Full wwPDB X-ray Structure Validation Report (i)

Jun 13, 2024 – 07:10 AM EDT

PDB ID	:	4IAP
Title	:	Crystal structure of PH domain of Osh3 from Saccharomyces cerevisiae
Authors	:	Tong, J.; Im, Y.J.
Deposited on	:	2012-12-07
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*
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 (i)) were used in the production of this report:

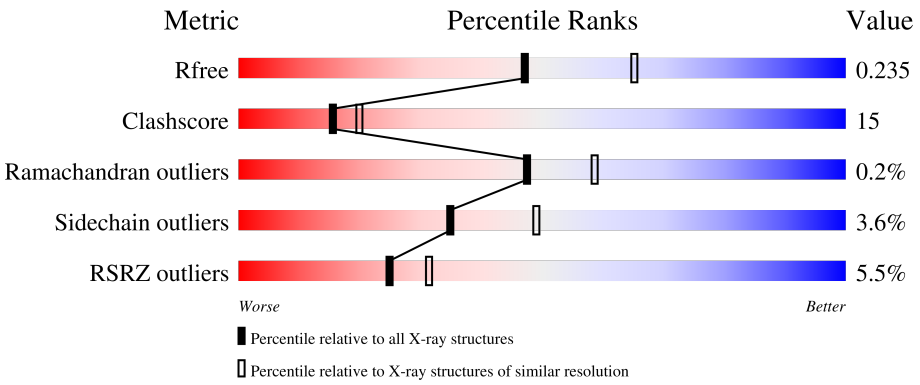
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 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}	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 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	260	5% 73% 25% • •
1	B	260	6% 66% 31% • •

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	SO4	A	1403	-	-	X	-

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 4283 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 Oxysterol-binding protein homolog 3,Endolysin,Oxysterol-binding protein homolog 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	256	2070	1312	370	381	7	0	0	0
1	B	256	2070	1312	370	381	7	0	0	0

There are 26 discrepancies between the modelled and reference sequences:

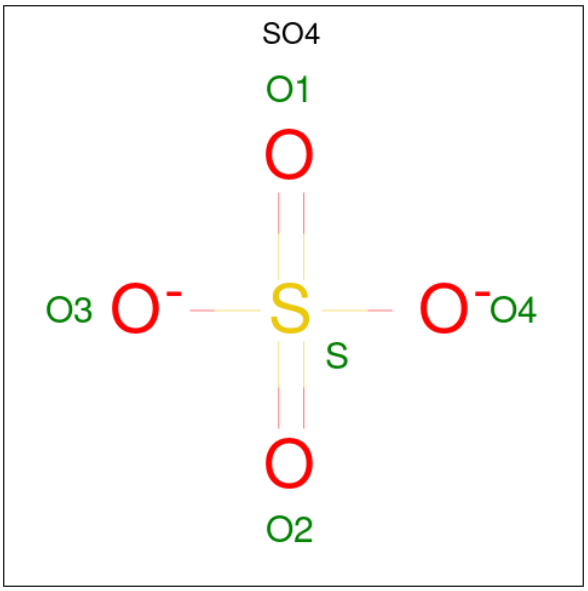
Chain	Residue	Modelled	Actual	Comment	Reference
A	217	GLY	-	expression tag	UNP P38713
A	218	SER	-	expression tag	UNP P38713
A	219	ALA	-	expression tag	UNP P38713
A	220	MET	-	expression tag	UNP P38713
A	1000	VAL	-	linker	UNP P38713
A	1001	ASP	-	linker	UNP P38713
A	1012	GLY	ARG	see sequence details	UNP P00720
A	1020	ASN	ASP	engineered mutation	UNP P00720
A	1054	THR	CYS	engineered mutation	UNP P00720
A	1097	ALA	CYS	engineered mutation	UNP P00720
A	1137	ARG	ILE	see sequence details	UNP P00720
A	1162	VAL	-	linker	UNP P00720
A	1163	ASP	-	linker	UNP P00720
B	217	GLY	-	expression tag	UNP P38713
B	218	SER	-	expression tag	UNP P38713
B	219	ALA	-	expression tag	UNP P38713
B	220	MET	-	expression tag	UNP P38713
B	1000	VAL	-	linker	UNP P38713
B	1001	ASP	-	linker	UNP P38713
B	1012	GLY	ARG	see sequence details	UNP P00720
B	1020	ASN	ASP	engineered mutation	UNP P00720
B	1054	THR	CYS	engineered mutation	UNP P00720
B	1097	ALA	CYS	engineered mutation	UNP P00720
B	1137	ARG	ILE	see sequence details	UNP P00720

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	1162	VAL	-	linker	UNP P00720
B	1163	ASP	-	linker	UNP P00720

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 3 is water.

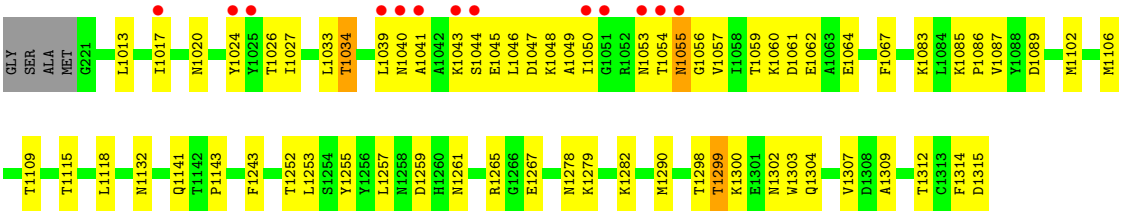
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	72	72	72	0	0
			Total	O		
3	B	31	31	31	0	0

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.

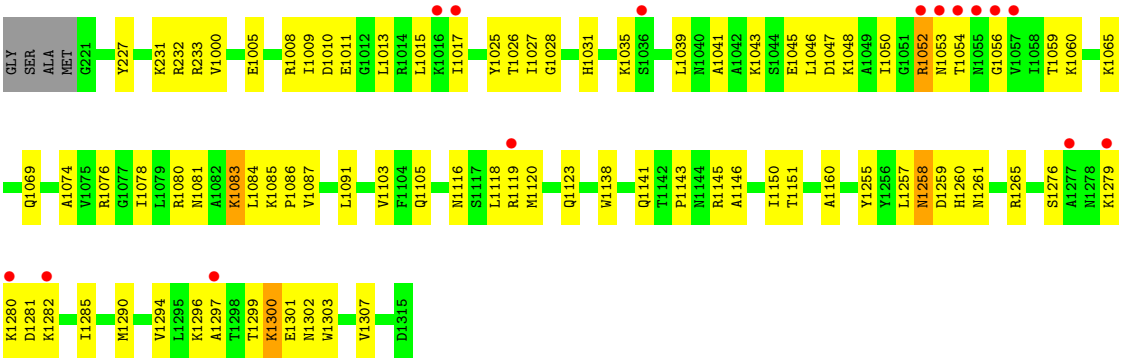
• Molecule 1: Oxysterol-binding protein homolog 3,Endolysin,Oxysterol-binding protein homolog 3

Chain A:



• Molecule 1: Oxysterol-binding protein homolog 3,Endolysin,Oxysterol-binding protein homolog 3

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	98.03Å 91.31Å 84.13Å 90.00° 81.42° 90.00°	Depositor
Resolution (Å)	40.02 – 2.30 40.02 – 2.28	Depositor EDS
% Data completeness (in resolution range)	99.4 (40.02-2.30) 97.8 (40.02-2.28)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.22 (at 2.27Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.242 , 0.274 0.242 , 0.235	Depositor DCC
R_{free} test set	1671 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	37.0	Xtriage
Anisotropy	0.112	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 43.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4283	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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: 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	0.39	0/2107	0.60	0/2839
1	B	0.33	0/2107	0.54	0/2839
All	All	0.36	0/4214	0.57	0/5678

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	2070	0	2089	50	0
1	B	2070	0	2089	74	0
2	A	25	0	0	3	0
2	B	15	0	0	1	0
3	A	72	0	0	1	0
3	B	31	0	0	0	0
All	All	4283	0	4178	124	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 15.

All (124) 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:1059:THR:HB	1:A:1062:GLU:HG3	1.44	0.97
1:B:1078:ILE:HD11	1:B:1103:VAL:HG21	1.46	0.94
1:B:1047:ASP:OD1	1:B:1054:THR:HA	1.72	0.90
1:A:1279:LYS:HD2	1:A:1300:LYS:HE3	1.54	0.86
1:A:1309:ALA:O	1:A:1312:THR:HG22	1.76	0.84
1:A:1083:LYS:HE3	1:A:1115:THR:HG22	1.68	0.75
1:B:1076:ARG:O	1:B:1080:ARG:HG3	1.87	0.73
1:B:1282:LYS:HE3	1:B:1300:LYS:HG3	1.71	0.72
1:B:1258:ASN:HD21	1:B:1261:ASN:H	1.38	0.71
1:B:1280:LYS:HD2	1:B:1281:ASP:OD2	1.91	0.70
1:B:1146:ALA:O	1:B:1150:ILE:HG12	1.92	0.70
1:B:1087:VAL:HG21	1:B:1118:LEU:HB3	1.73	0.69
1:A:1282:LYS:HZ2	1:A:1299:THR:HA	1.56	0.69
1:A:1083:LYS:O	1:A:1083:LYS:HD3	1.93	0.69
1:B:1258:ASN:ND2	1:B:1261:ASN:H	1.94	0.65
1:B:1085:LYS:HB3	1:B:1086:PRO:HD3	1.79	0.64
1:A:1314:PHE:O	1:A:1315:ASP:HB2	1.97	0.63
1:B:1074:ALA:O	1:B:1078:ILE:HG12	1.98	0.63
1:A:1039:LEU:O	1:A:1039:LEU:HD23	1.98	0.62
1:B:1039:LEU:HD11	1:B:1043:LYS:NZ	2.14	0.62
1:A:1059:THR:HG22	1:A:1060:LYS:N	2.16	0.61
1:B:1258:ASN:HD22	1:B:1258:ASN:C	2.03	0.61
1:B:1282:LYS:HE2	1:B:1299:THR:HA	1.82	0.61
1:B:1080:ARG:HG2	1:B:1080:ARG:HH11	1.65	0.61
1:A:1044:SER:HA	1:A:1047:ASP:HB2	1.82	0.61
1:B:1041:ALA:O	1:B:1045:GLU:HG2	2.01	0.61
1:B:227:TYR:OH	1:B:1259:ASP:HB2	2.00	0.60
1:B:1017:ILE:HD13	1:B:1027:ILE:HD12	1.84	0.60
1:B:232:ARG:HD3	1:B:1005:GLU:OE1	2.02	0.60
1:A:1143:PRO:HD2	2:A:1404:SO4:O3	2.03	0.59
1:B:231:LYS:HG3	1:B:1294:VAL:HB	1.85	0.59
1:B:1050:ILE:HD12	1:B:1053:ASN:HB2	1.86	0.58
1:B:1039:LEU:HD13	1:B:1039:LEU:O	2.05	0.57
1:A:1024:TYR:HB3	1:A:1034:THR:O	2.04	0.57
1:B:1258:ASN:ND2	1:B:1260:HIS:H	2.03	0.57
1:B:232:ARG:NH1	1:B:1008:ARG:HH12	2.02	0.56
1:B:1279:LYS:HB2	1:B:1303:TRP:CH2	2.40	0.56
1:B:1017:ILE:HD11	1:B:1046:LEU:HD22	1.88	0.55
1:B:1303:TRP:O	1:B:1307:VAL:HG23	2.05	0.55
1:B:1282:LYS:NZ	1:B:1300:LYS:HE3	2.21	0.55
1:B:232:ARG:HH11	1:B:1008:ARG:HH12	1.52	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1065:LYS:O	1:B:1069:GLN:HG3	2.08	0.54
1:A:1026:THR:HG22	1:A:1027:ILE:N	2.23	0.53
1:A:1304:GLN:HA	1:A:1307:VAL:CG1	2.39	0.53
1:B:1282:LYS:HE3	1:B:1300:LYS:N	2.23	0.53
1:A:1043:LYS:HZ2	1:A:1055:ASN:C	2.12	0.52
1:A:1059:THR:HG22	1:A:1061:ASP:H	1.74	0.52
1:B:1119:ARG:O	1:B:1123:GLN:HG3	2.10	0.52
1:A:1050:ILE:HD12	1:A:1050:ILE:N	2.24	0.52
1:B:1297:ALA:HB1	1:B:1302:ASN:HD22	1.76	0.51
1:A:1303:TRP:O	1:A:1307:VAL:HG12	2.11	0.51
1:A:1041:ALA:O	1:A:1045:GLU:HG2	2.11	0.51
1:B:1048:LYS:O	1:B:1048:LYS:HD3	2.10	0.51
1:A:1102:MET:O	1:A:1106:MET:HG2	2.11	0.51
1:B:1000:VAL:HG21	1:B:1009:ILE:CD1	2.41	0.50
1:B:1078:ILE:HD13	1:B:1084:LEU:HD13	1.93	0.50
1:B:1052:ARG:O	1:B:1054:THR:HG23	2.10	0.50
1:A:1054:THR:HB	1:A:1057:VAL:O	2.12	0.50
1:A:1087:VAL:HG21	1:A:1118:LEU:HB3	1.92	0.50
1:B:1015:LEU:HD22	1:B:1015:LEU:N	2.26	0.50
1:A:1054:THR:O	1:A:1055:ASN:HB3	2.12	0.50
1:A:1278:ASN:HA	2:A:1403:SO4:S	2.52	0.50
1:B:1047:ASP:CG	1:B:1054:THR:HG22	2.32	0.50
1:B:1080:ARG:HG2	1:B:1080:ARG:NH1	2.24	0.50
1:B:1116:ASN:O	1:B:1120:MET:HG3	2.12	0.49
1:B:1087:VAL:O	1:B:1091:LEU:HG	2.12	0.49
1:B:1059:THR:HG22	1:B:1060:LYS:N	2.27	0.49
1:A:1300:LYS:NZ	1:A:1300:LYS:HB2	2.28	0.49
1:A:1314:PHE:O	1:A:1315:ASP:CB	2.60	0.48
1:A:1017:ILE:CD1	1:A:1056:GLY:HA2	2.44	0.48
1:B:1265:ARG:HD3	2:B:1401:SO4:O3	2.13	0.48
1:B:1026:THR:HG22	1:B:1027:ILE:N	2.29	0.48
1:B:1039:LEU:HD11	1:B:1043:LYS:HZ3	1.79	0.47
1:B:1039:LEU:HD13	1:B:1039:LEU:C	2.34	0.47
1:B:1000:VAL:HG21	1:B:1009:ILE:HD11	1.96	0.47
1:A:1048:LYS:O	1:A:1048:LYS:HD3	2.14	0.47
1:A:1257:LEU:HB2	1:A:1265:ARG:CZ	2.45	0.47
1:B:1027:ILE:HG12	1:B:1028:GLY:N	2.30	0.47
1:B:1054:THR:C	1:B:1056:GLY:H	2.18	0.47
1:A:1299:THR:HG23	1:A:1302:ASN:CB	2.45	0.46
1:B:1081:ASN:OD1	1:B:1083:LYS:HB2	2.14	0.46
1:A:1282:LYS:HZ2	1:A:1299:THR:CA	2.27	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1020:ASN:ND2	1:A:1026:THR:OG1	2.49	0.46
1:A:1299:THR:HG23	1:A:1302:ASN:HB2	1.97	0.46
1:A:1304:GLN:HA	1:A:1307:VAL:HG12	1.97	0.46
1:A:1085:LYS:HB3	1:A:1086:PRO:HD3	1.98	0.46
1:B:1026:THR:HG23	1:B:1031:HIS:O	2.15	0.46
1:B:1276:SER:HB3	1:B:1285:ILE:HB	1.98	0.46
1:A:1047:ASP:OD2	1:A:1053:ASN:HA	2.15	0.46
1:A:1049:ALA:HB3	1:A:1050:ILE:HD12	1.98	0.46
1:A:1253:LEU:O	1:A:1267:GLU:HA	2.15	0.45
1:B:1141:GLN:C	1:B:1143:PRO:HD3	2.37	0.45
1:B:233:ARG:NH2	1:B:1285:ILE:HD13	2.31	0.45
1:A:1059:THR:CG2	1:A:1060:LYS:N	2.79	0.45
1:B:1035:LYS:O	1:B:1035:LYS:HG3	2.17	0.45
1:B:1027:ILE:HG12	1:B:1028:GLY:H	1.82	0.45
1:B:1255:TYR:CE1	1:B:1265:ARG:HB3	2.52	0.45
1:A:1043:LYS:HD3	1:A:1055:ASN:HA	2.00	0.44
1:B:1083:LYS:CA	1:B:1083:LYS:HE2	2.47	0.44
1:B:1083:LYS:HE2	1:B:1083:LYS:O	2.18	0.44
1:A:1298:THR:HG22	1:A:1298:THR:O	2.17	0.43
1:B:1010:ASP:HB3	1:B:1145:ARG:NE	2.33	0.43
1:B:1026:THR:HG23	1:B:1031:HIS:C	2.38	0.43
1:B:1151:THR:HB	1:B:1160:ALA:HB2	2.01	0.43
1:B:1105:GLN:HB2	1:B:1145:ARG:CZ	2.48	0.43
1:A:1278:ASN:HA	2:A:1403:SO4:O4	2.19	0.43
1:A:1085:LYS:NZ	1:A:1089:ASP:OD2	2.50	0.43
1:B:1300:LYS:HB2	1:B:1300:LYS:HZ3	1.84	0.43
1:B:1083:LYS:HE2	1:B:1083:LYS:HA	2.00	0.42
1:B:1039:LEU:HD11	1:B:1043:LYS:HZ2	1.85	0.42
1:A:1013:LEU:C	1:A:1013:LEU:HD23	2.39	0.42
1:A:1033:LEU:HD21	1:A:1046:LEU:HD13	2.02	0.42
1:B:1025:TYR:CE2	1:B:1039:LEU:HD23	2.54	0.42
1:B:1138:TRP:CZ2	1:B:1146:ALA:HA	2.54	0.42
1:A:1064:GLU:O	1:A:1067:PHE:HB3	2.20	0.42
1:B:1299:THR:HG23	1:B:1301:GLU:H	1.84	0.42
1:B:1008:ARG:HG3	1:B:1013:LEU:HD12	2.01	0.41
1:A:1257:LEU:HD22	1:A:1257:LEU:O	2.20	0.41
1:B:1279:LYS:HB2	1:B:1303:TRP:CZ3	2.55	0.41
1:A:1261:ASN:ND2	3:A:1513:HOH:O	2.54	0.40
1:B:1281:ASP:O	1:B:1296:LYS:HE3	2.21	0.40
1:A:1047:ASP:O	1:A:1050:ILE:O	2.38	0.40
1:A:1243:PHE:O	1:A:1255:TYR:HA	2.21	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1258:ASN:HD22	1:B:1260:HIS:H	1.68	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	254/260 (98%)	243 (96%)	10 (4%)	1 (0%)	34	42
1	B	254/260 (98%)	238 (94%)	16 (6%)	0	100	100
All	All	508/520 (98%)	481 (95%)	26 (5%)	1 (0%)	47	58

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1034	THR

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	220/222 (99%)	211 (96%)	9 (4%)	30	43
1	B	220/222 (99%)	213 (97%)	7 (3%)	39	54
All	All	440/444 (99%)	424 (96%)	16 (4%)	35	49

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1040	ASN
1	A	1055	ASN
1	A	1109	THR
1	A	1132	ASN
1	A	1141	GLN
1	A	1252	THR
1	A	1259	ASP
1	A	1290	MET
1	A	1299	THR
1	B	1011	GLU
1	B	1052	ARG
1	B	1083	LYS
1	B	1257	LEU
1	B	1258	ASN
1	B	1290	MET
1	B	1300	LYS

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

Mol	Chain	Res	Type
1	A	1055	ASN
1	A	1116	ASN
1	A	1122	GLN
1	A	1261	ASN
1	A	1302	ASN
1	A	1304	GLN
1	B	1122	GLN
1	B	1132	ASN
1	B	1141	GLN
1	B	1258	ASN
1	B	1261	ASN
1	B	1262	GLN
1	B	1302	ASN
1	B	1311	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

8 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	A	1405	-	4,4,4	0.37	0	6,6,6	0.10	0
2	SO4	B	1401	-	4,4,4	0.37	0	6,6,6	0.15	0
2	SO4	A	1402	-	4,4,4	0.38	0	6,6,6	0.10	0
2	SO4	A	1403	-	4,4,4	0.33	0	6,6,6	0.16	0
2	SO4	A	1401	-	4,4,4	0.26	0	6,6,6	0.20	0
2	SO4	A	1404	-	4,4,4	0.35	0	6,6,6	0.12	0
2	SO4	B	1402	-	4,4,4	0.37	0	6,6,6	0.11	0
2	SO4	B	1403	-	4,4,4	0.35	0	6,6,6	0.10	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.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1401	SO4	1	0
2	A	1403	SO4	2	0
2	A	1404	SO4	1	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 (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	256/260 (98%)	0.25	13 (5%)	28	35	17, 33, 78, 87	0
1	B	256/260 (98%)	0.49	15 (5%)	22	28	31, 47, 74, 93	0
All	All	512/520 (98%)	0.37	28 (5%)	25	31	17, 42, 76, 93	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1044	SER	5.6
1	A	1025	TYR	4.8
1	A	1039	LEU	4.3
1	B	1052	ARG	3.9
1	B	1056	GLY	3.6
1	A	1051	GLY	3.5
1	B	1057	VAL	3.5
1	B	1054	THR	3.4
1	A	1040	ASN	3.2
1	A	1053	ASN	3.2
1	B	1297	ALA	3.1
1	A	1017	ILE	3.0
1	A	1024	TYR	2.8
1	A	1041	ALA	2.7
1	B	1280	LYS	2.7
1	A	1054	THR	2.7
1	B	1036	SER	2.6
1	B	1017	ILE	2.5
1	B	1282	LYS	2.4
1	B	1279	LYS	2.4
1	B	1053	ASN	2.4
1	A	1055	ASN	2.3
1	B	1055	ASN	2.3
1	A	1050	ILE	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	1043	LYS	2.2
1	B	1016	LYS	2.2
1	B	1119	ARG	2.1
1	B	1277	ALA	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
2	SO4	A	1403	5/5	0.69	0.39	117,117,118,118	0
2	SO4	A	1405	5/5	0.86	0.18	102,102,103,103	0
2	SO4	A	1402	5/5	0.91	0.15	84,84,84,85	0
2	SO4	B	1401	5/5	0.94	0.18	59,60,62,62	0
2	SO4	B	1402	5/5	0.96	0.15	97,97,97,97	0
2	SO4	B	1403	5/5	0.98	0.16	53,55,56,57	0
2	SO4	A	1401	5/5	0.99	0.16	40,41,44,45	0
2	SO4	A	1404	5/5	0.99	0.12	33,33,36,37	0

6.5 Other polymers (i)

There are no such residues in this entry.