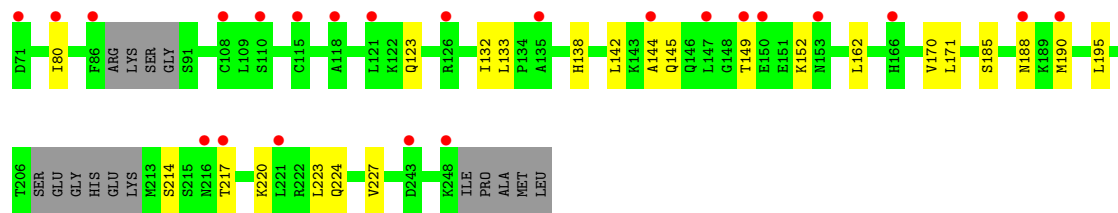
- Molecule 2 is UNKNOWN LIGAND (CCD ID: UNX) (formula: X).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total X 1 1	0	0
2	B	4	Total X 4 4	0	0
2	C	1	Total X 1 1	0	0

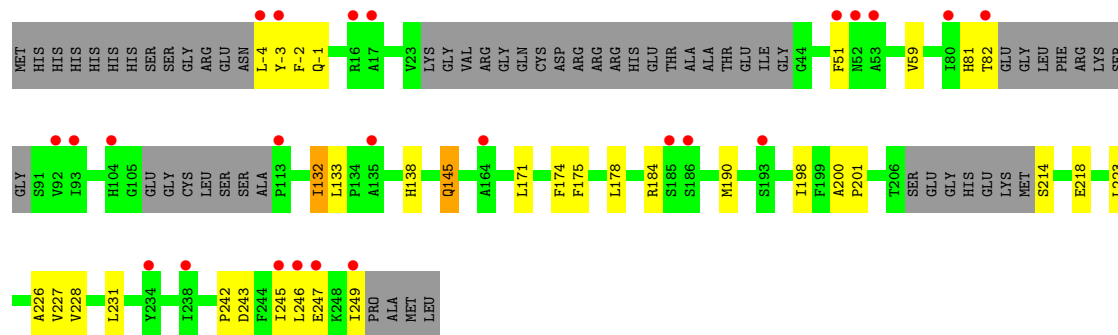
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	10	Total O 10 10	0	0
3	B	19	Total O 19 19	0	0
3	C	15	Total O 15 15	0	0
3	D	14	Total O 14 14	0	0





● Molecule 1: Rho GTPase-activating protein 11A



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	46.07Å 106.15Å 107.33Å 90.00° 97.16° 90.00°	Depositor
Resolution (Å)	20.00 – 2.30 20.00 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.1 (20.00-2.30) 97.9 (20.00-2.30)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.24 (at 2.30Å)	Xtrriage
Refinement program	REFMAC 5.4.0069, tlsmd, FFAS03/SCWRL	Depositor
R, $R_{free}$	0.227 , 0.277 0.262 , 0.301	Depositor DCC
$R_{free}$ test set	2233 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.5	Xtrriage
Anisotropy	0.028	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 68.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6525	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	60.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.87% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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](#)

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

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	0.95	0/1701	0.96	0/2321
1	B	0.95	0/1639	0.99	1/2230 (0.0%)
1	C	1.08	1/1645 (0.1%)	0.98	1/2235 (0.0%)
1	D	0.98	1/1610 (0.1%)	1.00	0/2192
All	All	0.99	2/6595 (0.0%)	0.98	2/8978 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	59	VAL	CA-CB	7.33	1.60	1.54
1	D	59	VAL	CA-CB	5.71	1.58	1.54

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	46	ILE	N-CA-C	6.29	116.59	111.62
1	C	80	ILE	CB-CA-C	-5.58	104.73	112.04

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	1665	0	1583	15	0
1	B	1606	0	1567	14	0
1	C	1613	0	1569	14	0
1	D	1577	0	1511	26	0
2	A	1	0	0	0	0
2	B	4	0	0	0	0
2	C	1	0	0	0	0
3	A	10	0	0	0	0
3	B	19	0	0	1	0
3	C	15	0	0	0	0
3	D	14	0	0	0	0
All	All	6525	0	6230	64	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 5.

All (64) 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:94:ARG:HH21	1:B:94:ARG:CG	1.64	1.10
1:B:94:ARG:HG2	1:B:94:ARG:NH2	1.46	1.01
1:A:1:MET:O	1:A:251:ALA:HB1	1.88	0.73
1:D:190:MET:HE1	1:D:198:ILE:CD1	2.29	0.62
1:C:223:LEU:O	1:C:227:VAL:HG23	2.01	0.61
1:C:3:ASP:O	1:C:7:VAL:HG23	2.04	0.57
1:C:190:MET:HG3	1:C:195:LEU:HG	1.87	0.56
1:B:94:ARG:HH21	1:B:94:ARG:HG2	0.68	0.56
1:A:200:ALA:HB3	1:A:201:PRO:HD3	1.88	0.55
1:B:185:SER:HA	1:B:188:ASN:OD1	2.06	0.55
1:D:223:LEU:O	1:D:227:VAL:HG23	2.06	0.55
1:C:142:LEU:HD21	1:C:224:GLN:HG3	1.88	0.54
1:B:94:ARG:CG	1:B:94:ARG:NH2	2.35	0.54
1:B:244:PHE:O	1:B:248:LYS:HD3	2.09	0.52
1:A:243:ASP:OD1	1:D:-3:TYR:CD2	2.62	0.52
1:D:81:HIS:O	1:D:82:THR:C	2.51	0.52
1:C:145:GLN:HB2	1:C:223:LEU:HD22	1.91	0.52
1:B:143:LYS:O	1:B:146:GLN:HG2	2.10	0.52
1:B:163:LEU:HD13	1:B:171:LEU:HD12	1.93	0.51
1:D:-4:LEU:O	1:D:-1:GLN:HG2	2.10	0.51
1:D:171:LEU:HD22	1:D:175:PHE:HE2	1.76	0.50
1:D:145:GLN:HG2	1:D:226:ALA:HB3	1.94	0.50
1:B:14:HIS:HE1	3:B:274:HOH:O	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:ALA:O	1:A:252:MET:C	2.55	0.49
1:A:-2:PHE:HB2	1:D:-2:PHE:HB2	1.95	0.49
1:A:149:THR:HG21	1:D:184:ARG:NH1	2.27	0.49
1:D:133:LEU:O	1:D:138:HIS:NE2	2.41	0.48
1:A:213:MET:SD	1:A:221:LEU:HD12	2.54	0.48
1:D:190:MET:HE1	1:D:198:ILE:HD11	1.97	0.47
1:C:214:SER:OG	1:C:217:THR:HG23	2.14	0.47
1:A:243:ASP:OD1	1:D:-3:TYR:CE2	2.67	0.47
1:C:132:ILE:HD13	1:C:171:LEU:HD21	1.97	0.47
1:D:242:PRO:HD2	1:D:245:ILE:HD13	1.98	0.46
1:B:2:TRP:CD1	1:B:7:VAL:HG21	2.51	0.46
1:D:171:LEU:HD22	1:D:175:PHE:CE2	2.50	0.45
1:A:200:ALA:HA	1:A:228:VAL:HG21	1.98	0.45
1:C:185:SER:HA	1:C:188:ASN:OD1	2.16	0.45
1:D:190:MET:HE1	1:D:198:ILE:HD12	1.97	0.45
1:D:171:LEU:HD23	1:D:171:LEU:HA	1.91	0.44
1:A:148:GLY:O	1:A:152:LYS:HG3	2.17	0.44
1:D:145:GLN:CG	1:D:226:ALA:HB3	2.48	0.44
1:A:168:VAL:O	1:A:172:ARG:HG3	2.17	0.44
1:C:144:ALA:O	1:C:152:LYS:HB2	2.18	0.44
1:B:178:LEU:HD22	1:B:195:LEU:HD13	1.99	0.44
1:B:184:ARG:HH11	1:C:149:THR:CB	2.31	0.43
1:D:243:ASP:O	1:D:247:GLU:HG3	2.19	0.43
1:B:95:LEU:HD13	1:B:116:ASP:HA	2.01	0.43
1:B:200:ALA:HA	1:B:228:VAL:HG21	2.01	0.42
1:C:123:GLN:HE21	1:C:123:GLN:HB2	1.69	0.42
1:D:214:SER:O	1:D:218:GLU:N	2.45	0.42
1:D:145:GLN:HB3	1:D:223:LEU:HD22	2.01	0.42
1:C:133:LEU:O	1:C:138:HIS:NE2	2.40	0.41
1:D:246:LEU:HA	1:D:249:ILE:HD12	2.02	0.41
1:C:51:PHE:CE1	1:C:170:VAL:HG21	2.55	0.41
1:D:174:PHE:CE2	1:D:178:LEU:HD11	2.56	0.41
1:D:227:VAL:O	1:D:231:LEU:HG	2.21	0.41
1:A:2:TRP:CE2	1:A:251:ALA:HB2	2.55	0.41
1:A:80:ILE:O	1:A:188:ASN:HB3	2.20	0.41
1:D:200:ALA:HA	1:D:228:VAL:HG21	2.02	0.41
1:A:210:HIS:O	1:A:213:MET:HE2	2.21	0.41
1:C:8:ARG:NH1	1:C:162:LEU:HD22	2.36	0.41
1:A:8:ARG:HD3	1:A:162:LEU:CD2	2.51	0.41
1:D:51:PHE:HZ	1:D:132:ILE:HD12	1.86	0.40
1:D:200:ALA:HB3	1:D:201:PRO:HD3	2.03	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	217/271 (80%)	211 (97%)	6 (3%)	0	100	100
1	B	203/271 (75%)	201 (99%)	2 (1%)	0	100	100
1	C	208/271 (77%)	204 (98%)	4 (2%)	0	100	100
1	D	202/271 (74%)	195 (96%)	7 (4%)	0	100	100
All	All	830/1084 (77%)	811 (98%)	19 (2%)	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	164/233 (70%)	162 (99%)	2 (1%)	63	79
1	B	163/233 (70%)	161 (99%)	2 (1%)	63	79
1	C	160/233 (69%)	159 (99%)	1 (1%)	78	89
1	D	156/233 (67%)	154 (99%)	2 (1%)	61	77
All	All	643/932 (69%)	636 (99%)	7 (1%)	65	81

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	103	ASP
1	A	208	GLU
1	B	94	ARG
1	B	189	LYS
1	C	220	LYS
1	D	132	ILE
1	D	145	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	HIS
1	A	79	HIS
1	B	104	HIS
1	B	145	GLN
1	C	194	ASN
1	C	202	ASN
1	D	153	ASN
1	D	169	HIS
1	D	194	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 oligosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 6 are unknown - 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

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	225/271 (83%)	1.13	26 (11%) <b>9</b> <b>10</b>	47, 60, 70, 77	0
1	B	213/271 (78%)	1.14	24 (11%) <b>10</b> <b>11</b>	51, 60, 68, 71	0
1	C	216/271 (79%)	1.24	31 (14%) <b>6</b> <b>7</b>	52, 60, 70, 77	0
1	D	212/271 (78%)	1.20	24 (11%) <b>10</b> <b>11</b>	53, 60, 70, 79	0
All	All	866/1084 (79%)	1.17	105 (12%) <b>8</b> <b>9</b>	47, 60, 70, 79	0

All (105) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	186	SER	4.1
1	B	2	TRP	4.0
1	C	217	THR	3.9
1	A	208	GLU	3.7
1	A	209	GLY	3.7
1	D	104	HIS	3.7
1	D	82	THR	3.7
1	B	117	ILE	3.7
1	B	215	SER	3.7
1	A	251	ALA	3.5
1	D	135	ALA	3.5
1	C	21	ILE	3.3
1	A	249	ILE	3.2
1	C	115	CYS	3.2
1	B	216	ASN	3.2
1	C	153	ASN	3.2
1	C	19	TYR	3.1
1	D	80	ILE	3.1
1	D	249	ILE	3.1
1	C	110	SER	3.1
1	C	135	ALA	3.0

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	C	166	HIS	3.0
1	B	53	ALA	3.0
1	C	18	PHE	2.9
1	D	-4	LEU	2.9
1	C	44	GLY	2.9
1	A	18	PHE	2.9
1	C	121	LEU	2.9
1	A	227	VAL	2.9
1	D	113	PRO	2.8
1	C	118	ALA	2.8
1	B	1	MET	2.8
1	C	86	PHE	2.8
1	A	210	HIS	2.8
1	D	93	ILE	2.8
1	B	102	VAL	2.7
1	D	185	SER	2.7
1	D	238	ILE	2.7
1	A	111	SER	2.6
1	B	82	THR	2.6
1	A	215	SER	2.6
1	C	108	CYS	2.6
1	C	144	ALA	2.5
1	B	165	ASP	2.5
1	D	-3	TYR	2.5
1	D	17	ALA	2.5
1	A	165	ASP	2.5
1	B	100	ASN	2.5
1	A	113	PRO	2.5
1	B	114	PRO	2.5
1	D	16	ARG	2.4
1	A	243	ASP	2.4
1	C	7	VAL	2.4
1	C	71	ASP	2.4
1	D	234	TYR	2.4
1	A	53	ALA	2.4
1	C	80	ILE	2.4
1	C	147	LEU	2.4
1	D	193	SER	2.3
1	B	79	HIS	2.3
1	B	200	ALA	2.3
1	C	14	HIS	2.3
1	C	150	GLU	2.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	A	51	PHE	2.3
1	A	45	LYS	2.3
1	C	221	LEU	2.3
1	C	216	ASN	2.3
1	C	190	MET	2.2
1	D	53	ALA	2.2
1	A	217	THR	2.2
1	D	51	PHE	2.2
1	C	243	ASP	2.2
1	D	52	ASN	2.2
1	B	89	SER	2.2
1	B	207	SER	2.2
1	C	149	THR	2.2
1	D	245	ILE	2.2
1	C	188	ASN	2.2
1	A	250	PRO	2.2
1	B	80	ILE	2.1
1	D	92	VAL	2.1
1	C	248	LYS	2.1
1	A	115	CYS	2.1
1	D	164	ALA	2.1
1	A	80	ILE	2.1
1	B	72	ALA	2.1
1	B	120	LEU	2.1
1	C	6	LEU	2.1
1	A	-3	TYR	2.1
1	B	52	ASN	2.1
1	A	181	VAL	2.1
1	B	63	GLY	2.1
1	B	75	SER	2.1
1	B	217	THR	2.1
1	A	213	MET	2.1
1	A	117	ILE	2.1
1	C	126	ARG	2.1
1	A	59	VAL	2.0
1	B	23	VAL	2.0
1	B	227	VAL	2.0
1	A	44	GLY	2.0
1	A	47	PHE	2.0
1	D	247	GLU	2.0
1	C	3	ASP	2.0
1	D	246	LEU	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 oligosaccharides 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	UNX	B	257	1/1	-0.47	1.57	2,2,2,2	1
2	UNX	C	254	1/1	-0.05	1.65	2,2,2,2	1
2	UNX	A	254	1/1	0.32	3.02	2,2,2,2	1
2	UNX	B	255	1/1	0.35	3.28	2,2,2,2	1
2	UNX	B	254	1/1	0.45	2.00	17,17,17,17	1
2	UNX	B	256	1/1	0.58	1.75	2,2,2,2	1

## 6.5 Other polymers [i](#)

There are no such residues in this entry.