



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 07:33 PM UTC

PDB ID : 6DEX / pdb_00006dex
Title : Structure of Eremothecium gossypii Shu1:Shu2 complex
Authors : Singh, N.; Corbett, K.D.
Deposited on : 2018-05-13
Resolution : 2.10 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (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

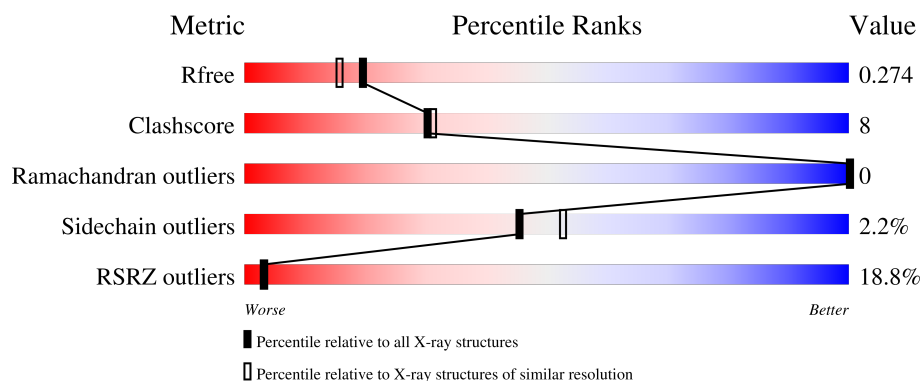
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	148	18% 70% 16% 12%
2	B	201	17% 80% 16% .

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5249 atoms, of which 2549 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 Suppressor of hydroxyurea sensitivity protein 1.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	130	Total	C	H	N	O	S	0	0	0
			2077	671	1034	183	187	2			

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	SER	-	expression tag	UNP Q75DL0
A	17	ASN	-	expression tag	UNP Q75DL0
A	18	ALA	-	expression tag	UNP Q75DL0

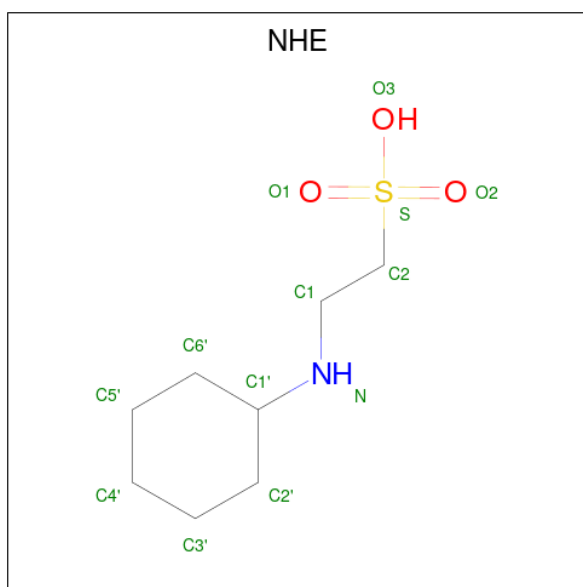
- Molecule 2 is a protein called Suppressor of hydroxyurea sensitivity protein 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	B	195	Total	C	H	N	O	S	0	0	0
			3042	999	1499	255	279	10			

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 2-[N-CYCLOHEXYLAMINO]ETHANE SULFONIC ACID (CCD ID: NHE) (formula: C₈H₁₇NO₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
4	A	1	Total	C	H	N	O	S	0	0
			29	8	16	1	3	1		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

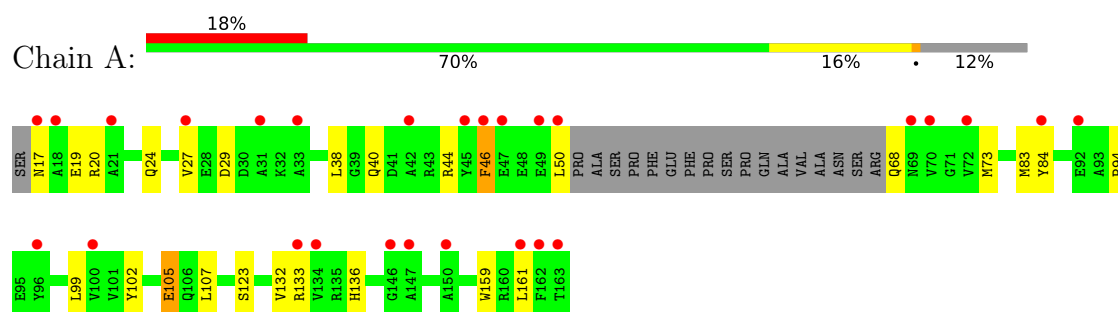
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	50	Total	O	0	0
			50	50		
6	B	49	Total	O	0	0
			49	49		

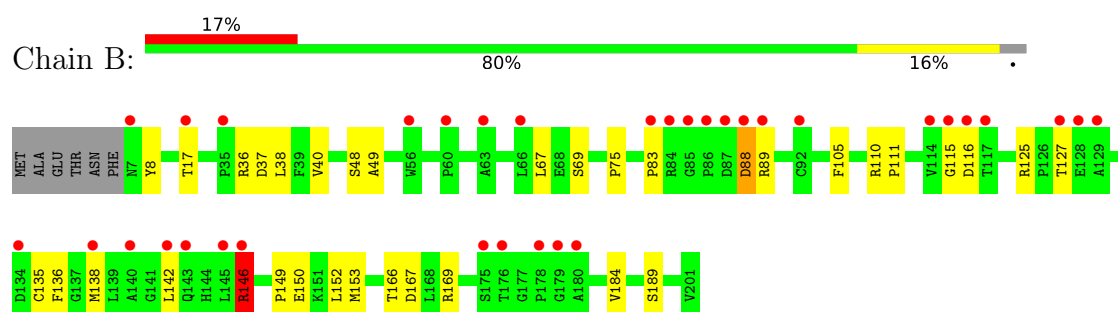
3 Residue-property plots [i](#)

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: Suppressor of hydroxyurea sensitivity protein 1



- Molecule 2: Suppressor of hydroxyurea sensitivity protein 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	37.25Å 83.91Å 107.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.06 – 2.10 39.06 – 2.10	Depositor EDS
% Data completeness (in resolution range)	90.0 (39.06-2.10) 96.4 (39.06-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, R_{free}	0.251 , 0.270 0.252 , 0.274	Depositor DCC
R_{free} test set	952 reflections (4.68%)	wwPDB-VP
Wilson B-factor (Å ²)	40.1	Xtriage
Anisotropy	0.707	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 49.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5249	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.02% 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](#)

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

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	0.33	0/1062	0.55	1/1438 (0.1%)
2	B	0.37	1/1586 (0.1%)	0.53	0/2167
All	All	0.36	1/2648 (0.0%)	0.54	1/3605 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	146	ARG	CZ-NH2	-5.08	1.26	1.33

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	133	ARG	CG-CD-NE	-5.15	100.66	112.00

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	1043	1034	1033	18	0
2	B	1543	1499	1499	26	0
3	A	1	0	0	0	0
4	A	13	16	17	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	1	0	0	0	0
6	A	50	0	0	2	0
6	B	49	0	0	1	0
All	All	2700	2549	2549	43	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 8.

All (43) 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:83:PRO:HB3	2:B:88:ASP:HB3	1.56	0.88
1:A:105:GLU:OE2	6:A:301:HOH:O	1.95	0.82
2:B:125:ARG:NH2	2:B:146:ARG:NH2	2.31	0.79
2:B:125:ARG:CZ	2:B:146:ARG:NH2	2.46	0.79
2:B:125:ARG:CZ	2:B:146:ARG:HH21	2.01	0.74
1:A:73:MET:HE1	1:A:84:TYR:CZ	2.28	0.69
2:B:89:ARG:NH1	6:B:401:HOH:O	2.27	0.68
2:B:36:ARG:NH2	2:B:150:GLU:O	2.28	0.67
1:A:161:LEU:HB3	2:B:142:LEU:HD21	1.77	0.65
1:A:44:ARG:NH2	6:A:302:HOH:O	2.31	0.64
2:B:127:THR:HG22	2:B:146:ARG:HG3	1.87	0.57
1:A:38:LEU:HB3	1:A:107:LEU:HD12	1.87	0.56
2:B:125:ARG:NH2	2:B:146:ARG:HH22	2.03	0.56
2:B:115:GLY:O	2:B:116:ASP:CB	2.54	0.55
1:A:123:SER:HB3	1:A:159:TRP:CH2	2.44	0.53
1:A:29:ASP:OD2	1:A:68:GLN:HG2	2.08	0.52
1:A:24:GLN:HA	1:A:27:VAL:HG12	1.91	0.51
2:B:125:ARG:NE	2:B:146:ARG:HH21	2.08	0.51
2:B:83:PRO:HB3	2:B:88:ASP:CB	2.33	0.51
2:B:105:PHE:CE1	2:B:152:LEU:HD21	2.46	0.51
2:B:48:SER:O	2:B:49:ALA:HB3	2.11	0.50
1:A:94:PRO:HB3	1:A:136:HIS:HB3	1.92	0.50
2:B:69:SER:OG	2:B:75:PRO:HG3	2.11	0.50
2:B:38:LEU:HD13	2:B:153:MET:HE3	1.93	0.49
2:B:8:TYR:CZ	2:B:149:PRO:HG2	2.50	0.47
1:A:40:GLN:O	1:A:44:ARG:HG3	2.14	0.47
1:A:24:GLN:HA	1:A:27:VAL:CG1	2.45	0.47
2:B:38:LEU:HD13	2:B:153:MET:CE	2.44	0.46
1:A:46:PHE:O	1:A:50:LEU:HB2	2.16	0.46
2:B:67:LEU:CD2	2:B:184:VAL:HG21	2.46	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:MET:HG3	4:A:202:NHE:H5'1	1.99	0.44
1:A:73:MET:HE1	1:A:84:TYR:CE2	2.52	0.43
2:B:8:TYR:HB2	2:B:136:PHE:HB3	2.01	0.43
1:A:99:LEU:HD11	1:A:132:VAL:HG11	2.00	0.43
1:A:83:MET:HG3	4:A:202:NHE:H6'1	2.01	0.42
1:A:19:GLU:OE2	1:A:102:TYR:OH	2.28	0.42
2:B:110:ARG:N	2:B:111:PRO:HD2	2.35	0.41
2:B:37:ASP:HB3	2:B:40:VAL:CG1	2.51	0.41
1:A:20:ARG:HE	1:A:20:ARG:HB3	1.70	0.41
2:B:138:MET:HE2	2:B:138:MET:HB3	1.95	0.41
2:B:135:CYS:HA	2:B:138:MET:HG3	2.03	0.41
2:B:166:THR:OG1	2:B:167:ASP:N	2.54	0.40
2:B:17:THR:O	2:B:169:ARG:HD2	2.21	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	126/148 (85%)	125 (99%)	1 (1%)	0	100	100
2	B	193/201 (96%)	188 (97%)	5 (3%)	0	100	100
All	All	319/349 (91%)	313 (98%)	6 (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	104/121 (86%)	101 (97%)	3 (3%)	37	42
2	B	169/179 (94%)	166 (98%)	3 (2%)	51	60
All	All	273/300 (91%)	267 (98%)	6 (2%)	45	53

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	ASN
1	A	46	PHE
1	A	105	GLU
2	B	88	ASP
2	B	146	ARG
2	B	189	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
4	NHE	A	202	-	13,13,13	0.91	1 (7%)	16,17,17	4.21	9 (56%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NHE	A	202	-	-	7/7/15/15	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	202	NHE	O2-S	2.57	1.52	1.45

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	202	NHE	O2-S-O1	-9.54	82.78	113.82
4	A	202	NHE	O1-S-C2	8.60	119.73	106.73
4	A	202	NHE	O3-S-O1	7.55	130.29	111.40
4	A	202	NHE	C1-N-C1'	-4.05	106.38	114.18
4	A	202	NHE	C4'-C5'-C6'	4.01	119.67	111.42
4	A	202	NHE	C3'-C2'-C1'	2.72	115.97	111.09
4	A	202	NHE	C5'-C6'-C1'	2.36	115.33	111.09
4	A	202	NHE	C6'-C1'-C2'	2.05	114.35	110.80
4	A	202	NHE	O3-S-O2	-2.03	106.31	111.40

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	202	NHE	C2-C1-N-C1'

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Mol	Chain	Res	Type	Atoms
4	A	202	NHE	N-C1-C2-S
4	A	202	NHE	C1-C2-S-O2
4	A	202	NHE	C1-C2-S-O3
4	A	202	NHE	C2'-C1'-N-C1
4	A	202	NHE	C1-C2-S-O1
4	A	202	NHE	C6'-C1'-N-C1

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	202	NHE	2	0

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	130/148 (87%)	1.30	27 (20%) 2 2	35, 62, 104, 121	0
2	B	195/201 (97%)	1.18	34 (17%) 4 4	33, 54, 95, 107	0
All	All	325/349 (93%)	1.22	61 (18%) 3 3	33, 56, 99, 121	0

All (61) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	116	ASP	4.3
2	B	114	VAL	4.2
1	A	27	VAL	4.1
1	A	31	ALA	4.1
2	B	83	PRO	3.5
2	B	66	LEU	3.5
1	A	46	PHE	3.4
1	A	45	TYR	3.4
1	A	163	THR	3.4
2	B	117	THR	3.4
1	A	96	TYR	3.3
2	B	85	GLY	3.3
2	B	115	GLY	3.2
1	A	42	ALA	3.1
2	B	140	ALA	3.0
2	B	63	ALA	3.0
2	B	129	ALA	3.0
2	B	88	ASP	3.0
1	A	50	LEU	2.9
2	B	86	PRO	2.9
1	A	92	GLU	2.9
1	A	33	ALA	2.8
2	B	92	CYS	2.8
1	A	70	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	180	ALA	2.7
1	A	17	ASN	2.7
2	B	128	GLU	2.7
1	A	72	VAL	2.7
1	A	49	GLU	2.6
2	B	142	LEU	2.6
2	B	178	PRO	2.6
2	B	7	ASN	2.6
1	A	147	ALA	2.6
2	B	145	LEU	2.5
1	A	18	ALA	2.5
1	A	69	ASN	2.4
2	B	146	ARG	2.4
2	B	175	SER	2.3
2	B	17	THR	2.3
2	B	84	ARG	2.3
1	A	47	GLU	2.3
1	A	100	VAL	2.3
2	B	87	ASP	2.3
2	B	56	TRP	2.3
2	B	127	THR	2.2
2	B	134	ASP	2.2
2	B	143	GLN	2.2
1	A	84	TYR	2.2
1	A	150	ALA	2.2
1	A	161	LEU	2.2
2	B	89	ARG	2.1
2	B	60	PRO	2.1
2	B	176	THR	2.1
1	A	162	PHE	2.1
2	B	179	GLY	2.1
1	A	146	GLY	2.1
1	A	134	VAL	2.1
1	A	21	ALA	2.1
2	B	35	PRO	2.1
2	B	138	MET	2.0
1	A	133	ARG	2.0

6.2 Non-standard residues in protein, DNA, RNA chains

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, 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($\text{\AA}^2$)	Q<0.9
4	NHE	A	202	13/13	0.78	0.28	131,157,166,167	0
3	MG	A	201	1/1	0.86	0.19	38,38,38,38	0
5	ZN	B	301	1/1	0.95	0.08	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.