



# Full wwPDB X-ray Structure Validation Report i

May 17, 2020 – 02:22 am BST

PDB ID : 5Z1G  
Title : Structure of the Brx1 and Ebp2 complex  
Authors : Zheng, S.; Ye, K.  
Deposited on : 2017-12-26  
Resolution : 2.29 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)  
A user guide is available at  
<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>  
with specific help available everywhere you see the i symbol.

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The following versions of software and data (see [references](#) ①) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
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) : 2.11

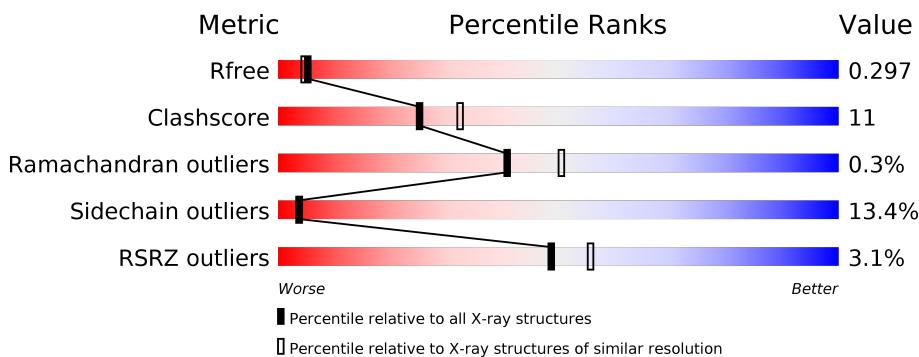
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

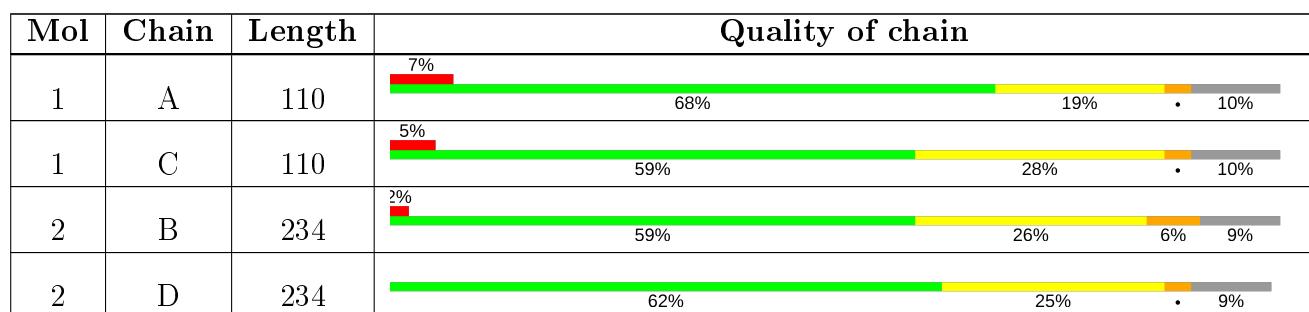
The reported resolution of this entry is 2.29 Å.

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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (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 on 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.



## 2 Entry composition [\(i\)](#)

There are 4 unique types of molecules in this entry. The entry contains 5459 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.

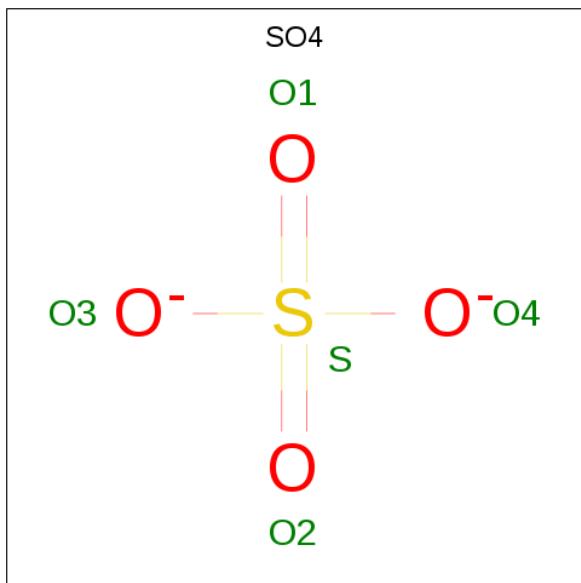
- Molecule 1 is a protein called rRNA-processing protein EBP2.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	99	Total	C 826	N 523	O 145	S 155	3	0
1	C	99	Total	C 826	N 523	O 145	S 155	3	0

- Molecule 2 is a protein called Ribosome biogenesis protein BRX1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	B	212	Total	C 1747	N 1125	O 309	S 307	6	0
2	D	212	Total	C 1747	N 1125	O 309	S 307	6	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	D	1	Total O S 5 4 1	0	0

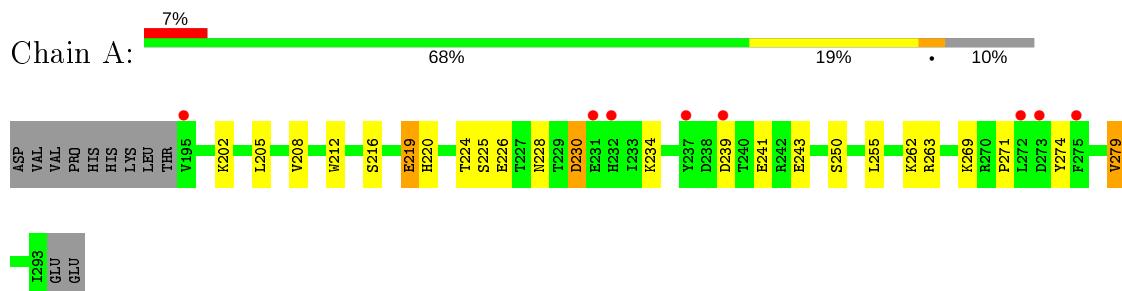
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	59	Total O 59 59	0	0
4	B	98	Total O 98 98	0	0
4	C	57	Total O 57 57	0	0
4	D	94	Total O 94 94	0	0

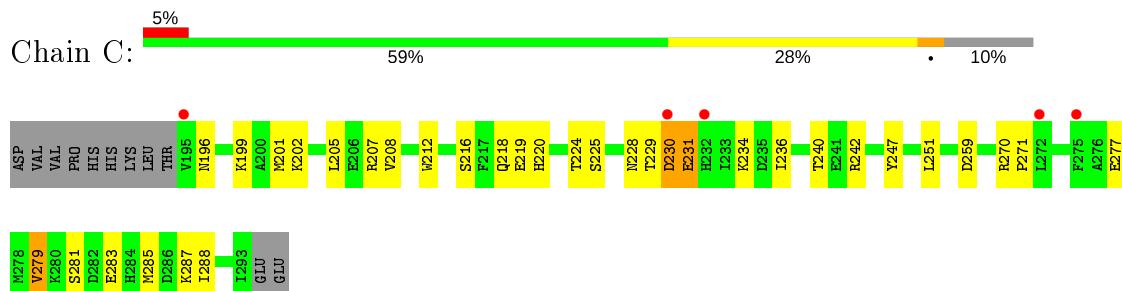
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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.

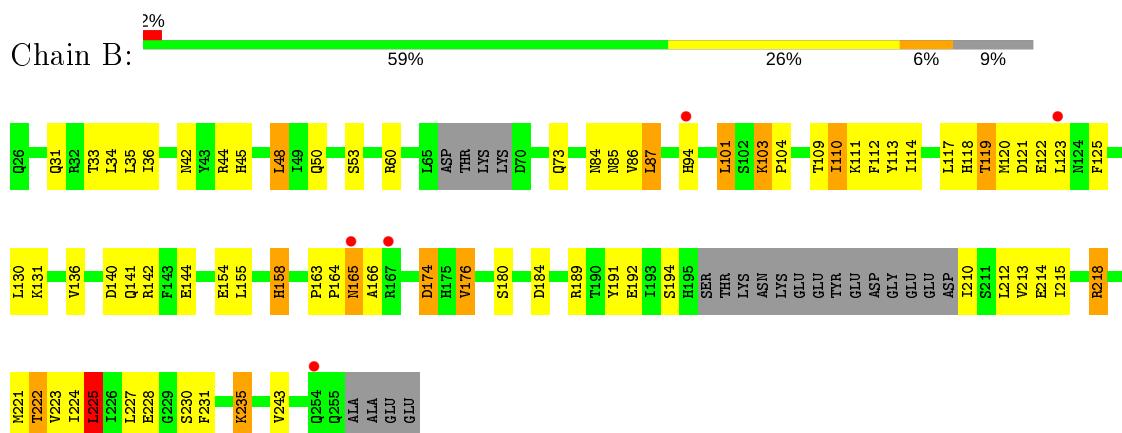
- Molecule 1: rRNA-processing protein EBP2

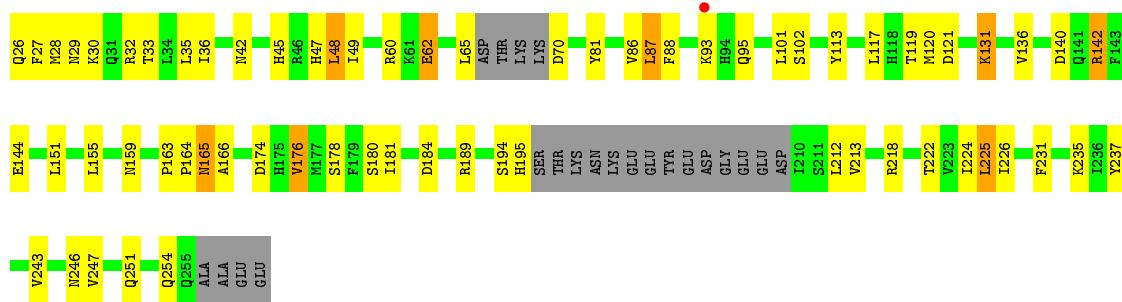


- Molecule 1: rRNA-processing protein EBP2



- Molecule 2: Ribosome biogenesis protein BRX1





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.93 Å    47.35 Å    100.69 Å 90.00°    94.10°    90.00°	Depositor
Resolution (Å)	24.91 – 2.29 24.91 – 2.29	Depositor EDS
% Data completeness (in resolution range)	96.1 (24.91-2.29) 96.3 (24.91-2.29)	Depositor EDS
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) >$ <sup>1</sup>	1.45 (at 2.28 Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
$R$ , $R_{free}$	0.230 , 0.297 0.230 , 0.297	Depositor DCC
$R_{free}$ test set	1685 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtriage
Anisotropy	0.101	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 40.9	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.51$ , $< L^2 > = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	5459	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 40.02 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.9126e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

<sup>2</sup>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:  
SO4

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	0.41	0/842	0.57	0/1130
1	C	0.43	0/842	0.56	0/1130
2	B	0.43	0/1790	0.68	2/2418 (0.1%)
2	D	0.43	0/1790	0.66	1/2418 (0.0%)
All	All	0.42	0/5264	0.64	3/7096 (0.0%)

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
1	A	0	1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
2	B	101	LEU	CA-CB-CG	7.30	132.09	115.30
2	B	225	LEU	CA-CB-CG	7.14	131.72	115.30
2	D	225	LEU	CA-CB-CG	6.00	129.11	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	230	ASP	Peptide

## 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	826	0	828	15	0
1	C	826	0	828	18	0
2	B	1747	0	1759	49	0
2	D	1747	0	1759	39	0
3	D	5	0	0	0	0
4	A	59	0	0	5	0
4	B	98	0	0	7	0
4	C	57	0	0	9	0
4	D	94	0	0	7	0
All	All	5459	0	5174	110	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 11.

All (110) 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)
2:B:31:GLN:HE21	2:B:85:ASN:HD21	1.27	0.79
2:D:142:ARG:HB3	2:D:181:ILE:HD12	1.62	0.79
2:B:44:ARG:NH2	2:B:122:GLU:OE2	2.16	0.79
2:D:164:PRO:O	4:D:401:HOH:O	2.02	0.76
1:A:262:LYS:NZ	4:A:303:HOH:O	2.20	0.74
2:B:210:ILE:N	4:B:303:HOH:O	2.21	0.73
1:C:285:MET:SD	4:C:309:HOH:O	2.46	0.73
2:D:101:LEU:HD11	2:D:159:ASN:ND2	2.04	0.72
2:D:60:ARG:NH2	4:D:403:HOH:O	2.19	0.72
2:B:164:PRO:O	4:B:301:HOH:O	2.08	0.71
2:B:103:LYS:NZ	2:B:158:HIS:HD2	1.89	0.70
2:B:42:ASN:H	2:B:45:HIS:CD2	2.11	0.67
2:B:119:THR:O	2:B:122:GLU:HG2	1.95	0.67
2:D:70:ASP:OD2	4:D:402:HOH:O	2.15	0.65
2:D:26:GLN:HG3	2:D:27:PHE:H	1.62	0.65
2:B:235:LYS:HE3	2:B:235:LYS:H	1.61	0.65
1:C:277:GLU:OE2	4:C:301:HOH:O	2.14	0.64
2:B:42:ASN:HB2	2:B:45:HIS:CD2	2.32	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:111:LYS:HB3	2:B:225:LEU:HD22	1.79	0.64
2:B:60:ARG:NH2	4:B:306:HOH:O	2.32	0.63
1:C:234:LYS:NZ	4:C:303:HOH:O	2.27	0.63
2:D:47:HIS:CE1	2:D:121:ASP:HB2	2.34	0.62
1:A:279:VAL:HG13	2:D:120:MET:HE1	1.81	0.62
1:C:287:LYS:NZ	4:C:302:HOH:O	2.18	0.61
2:D:42:ASN:HB2	2:D:45:HIS:CG	2.36	0.61
2:D:29:ASN:O	4:D:401:HOH:O	2.16	0.60
2:D:136:VAL:HB	2:D:176:VAL:HG13	1.84	0.60
2:B:31:GLN:NE2	2:B:85:ASN:HD21	1.99	0.59
2:B:42:ASN:HB2	2:B:45:HIS:CG	2.39	0.58
2:B:192:GLU:HB2	2:B:215:ILE:HD11	1.87	0.57
2:D:33:THR:HG21	2:D:87:LEU:HD22	1.86	0.57
1:C:196:ASN:N	4:C:307:HOH:O	2.38	0.57
2:D:87:LEU:HD13	2:D:101:LEU:HD13	1.86	0.57
2:B:163:PRO:HG2	2:B:166:ALA:HB2	1.88	0.55
1:A:234:LYS:N	4:A:301:HOH:O	2.16	0.55
1:A:228:ASN:ND2	4:A:309:HOH:O	2.40	0.54
2:D:189:ARG:NH2	4:D:415:HOH:O	2.40	0.54
2:B:114:ILE:HD13	2:B:221:MET:HG2	1.90	0.54
2:D:246:ASN:ND2	4:D:412:HOH:O	2.34	0.54
1:C:231:GLU:N	4:C:310:HOH:O	2.41	0.52
2:B:140:ASP:HB2	2:B:180:SER:HA	1.92	0.52
2:B:48:LEU:HG	2:B:117:LEU:HD11	1.92	0.51
1:A:241:GLU:OE1	4:A:301:HOH:O	2.19	0.51
1:A:271:PRO:HG2	1:A:274:TYR:HB2	1.92	0.50
2:B:113:TYR:HB3	2:B:222:THR:HG23	1.93	0.50
2:D:163:PRO:HG2	2:D:166:ALA:HB2	1.94	0.50
2:B:109:THR:HB	2:B:227:LEU:HD13	1.95	0.49
2:D:189:ARG:CZ	2:D:218:ARG:HG3	2.42	0.49
2:D:165:ASN:OD1	2:D:165:ASN:N	2.42	0.49
2:B:86:VAL:HG21	2:B:231:PHE:CE2	2.47	0.49
2:D:140:ASP:HB2	2:D:180:SER:HA	1.94	0.49
2:B:136:VAL:HB	2:B:176:VAL:HG13	1.94	0.49
2:B:222:THR:HG22	4:B:335:HOH:O	2.12	0.48
1:C:218:GLN:NE2	4:C:308:HOH:O	2.39	0.48
2:D:62:GLU:HG2	2:D:81:TYR:CE2	2.48	0.48
2:D:32:ARG:HH11	2:D:60:ARG:HE	1.62	0.48
2:B:110:ILE:HG12	2:B:112:PHE:CZ	2.49	0.47
2:B:130:LEU:N	2:B:174:ASP:OD2	2.34	0.47
2:B:103:LYS:HZ3	2:B:158:HIS:HD2	1.61	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:53:SER:OG	4:B:302:HOH:O	2.13	0.47
2:B:34:LEU:HG	2:B:36:ILE:HG13	1.96	0.47
2:B:73:GLN:HA	4:B:305:HOH:O	2.13	0.47
2:B:154:GLU:OE1	2:B:158:HIS:HE1	1.98	0.46
1:A:225:SER:OG	4:A:302:HOH:O	2.19	0.46
2:B:164:PRO:HA	2:B:165:ASN:HA	1.61	0.46
2:D:247:VAL:O	2:D:251:GLN:HG2	2.15	0.46
1:C:207:ARG:NH2	4:C:315:HOH:O	2.48	0.46
2:B:33:THR:HG21	2:B:87:LEU:HD22	1.97	0.46
2:B:44:ARG:HG2	2:B:117:LEU:HD23	1.98	0.45
2:B:174:ASP:OD1	1:C:270:ARG:NH1	2.36	0.45
2:B:214:GLU:OE2	2:B:218:ARG:HD2	2.15	0.45
2:B:118:HIS:NE2	4:B:304:HOH:O	2.26	0.45
2:D:194:SER:O	2:D:195:HIS:HB2	2.16	0.45
2:B:192:GLU:HB3	2:B:213:VAL:HG13	1.99	0.45
1:A:271:PRO:HB3	1:C:271:PRO:HB3	1.99	0.45
1:C:228:ASN:C	1:C:230:ASP:H	2.19	0.45
2:D:189:ARG:NE	2:D:218:ARG:HG3	2.31	0.45
2:D:226:ILE:HB	2:D:237:TYR:HB3	1.99	0.45
1:A:279:VAL:HG13	2:D:120:MET:CE	2.47	0.44
1:A:279:VAL:HG13	2:D:120:MET:SD	2.58	0.44
1:C:242:ARG:NH2	4:C:312:HOH:O	2.45	0.44
2:D:113:TYR:HB2	2:D:224:ILE:HD11	1.99	0.44
2:D:131:LYS:HB2	2:D:131:LYS:HE3	1.83	0.43
2:D:86:VAL:HG21	2:D:231:PHE:CE2	2.53	0.43
1:A:250:SER:OG	2:D:178:SER:HB3	2.17	0.43
1:C:199:LYS:HB2	1:C:199:LYS:HE2	1.80	0.43
2:B:110:ILE:CD1	2:B:223:VAL:HG13	2.48	0.43
1:A:263:ARG:HE	1:A:263:ARG:HB2	1.64	0.42
2:B:119:THR:CG2	2:B:121:ASP:HB2	2.49	0.42
1:C:281:SER:O	1:C:285:MET:HG2	2.18	0.42
2:B:110:ILE:HD11	2:B:223:VAL:HG13	2.00	0.42
2:D:101:LEU:HD11	2:D:159:ASN:HD21	1.80	0.42
2:D:246:ASN:ND2	4:D:423:HOH:O	2.51	0.42
2:B:176:VAL:HG23	2:B:191:TYR:HB2	2.01	0.42
2:B:113:TYR:HB2	2:B:224:ILE:HD11	2.01	0.41
2:B:212:LEU:HB2	1:C:247:TYR:CE2	2.55	0.41
1:A:219:GLU:HG2	2:D:28:MET:HE3	2.02	0.41
2:B:125:PHE:HZ	2:B:218:ARG:HD3	1.84	0.41
2:B:141:GLN:HB2	1:C:225:SER:O	2.20	0.41
2:B:109:THR:OG1	2:B:230:SER:HA	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:93:LYS:O	2:D:95:GLN:HG2	2.20	0.41
1:A:212:TRP:CZ3	1:A:220:HIS:HB3	2.56	0.41
2:B:120:MET:HE3	1:C:279:VAL:HG13	2.03	0.41
1:C:212:TRP:CZ3	1:C:220:HIS:HB3	2.56	0.41
2:D:48:LEU:HG	2:D:117:LEU:HD11	2.02	0.41
2:B:84:ASN:O	2:B:104:PRO:HD2	2.21	0.41
1:A:243:GLU:OE1	2:D:189:ARG:NH1	2.54	0.40
2:D:235:LYS:HE3	2:D:235:LYS:HB2	1.91	0.40
2:D:36:ILE:O	2:D:88:PHE:HA	2.20	0.40
2:B:86:VAL:HG21	2:B:231:PHE:HE2	1.86	0.40

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
1	A	97/110 (88%)	93 (96%)	4 (4%)	0	100 100
1	C	97/110 (88%)	94 (97%)	1 (1%)	2 (2%)	7 5
2	B	206/234 (88%)	197 (96%)	9 (4%)	0	100 100
2	D	206/234 (88%)	201 (98%)	5 (2%)	0	100 100
All	All	606/688 (88%)	585 (96%)	19 (3%)	2 (0%)	41 50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	229	THR
1	C	236	ILE

### 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	92/103 (89%)	80 (87%)	12 (13%)	4 4
1	C	92/103 (89%)	77 (84%)	15 (16%)	2 2
2	B	198/217 (91%)	171 (86%)	27 (14%)	3 3
2	D	198/217 (91%)	174 (88%)	24 (12%)	5 5
All	All	580/640 (91%)	502 (87%)	78 (13%)	4 4

All (78) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	202	LYS
1	A	205	LEU
1	A	208	VAL
1	A	216	SER
1	A	219	GLU
1	A	224	THR
1	A	226	GLU
1	A	230	ASP
1	A	239	ASP
1	A	255	LEU
1	A	269	LYS
1	A	279	VAL
2	B	35	LEU
2	B	48	LEU
2	B	50	GLN
2	B	87	LEU
2	B	94	HIS
2	B	101	LEU
2	B	103	LYS
2	B	110	ILE
2	B	119	THR
2	B	123	LEU
2	B	131	LYS
2	B	142	ARG

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Mol	Chain	Res	Type
2	B	144	GLU
2	B	155	LEU
2	B	158	HIS
2	B	165	ASN
2	B	174	ASP
2	B	176	VAL
2	B	184	ASP
2	B	189	ARG
2	B	194	SER
2	B	218	ARG
2	B	222	THR
2	B	225	LEU
2	B	228	GLU
2	B	235	LYS
2	B	243	VAL
1	C	201	MET
1	C	202	LYS
1	C	205	LEU
1	C	208	VAL
1	C	216	SER
1	C	219	GLU
1	C	224	THR
1	C	230	ASP
1	C	231	GLU
1	C	240	THR
1	C	251	LEU
1	C	259	ASP
1	C	279	VAL
1	C	283	GLU
1	C	288	ILE
2	D	30	LYS
2	D	35	LEU
2	D	48	LEU
2	D	49	ILE
2	D	62	GLU
2	D	65	LEU
2	D	87	LEU
2	D	102	SER
2	D	119	THR
2	D	131	LYS
2	D	142	ARG
2	D	144	GLU

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Mol	Chain	Res	Type
2	D	151	LEU
2	D	155	LEU
2	D	165	ASN
2	D	174	ASP
2	D	176	VAL
2	D	184	ASP
2	D	212	LEU
2	D	213	VAL
2	D	222	THR
2	D	225	LEU
2	D	243	VAL
2	D	254	GLN

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

Mol	Chain	Res	Type
1	A	215	HIS
1	A	228	ASN
2	B	31	GLN
2	B	45	HIS
2	B	158	HIS
2	B	254	GLN
1	C	218	GLN
2	D	95	GLN

### 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 carbohydrates in this entry.

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

1 ligand is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	SO4	D	301	-	4,4,4	0.21	0	6,6,6	0.24	0

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, 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	99/110 (90%)	0.29	8 (8%) 12 16	18, 27, 48, 68	0
1	C	99/110 (90%)	0.29	5 (5%) 28 35	18, 29, 44, 73	0
2	B	212/234 (90%)	0.05	5 (2%) 59 66	14, 21, 41, 56	0
2	D	212/234 (90%)	-0.07	1 (0%) 91 94	13, 21, 38, 44	0
All	All	622/688 (90%)	0.09	19 (3%) 49 56	13, 23, 43, 73	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	232	HIS	8.8
1	A	232	HIS	5.9
1	A	272	LEU	3.7
2	B	94	HIS	3.6
1	A	275	PHE	3.2
1	A	237	TYR	3.0
1	C	272	LEU	2.8
1	A	273	ASP	2.5
2	B	123	LEU	2.4
1	A	231	GLU	2.4
2	D	93	LYS	2.4
1	A	195	VAL	2.4
1	A	239	ASP	2.2
1	C	275	PHE	2.2
1	C	195	VAL	2.1
2	B	165	ASN	2.1
2	B	254	GLN	2.1
2	B	167	ARG	2.1
1	C	230	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 carbohydrates 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
3	SO4	D	301	5/5	0.94	0.25	39,41,49,54	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.