



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 06:59 am BST

PDB ID : 2VO1
Title : CRYSTAL STRUCTURE OF THE SYNTHETASE DOMAIN OF HUMAN CTP SYNTHETASE
Authors : Stenmark, P.; Kursula, P.; Arrowsmith, C.; Berglund, H.; Edwards, A.; Ehn, M.; Flodin, S.; Graslund, S.; Hammarstrom, M.; Hallberg, B.M.; Holmberg-Schiavone, L.; Kotenyoa, T.; Moche, M.; Nilsson-Ehle, P.; Ogg, D.; Persson, C.; Sagemark, J.; Schuler, H.; Sundstrom, M.; Thorsell, A.G.; Van Den Berg, S.; Weigelt, J.; Nordlund, P.
Deposited on : 2008-02-08
Resolution : 2.80 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 following versions of software and data (see [references ⓘ](#)) 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

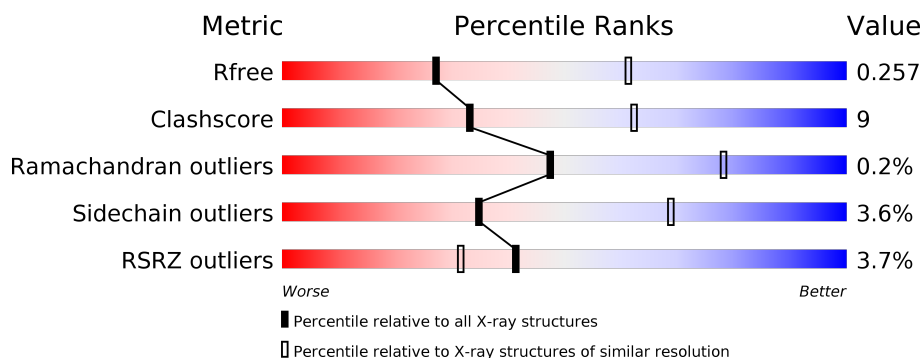
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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 ≥ 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	295	<div> <div>2%</div> <div> <div></div> <div>66%</div> <div>13%</div> <div>•</div> <div>20%</div> </div> </div>
1	B	295	<div> <div>3%</div> <div> <div></div> <div>61%</div> <div>16%</div> <div>23%</div> </div> </div>

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 3661 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 CTP SYNTHASE 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	235	Total	C	N	O	S	0	1	0
			1843	1172	312	348	11			
1	B	228	Total	C	N	O	S	0	0	0
			1779	1137	302	329	11			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	11	Total	O	0	0
			11	11		
3	B	3	Total	O	0	0
			3	3		

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 ($\text{RSRZ} > 2$). 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.

Chain A:

Sequence logo for Chain A. The y-axis represents information content in bits (0.00 to 2.00). The x-axis lists amino acids. A color scale at the top indicates conservation levels: 29% (red), 66% (green), 13% (yellow), and 20% (grey).

Position	Amino Acid	Information Content (bits)
1	Met	0.00
2	His	0.00
3	His	0.00
4	His	0.00
5	His	0.00
6	His	0.00
7	His	0.00
8	His	0.00
9	Ser	0.00
10	Ser	0.00
11	Gly	0.00
12	Val	0.00
13	Asp	0.00
14	Leu	0.00
15	Gly	0.00
16	Thr	0.00
17	Glu	0.00
18	Asn	0.00
19	Leu	0.00
20	Tyr	0.00
21	Phe	0.00
22	Q-1	0.00
23	I14	0.00
24	I37	0.00
25	I43	0.00
26	N44	0.00
27	I45	0.00
28	Asp	0.00
29	Ala	0.00
30	Gly	0.00
31	Thr	0.00
32	Phe	0.00
33	Ser	0.00
34	Pro	0.00
35	Tyr	0.00
36	Glu	0.00
37	His	0.00
38	Gly	0.00
39	Glu	0.00
40	Val	0.00
41	Phe	0.00
42	Val	0.00
43	Leu	0.00
44	Asp	0.00
45	Asp	0.00
46	Gly	0.00
47	Gly	0.00
48	Glu	0.00
49	Val	0.00
50	Asp	0.00
51	Leu	0.00
52	Asp	0.00
53	Gly	0.00
54	Asn	0.00
55	Tyr	0.00
56	Glu	0.00
57	Val	0.00
58	Pro	0.00
59	His	0.00
60	Thr	0.00
61	Leu	0.00
62	Val	0.00
63	Asp	0.00
64	Gly	0.00
65	Ala	0.00
66	Thr	0.00
67	Val	0.00
68	Leu	0.00
69	Asp	0.00
70	Gly	0.00
71	Val	0.00
72	Thr	0.00
73	Leu	0.00
74	Val	0.00
75	Asp	0.00
76	Gly	0.00
77	Val	0.00
78	Thr	0.00
79	Leu	0.00
80	Val	0.00
81	Asp	0.00
82	Gly	0.00
83	Val	0.00
84	Thr	0.00
85	Leu	0.00
86	Val	0.00
87	Asp	0.00
88	Gly	0.00
89	Val	0.00
90	Thr	0.00
91	Leu	0.00
92	Val	0.00
93	Asp	0.00
94	Gly	0.00
95	Val	0.00
96	Thr	0.00
97	Leu	0.00
98	Val	0.00
99	Asp	0.00
100	Gly	0.00

Chain B:

3% 61% 16% 23%

Label	Color
MET	Grey
HIS	Grey
HIS	Grey
HIS	Grey
HIS	Grey
HIS	Grey
HIS	Grey
SER	Grey
SER	Grey
GLY	Green
VAL	Green
ASP	Green
LEU	Green
GLY	Green
THR	Green
GLU	Green
ASN	Green
LEU	Green
TYR	Green
PHE	Green
GLN	Green
S0	Green
M1	Yellow
K2	Yellow
T7	Yellow
I18	Yellow
S22	Yellow
S36	Yellow
I37	Yellow
P41	Yellow
I42	Yellow
I43	Yellow
M44	Yellow
I45	Yellow
D46	Yellow
ALA	Red
GLY	Grey
THR	Grey
PHE	Grey
SER	Grey
PRO	Grey
TYR	Grey
GLU	Grey
HIS	Grey
GLY	Grey
GLU	Grey
VAL	Grey
PHE	Grey
VAL	Grey
LEU	Grey
ASP	Grey
ASP	Grey
GLY	Grey
GLY	Grey

Label	Color
VAL	Grey
ASP	Grey
LEU	Grey
ASP	Grey
LEU	Grey
GLY	Grey
ASN	Grey
TYR	Grey
GLU	Grey
ARG	Grey
PHE	Grey
LEU	Grey
ASP	Grey
ILE	Grey
ARG	Grey
THR	Grey
LYS	Grey
ASP	Grey
ASN	Grey
N87	Grey
L88	Yellow
R102	Yellow
K109	Yellow
V114	Yellow
I121	Yellow
W124	Yellow
V125	Yellow
Q128	Orange
I131	Red
P132	Red
VAL	Green
ASP	Green
GLU	Green
ASP	Green
G137	Red
L138	Red
C143	Red
L147	Yellow
E155	Yellow
R164	Yellow
Q165	Yellow
E173	Red
C176	Yellow
N177	Yellow
I178	Yellow

4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	98.42Å 98.42Å 120.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	76.25 – 2.80 19.69 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (76.25-2.80) 99.9 (19.69-2.80)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.78 (at 2.79Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.201 , 0.259 0.206 , 0.257	Depositor DCC
R_{free} test set	757 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.001	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 65.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3661	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.92% 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: 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	0.53	1/1874 (0.1%)	0.62	0/2537
1	B	0.46	0/1809	0.60	0/2447
All	All	0.50	1/3683 (0.0%)	0.61	0/4984

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	176	CYS	CB-SG	-6.03	1.72	1.82

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	136	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	1843	0	1881	35	0
1	B	1779	0	1831	31	0
2	A	15	0	0	0	0
2	B	10	0	0	0	0
3	A	11	0	0	0	0
3	B	3	0	0	0	0
All	All	3661	0	3712	63	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 (63) 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:232:MET:HE1	1:B:165:GLN:HG2	1.61	0.81
1:A:126:MET:O	1:A:130:LEU:HD23	1.80	0.80
1:A:85:ASP:HA	1:A:86:ASN:HB2	1.63	0.80
1:A:94:TYR:CZ	1:A:117:ILE:HD13	2.20	0.76
1:A:232:MET:HE2	1:B:164:ARG:HH12	1.53	0.73
1:B:178:ILE:HD12	1:B:213:LEU:HB2	1.70	0.72
1:A:133:VAL:HG12	1:A:133:VAL:O	1.90	0.70
1:A:85:ASP:HA	1:A:86:ASN:CB	2.23	0.69
1:B:218:CYS:SG	1:B:222:LEU:HG	2.36	0.66
1:A:14:ILE:O	1:A:217:ARG:HG3	1.99	0.61
1:A:88:LEU:HD13	1:A:124:TRP:CD2	2.36	0.59
1:B:18:ILE:N	1:B:18:ILE:HD12	2.19	0.58
1:A:178:ILE:HD11	1:A:266:PHE:HZ	1.69	0.57
1:A:113:VAL:HA	1:A:117:ILE:HD12	1.88	0.55
1:B:37:ILE:CD1	1:B:128:GLN:HB3	2.36	0.55
1:B:88:LEU:HD13	1:B:124:TRP:CE2	2.42	0.54
1:A:88:LEU:HD13	1:A:124:TRP:CG	2.43	0.54
1:B:214:VAL:HG23	1:B:241:VAL:HG13	1.88	0.54
1:A:183:VAL:HG13	1:A:193:LYS:O	2.07	0.54
1:B:37:ILE:HD11	1:B:128:GLN:HB3	1.89	0.54
1:A:267:LEU:HD23	1:A:272:LEU:HB2	1.90	0.53
1:B:41:PRO:HB2	1:B:155:GLU:HB3	1.90	0.53
1:A:232:MET:O	1:A:232:MET:HE2	2.10	0.52
1:B:18:ILE:N	1:B:18:ILE:CD1	2.73	0.52
1:A:43:ILE:O	1:A:43:ILE:CG2	2.58	0.50
1:B:121:ILE:O	1:B:125:VAL:HG23	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:121:ILE:HD12	1:A:159:PHE:CD2	2.47	0.50
1:A:218:CYS:O	1:A:245:HIS:HA	2.13	0.49
1:A:133:VAL:O	1:A:133:VAL:CG1	2.61	0.49
1:A:88:LEU:HD11	1:A:93:ILE:HG12	1.96	0.48
1:A:43:ILE:HG22	1:A:43:ILE:O	2.14	0.47
1:B:36:SER:O	1:B:37:ILE:HD13	2.13	0.47
1:A:93:ILE:HD12	1:A:120:ALA:HB1	1.97	0.47
1:B:22:SER:HB3	1:B:257:LEU:HD12	1.96	0.47
1:A:93:ILE:HD12	1:A:120:ALA:CB	2.45	0.47
1:A:121:ILE:CD1	1:A:159:PHE:CE2	2.98	0.47
1:A:85:ASP:CA	1:A:86:ASN:CB	2.91	0.47
1:B:236:VAL:HB	1:B:240:GLN:HB2	1.95	0.46
1:A:232:MET:HG3	1:A:233:PHE:N	2.30	0.45
1:B:1:MET:HE3	1:B:2:LYS:N	2.32	0.45
1:A:94:TYR:CZ	1:A:117:ILE:CD1	2.95	0.44
1:B:234:CYS:O	1:B:235:HIS:HB2	2.17	0.44
1:B:214:VAL:HG23	1:B:214:VAL:O	2.18	0.44
1:A:37:ILE:CG2	1:A:124:TRP:HZ3	2.31	0.44
1:A:192:GLN:HE22	1:A:222:LEU:HA	1.81	0.44
1:B:244:VAL:HG13	1:B:256:LEU:HD23	2.00	0.44
1:B:213:LEU:HD21	1:B:265:TYR:CD2	2.53	0.44
1:A:88:LEU:HB2	1:A:124:TRP:CZ3	2.53	0.43
1:B:45:ILE:HG22	1:B:45:ILE:O	2.18	0.43
1:B:7:THR:HG22	1:B:147:LEU:HD23	1.99	0.43
1:A:177:ASN:ND2	1:A:211:PRO:HA	2.33	0.43
1:B:88:LEU:HB2	1:B:124:TRP:CZ3	2.52	0.43
1:B:212:ASP:HB3	1:B:265:TYR:OH	2.18	0.43
1:A:201:VAL:HG11	1:A:234:CYS:HB3	2.00	0.42
1:B:2:LYS:HG3	1:B:272:LEU:HD21	2.01	0.42
1:B:1:MET:HE1	1:B:143:CYS:N	2.35	0.42
1:B:237:GLU:HG3	1:B:238:PRO:HD2	2.01	0.42
1:B:43:ILE:HG22	1:B:43:ILE:O	2.19	0.42
1:A:245:HIS:CE1	1:A:256:LEU:HD21	2.55	0.41
1:B:114:VAL:HG13	1:B:165:GLN:HE22	1.85	0.41
1:A:232:MET:CE	1:B:164:ARG:HH12	2.28	0.41
1:B:37:ILE:CG2	1:B:124:TRP:HZ3	2.33	0.41
1:A:94:TYR:CE2	1:A:117:ILE:HD11	2.56	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	230/295 (78%)	221 (96%)	8 (4%)	1 (0%)	34	66
1	B	220/295 (75%)	209 (95%)	11 (5%)	0	100	100
All	All	450/590 (76%)	430 (96%)	19 (4%)	1 (0%)	47	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	133	VAL

5.3.2 Protein sidechains

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	214/265 (81%)	208 (97%)	6 (3%)	43	77
1	B	206/265 (78%)	197 (96%)	9 (4%)	28	61
All	All	420/530 (79%)	405 (96%)	15 (4%)	35	69

All (15) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ILE
1	A	121	ILE
1	A	170	VAL
1	A	173	GLU
1	A	210	SER

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Mol	Chain	Res	Type
1	A	232	MET
1	B	46	ASP
1	B	87	ASN
1	B	102	ARG
1	B	109	LYS
1	B	128	GLN
1	B	176	CYS
1	B	210	SER
1	B	228	GLU
1	B	263	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	95	GLN
1	A	99	ASN
1	A	174	ASN
1	A	177	ASN
1	A	185	GLN
1	A	198	GLN
1	A	245	HIS
1	B	87	ASN
1	B	177	ASN
1	B	185	GLN
1	B	198	GLN
1	B	199	ASN
1	B	220	ASN
1	B	240	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 ligands are 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	$\# Z > 2$
2	SO4	B	1274	-	4,4,4	0.13	0	6,6,6	0.22	0
2	SO4	A	1274	-	4,4,4	0.15	0	6,6,6	0.28	0
2	SO4	A	1273	-	4,4,4	0.18	0	6,6,6	0.18	0
2	SO4	B	1273	-	4,4,4	0.14	0	6,6,6	0.18	0
2	SO4	A	1275	-	4,4,4	0.14	0	6,6,6	0.20	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, 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	235/295 (79%)	-0.23	7 (2%)	50 40	33, 38, 47, 54	1 (0%)
1	B	228/295 (77%)	0.04	10 (4%)	34 24	31, 39, 46, 48	0
All	All	463/590 (78%)	-0.09	17 (3%)	41 31	31, 38, 46, 54	1 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	135	GLU	4.9
1	B	248	SER	4.3
1	B	251	TYR	4.0
1	A	188	SER	3.9
1	A	243	CYS	3.7
1	B	131	ILE	3.3
1	A	134	ASP	3.2
1	B	138	LEU	3.1
1	B	137	GLY	3.0
1	A	187	SER	2.4
1	B	46	ASP	2.3
1	A	133	VAL	2.2
1	B	187	SER	2.1
1	B	143	CYS	2.1
1	A	251	TYR	2.1
1	B	132	PRO	2.0
1	B	173	GLU	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, 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(\AA^2)	Q<0.9
2	SO4	B	1274	5/5	0.80	0.35	103,103,103,103	0
2	SO4	A	1274	5/5	0.93	0.18	77,77,77,77	0
2	SO4	A	1275	5/5	0.94	0.36	76,76,76,76	0
2	SO4	B	1273	5/5	0.98	0.10	51,51,52,52	0
2	SO4	A	1273	5/5	0.98	0.13	41,41,41,41	0

6.5 Other polymers [i](#)

There are no such residues in this entry.