Full wwPDB X-ray Structure Validation Report (i)

Jan 31, 2016 – 09:22 PM GMT

PDB ID	:	1OPX
Title	:	Crystal structure of the traffic ATPase (HP0525) of the Helicobacter pylori type IV secretion system bound by sulfate
Authors	:	Savvides, S.N.; Yeo, H.J.; Beck, M.R.; Blaesing, F.; Lurz, R.; Lanka, E.; Buhrdorf, R.; Fischer, W.; Haas, R.; Waksman, G.
Deposited on	:	2003-03-06
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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

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

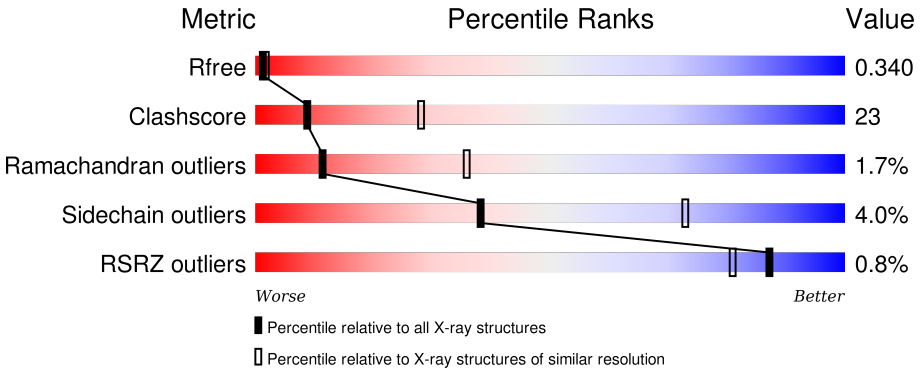
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 2.80 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}	91344	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (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. 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	330	% 58% 36%
1	B	330	% 56% 38%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 5128 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.

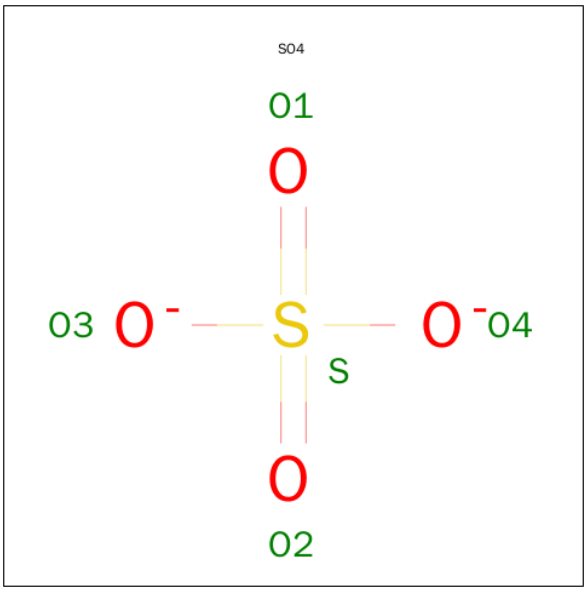
- Molecule 1 is a protein called virB11 homolog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	Se	0	0	0
			2531	1607	431	479	8	6			
1	B	323	Total	C	N	O	S	Se	0	0	0
			2536	1609	432	481	8	6			

There are 12 discrepancies between the modelled and reference sequences:

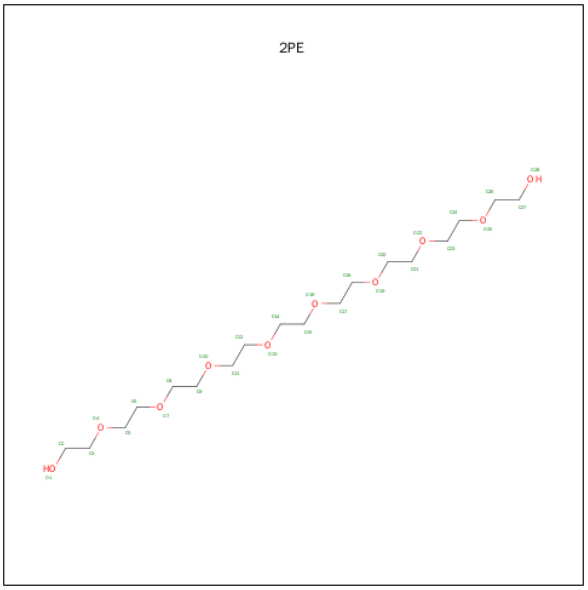
Chain	Residue	Modelled	Actual	Comment	Reference
A	42	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
A	82	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
A	192	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
A	239	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
A	287	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
A	312	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
B	1042	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
B	1082	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
B	1192	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
B	1239	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
B	1287	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04
B	1312	MSE	MET	MODIFIED RESIDUE	UNP Q7BK04

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



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

- Molecule 3 is NONAETHYLENE GLYCOL (three-letter code: 2PE) (formula: $C_{18}H_{38}O_{10}$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 28 18 10	0	0

- Molecule 4 is water.

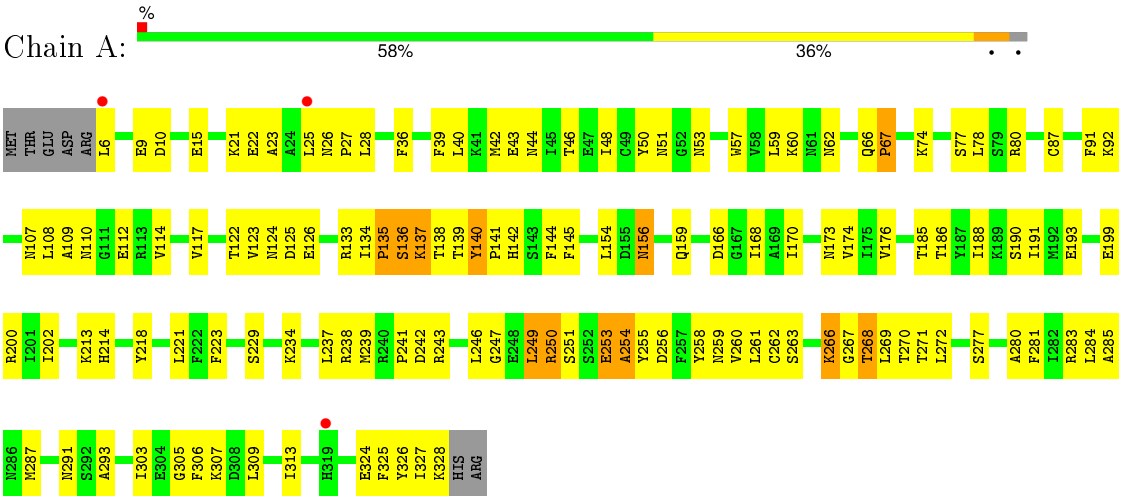
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	19	Total O 19 19	0	0
4	B	4	Total O 4 4	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

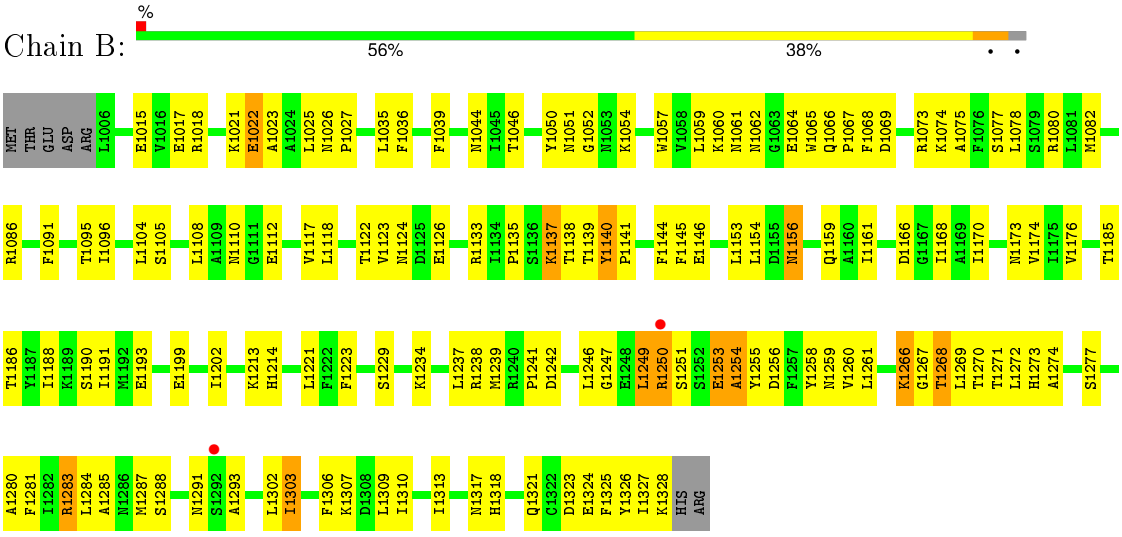
- Molecule 1: virB11 homolog

Chain A:



- Molecule 1: virB11 homolog

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α, β, γ	111.28Å 111.28Å 230.24Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.63 – 2.80 29.63 – 2.80	Depositor EDS
% Data completeness (in resolution range)	72.3 (29.63-2.80) 80.8 (29.63-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.12	Depositor
$< I/\sigma(I) >$ [1]	7.84 (at 2.80Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.250 , 0.324 0.266 , 0.340	Depositor DCC
R_{free} test set	861 reflections (5.19%)	DCC
Wilson B-factor (Å^2)	28.9	Xtriage
Anisotropy	0.367	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 65.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Outliers	0 of 18872 reflections	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	5128	wwPDB-VP
Average B, all atoms (Å^2)	31.0	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 54.01 % 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 3.8824e-05.The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 2PE, 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	0.48	0/2574	0.67	0/3465
1	B	0.47	0/2579	0.66	0/3470
All	All	0.47	0/5153	0.67	0/6935

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

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	2531	0	2474	122	0
1	B	2536	0	2480	127	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	B	28	0	38	5	0
4	A	19	0	0	1	0
4	B	4	0	0	0	0
All	All	5128	0	4992	237	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 23.

All (237) 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:145:PHE:HZ	1:A:186:THR:HG22	1.36	0.89
1:B:1145:PHE:HZ	1:B:1186:THR:HG22	1.37	0.88
1:B:1139:THR:HB	1:B:1213:LYS:HE2	1.57	0.85
1:A:139:THR:HB	1:A:213:LYS:HE2	1.59	0.84
1:A:237:LEU:HD11	1:A:260:VAL:HG22	1.61	0.83
1:B:1073:ARG:NH2	3:B:2000:2PE:H121	1.93	0.82
1:B:1174:VAL:HG13	1:B:1269:LEU:HD13	1.61	0.82
1:B:1108:LEU:HD12	1:B:1112:GLU:HG3	1.62	0.82
1:B:1237:LEU:HD11	1:B:1260:VAL:HG22	1.62	0.82
1:A:174:VAL:HG13	1:A:269:LEU:HD13	1.63	0.79
1:B:1156:ASN:HB2	1:B:1159:GLN:HE21	1.48	0.77
1:A:266:LYS:HD3	1:B:1318:HIS:CE1	2.20	0.77
1:A:266:LYS:HD3	1:B:1318:HIS:HE1	1.49	0.76
1:B:1069:ASP:HB2	3:B:2000:2PE:H52	1.65	0.76
1:A:156:ASN:HB2	1:A:159:GLN:HE21	1.51	0.75
1:B:1025:LEU:HD13	1:B:1091:PHE:CE1	2.21	0.75
1:B:1104:LEU:HD12	1:B:1105:SER:H	1.54	0.73
1:B:1284:LEU:HD13	1:B:1306:PHE:CD2	2.23	0.72
1:B:1156:ASN:HB2	1:B:1159:GLN:NE2	2.04	0.72
1:B:1110:ASN:HB2	1:B:1112:GLU:OE2	1.89	0.72
1:B:1108:LEU:HD12	1:B:1112:GLU:CG	2.20	0.71
1:B:1246:LEU:HB2	1:B:1270:THR:HB	1.72	0.70
1:A:168:ILE:HD11	1:A:191:ILE:HD12	1.73	0.70
1:B:1168:ILE:HD11	1:B:1191:ILE:HD12	1.74	0.69
1:A:246:LEU:HB2	1:A:270:THR:HB	1.73	0.68
1:B:1173:ASN:OD1	1:B:1268:THR:HB	1.92	0.68
1:A:156:ASN:HB2	1:A:159:GLN:NE2	2.09	0.68
1:A:261:LEU:HB3	1:A:309:LEU:HD13	1.75	0.68
1:A:173:ASN:OD1	1:A:268:THR:HB	1.93	0.68
1:A:199:GLU:OE1	1:A:242:ASP:HB3	1.94	0.68
1:A:272:LEU:HD11	1:A:287:MSE:HE1	1.76	0.67
1:A:263:SER:HB2	1:B:1273:HIS:HB3	1.77	0.66
1:B:1139:THR:CB	1:B:1213:LYS:HE2	2.26	0.66
1:B:1234:LYS:HE2	1:B:1238:ARG:HH21	1.61	0.65
1:B:1193:GLU:HA	1:B:1214:HIS:HD2	1.63	0.64
1:A:193:GLU:HA	1:A:214:HIS:CD2	2.33	0.64
1:B:1096:ILE:HG12	1:B:1118:LEU:HD11	1.81	0.63
1:B:1199:GLU:OE1	1:B:1242:ASP:HB3	1.97	0.63
1:A:139:THR:CB	1:A:213:LYS:HE2	2.29	0.63
1:B:1272:LEU:HD11	1:B:1287:MSE:HE1	1.79	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1193:GLU:HA	1:B:1214:HIS:CD2	2.34	0.62
1:B:1256:ASP:O	1:B:1260:VAL:HG23	1.99	0.62
1:A:176:VAL:O	1:A:271:THR:HA	1.99	0.62
1:A:193:GLU:HA	1:A:214:HIS:HD2	1.65	0.62
1:B:1017:GLU:HB3	1:B:1021:LYS:HE2	1.80	0.62
1:B:1261:LEU:HB3	1:B:1309:LEU:HD13	1.82	0.62
1:B:1017:GLU:O	1:B:1021:LYS:HG3	2.00	0.61
1:B:1285:ALA:HB2	1:B:1303:ILE:HG12	1.82	0.61
1:A:284:LEU:HD13	1:A:306:PHE:CD2	2.35	0.61
1:A:40:LEU:HD23	1:A:48:ILE:HD12	1.81	0.61
1:A:234:LYS:HE2	1:A:238:ARG:HH21	1.66	0.61
1:B:1133:ARG:HG3	1:B:1133:ARG:HH11	1.66	0.60
1:B:1104:LEU:HD12	1:B:1105:SER:N	2.14	0.60
1:A:36:PHE:O	1:A:40:LEU:HG	2.01	0.60
1:A:261:LEU:CB	1:A:309:LEU:HD13	2.32	0.60
1:A:6:LEU:HD12	1:B:1054:LYS:NZ	2.17	0.60
1:A:229:SER:OG	1:A:253:GLU:HG2	2.01	0.59
1:A:256:ASP:O	1:A:260:VAL:HG23	2.02	0.59
1:A:25:LEU:HD13	1:A:91:PHE:CE1	2.37	0.59
1:B:1176:VAL:O	1:B:1271:THR:HA	2.03	0.59
1:B:1073:ARG:HH22	3:B:2000:2PE:H121	1.66	0.58
1:B:1223:PHE:HE2	1:B:1250:ARG:HH21	1.51	0.58
1:A:135:PRO:O	1:A:136:SER:C	2.41	0.58
1:A:43:GLU:OE1	1:A:43:GLU:HA	2.03	0.58
1:B:1193:GLU:HG2	1:B:1214:HIS:NE2	2.18	0.58
1:A:40:LEU:HD23	1:A:48:ILE:CD1	2.34	0.58
1:B:1133:ARG:HG3	1:B:1133:ARG:NH1	2.17	0.58
1:B:1168:ILE:CD1	1:B:1191:ILE:HD12	2.33	0.57
1:B:1325:PHE:CE2	1:B:1327:ILE:HD11	2.38	0.57
1:B:1064:GLU:OE2	1:B:1066:GLN:HG3	2.03	0.57
1:A:327:ILE:HG22	1:A:328:LYS:N	2.19	0.57
1:A:168:ILE:CD1	1:A:191:ILE:HD12	2.33	0.57
1:B:1096:ILE:HG12	1:B:1118:LEU:CD1	2.34	0.57
1:B:1153:LEU:HG	1:B:1321:GLN:NE2	2.20	0.57
1:B:1325:PHE:CD2	1:B:1327:ILE:HD11	2.40	0.56
1:B:1174:VAL:CG1	1:B:1269:LEU:HD13	2.33	0.56
1:A:125:ASP:OD1	1:A:126:GLU:HG3	2.05	0.56
1:A:108:LEU:HB2	1:A:112:GLU:OE1	2.05	0.56
1:A:60:LYS:HB2	1:A:62:ASN:OD1	2.04	0.56
1:B:1060:LYS:HB2	1:B:1062:ASN:OD1	2.05	0.56
1:A:10:ASP:HB3	1:B:1078:LEU:HD12	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:193:GLU:HG2	1:A:214:HIS:NE2	2.21	0.56
1:A:60:LYS:HE3	1:A:66:GLN:OE1	2.06	0.56
1:A:188:ILE:HA	1:A:191:ILE:HG12	1.88	0.55
1:B:1281:PHE:CE2	1:B:1307:LYS:HA	2.42	0.55
1:A:281:PHE:CE2	1:A:307:LYS:HA	2.41	0.55
1:B:1223:PHE:HE2	1:B:1250:ARG:NH2	2.04	0.55
1:A:50:TYR:C	1:A:51:ASN:HD22	2.10	0.55
1:A:154:LEU:HB3	1:A:156:ASN:ND2	2.22	0.54
1:A:305:GLY:O	1:A:309:LEU:HG	2.08	0.54
1:A:137:LYS:O	1:A:138:THR:OG1	2.25	0.54
1:B:1280:ALA:O	1:B:1284:LEU:HG	2.07	0.54
1:A:221:LEU:HD21	1:A:239:MSE:HE1	1.90	0.54
1:A:26:ASN:HB3	1:A:27:PRO:HD3	1.90	0.54
1:B:1145:PHE:HZ	1:B:1186:THR:CG2	2.17	0.54
1:A:140:TYR:HD1	1:A:140:TYR:H	1.56	0.54
1:B:1026:ASN:HB3	1:B:1027:PRO:HD3	1.89	0.54
1:A:28:LEU:HD13	1:A:87:CYS:HB3	1.90	0.54
1:B:1327:ILE:HG22	1:B:1328:LYS:N	2.23	0.53
1:B:1124:ASN:OD1	1:B:1126:GLU:N	2.36	0.53
1:B:1108:LEU:HB2	1:B:1112:GLU:HG2	1.90	0.53
1:B:1154:LEU:HB3	1:B:1156:ASN:ND2	2.24	0.53
1:B:1188:ILE:HA	1:B:1191:ILE:HG12	1.90	0.53
1:B:1261:LEU:CB	1:B:1309:LEU:HD13	2.38	0.53
1:A:223:PHE:HE2	1:A:250:ARG:HH21	1.57	0.53
1:B:1234:LYS:CE	1:B:1238:ARG:HH21	2.22	0.53
1:B:1135:PRO:HG2	1:B:1137:LYS:HE2	1.89	0.53
1:B:1140:TYR:HD1	1:B:1140:TYR:H	1.55	0.52
1:B:1035:LEU:HD12	1:B:1075:ALA:HB1	1.91	0.52
1:A:74:LYS:O	1:A:80:ARG:HG3	2.09	0.52
1:A:133:ARG:NH1	1:A:134:ILE:O	2.43	0.52
1:B:1188:ILE:HG22	1:B:1269:LEU:HD11	1.91	0.52
1:A:138:THR:HB	1:A:140:TYR:CE1	2.45	0.52
1:B:1050:TYR:C	1:B:1051:ASN:HD22	2.13	0.52
1:A:92:LYS:HZ2	1:A:107:ASN:HB2	1.75	0.52
1:A:46:THR:CG2	1:A:59:LEU:HG	2.40	0.52
1:B:1185:THR:O	1:B:1188:ILE:HG12	2.10	0.51
1:A:280:ALA:O	1:A:284:LEU:HG	2.10	0.51
1:B:1317:ASN:HD22	1:B:1323:ASP:HB3	1.75	0.51
1:A:277:SER:HB2	1:A:324:GLU:CD	2.31	0.51
1:A:277:SER:HB2	1:A:324:GLU:OE2	2.10	0.51
1:B:1036:PHE:HA	1:B:1039:PHE:HD1	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:174:VAL:CG1	1:A:269:LEU:HD13	2.36	0.51
1:A:188:ILE:HG22	1:A:269:LEU:HD11	1.92	0.51
1:B:1082:MSE:O	1:B:1086:ARG:HG3	2.10	0.51
1:A:145:PHE:HZ	1:A:186:THR:CG2	2.18	0.51
1:A:185:THR:O	1:A:188:ILE:HG12	2.10	0.51
1:B:1291:ASN:HD22	1:B:1293:ALA:HB3	1.77	0.50
1:A:166:ASP:O	1:A:170:ILE:HG12	2.11	0.50
1:B:1057:TRP:CZ3	1:B:1067:PRO:HB3	2.46	0.50
1:A:156:ASN:HD22	1:A:156:ASN:C	2.14	0.50
1:B:1166:ASP:O	1:B:1170:ILE:HG12	2.12	0.50
1:A:223:PHE:HE2	1:A:250:ARG:NH2	2.09	0.50
1:B:1018:ARG:O	1:B:1022:GLU:HB2	2.11	0.50
1:A:202:ILE:HG13	1:A:241:PRO:HB3	1.94	0.50
1:B:1229:SER:OG	1:B:1253:GLU:HG2	2.12	0.49
1:A:234:LYS:CE	1:A:238:ARG:HH21	2.25	0.49
1:A:266:LYS:HG3	1:A:267:GLY:N	2.27	0.49
1:B:1249:LEU:CB	1:B:1272:LEU:HD13	2.43	0.49
1:A:272:LEU:CD1	1:A:287:MSE:HE1	2.42	0.49
1:B:1221:LEU:HD21	1:B:1239:MSE:HE1	1.94	0.49
1:B:1140:TYR:CD1	1:B:1140:TYR:N	2.78	0.48
1:B:1190:SER:O	1:B:1193:GLU:HG3	2.14	0.48
1:A:199:GLU:OE2	1:A:243:ARG:NE	2.44	0.48
1:A:140:TYR:N	1:A:140:TYR:CD1	2.78	0.48
1:B:1310:ILE:N	1:B:1310:ILE:HD12	2.28	0.48
1:B:1057:TRP:CE3	1:B:1067:PRO:HB3	2.48	0.48
1:A:263:SER:HA	1:B:1274:ALA:HA	1.96	0.47
1:A:51:ASN:N	1:A:51:ASN:HD22	2.12	0.47
1:A:6:LEU:HD12	1:B:1054:LYS:HZ2	1.77	0.47
1:A:43:GLU:CD	1:A:44:ASN:H	2.18	0.47
1:B:1266:LYS:HG3	1:B:1267:GLY:N	2.29	0.47
1:B:1138:THR:HB	1:B:1140:TYR:CE1	2.49	0.47
1:B:1044:ASN:HB3	1:B:1061:ASN:HD22	1.79	0.47
1:B:1255:TYR:CE2	1:B:1259:ASN:ND2	2.78	0.47
1:A:117:VAL:HG12	1:A:122:THR:HG23	1.96	0.47
1:A:291:ASN:HD22	1:A:293:ALA:HB3	1.80	0.47
1:A:258:TYR:HB2	1:A:306:PHE:CZ	2.49	0.47
1:B:1068:PHE:HB3	3:B:2000:2PE:H112	1.97	0.47
1:A:200:ARG:HD3	1:B:1065:TRP:CZ2	2.51	0.46
1:A:92:LYS:NZ	1:A:107:ASN:HB2	2.30	0.46
1:B:1202:ILE:HG13	1:B:1241:PRO:HB3	1.96	0.46
1:A:26:ASN:N	1:A:27:PRO:CD	2.78	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:TRP:CZ3	1:A:67:PRO:HB3	2.50	0.46
1:B:1258:TYR:HB2	1:B:1306:PHE:CZ	2.51	0.46
1:A:272:LEU:HD12	4:A:3022:HOH:O	2.16	0.45
1:A:137:LYS:HG2	1:A:137:LYS:H	1.44	0.45
1:A:190:SER:O	1:A:193:GLU:HG3	2.16	0.45
1:A:170:ILE:HG22	1:A:170:ILE:O	2.17	0.45
1:A:249:LEU:CB	1:A:272:LEU:HD13	2.47	0.45
1:A:78:LEU:HD21	1:A:126:GLU:HA	1.98	0.45
1:B:1117:VAL:HG12	1:B:1122:THR:HG23	1.98	0.45
1:A:145:PHE:CZ	1:A:186:THR:HG22	2.29	0.45
1:B:1254:ALA:CB	1:B:1287:MSE:HB3	2.47	0.45
1:B:1077:SER:O	1:B:1080:ARG:N	2.50	0.45
1:A:325:PHE:CE2	1:A:327:ILE:HD11	2.52	0.45
1:A:51:ASN:ND2	1:A:51:ASN:N	2.64	0.45
1:B:1077:SER:O	1:B:1078:LEU:C	2.55	0.45
1:B:1249:LEU:HB2	1:B:1272:LEU:HD13	1.99	0.45
1:A:327:ILE:CG2	1:A:328:LYS:N	2.79	0.45
1:B:1272:LEU:CD1	1:B:1287:MSE:HE1	2.46	0.44
1:B:1021:LYS:C	1:B:1023:ALA:H	2.21	0.44
1:B:1285:ALA:CB	1:B:1303:ILE:HG12	2.46	0.44
1:A:25:LEU:HD11	1:A:109:ALA:HA	1.98	0.44
1:B:1288:SER:HB2	1:B:1302:LEU:HD13	1.99	0.44
1:A:285:ALA:HB2	1:A:303:ILE:HG12	1.98	0.44
1:B:1156:ASN:C	1:B:1156:ASN:HD22	2.19	0.44
1:A:123:VAL:HG13	1:A:124:ASN:N	2.33	0.44
1:B:1170:ILE:HG22	1:B:1170:ILE:O	2.18	0.44
1:B:1156:ASN:ND2	1:B:1156:ASN:H	2.15	0.44
1:A:77:SER:O	1:A:80:ARG:N	2.51	0.44
1:A:60:LYS:CB	1:A:62:ASN:OD1	2.65	0.44
1:B:1046:THR:CG2	1:B:1059:LEU:HG	2.48	0.44
1:B:1123:VAL:HG13	1:B:1124:ASN:N	2.33	0.44
1:A:325:PHE:CD2	1:A:327:ILE:HD11	2.53	0.43
1:B:1050:TYR:CE2	1:B:1052:GLY:HA2	2.53	0.43
1:B:1046:THR:HG22	1:B:1059:LEU:HG	2.00	0.43
1:A:39:PHE:CD2	1:A:42:MSE:HE3	2.54	0.43
1:A:254:ALA:CB	1:A:287:MSE:HB3	2.48	0.43
1:A:262:CYS:HB3	1:B:1283:ARG:HD2	2.00	0.43
1:B:1139:THR:HB	1:B:1213:LYS:CE	2.39	0.43
1:B:1051:ASN:N	1:B:1051:ASN:ND2	2.66	0.43
1:A:262:CYS:HB3	1:B:1283:ARG:CD	2.48	0.43
1:B:1327:ILE:CG2	1:B:1328:LYS:N	2.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:1068:PHE:HA	3:B:2000:2PE:H61	2.00	0.43
1:A:313:ILE:HB	1:A:326:TYR:HB3	2.00	0.43
1:A:253:GLU:O	1:A:254:ALA:C	2.56	0.42
1:A:199:GLU:OE2	1:A:243:ARG:NH2	2.49	0.42
1:B:1277:SER:HB2	1:B:1324:GLU:CD	2.39	0.42
1:A:156:ASN:H	1:A:156:ASN:ND2	2.16	0.42
1:B:1246:LEU:O	1:B:1247:GLY:C	2.58	0.42
1:A:249:LEU:HD23	1:A:270:THR:HG21	2.01	0.42
1:A:255:TYR:CE2	1:A:259:ASN:ND2	2.84	0.42
1:A:77:SER:O	1:A:78:LEU:C	2.57	0.42
1:A:21:LYS:C	1:A:23:ALA:H	2.23	0.42
1:B:1026:ASN:N	1:B:1027:PRO:CD	2.82	0.42
1:B:1253:GLU:O	1:B:1254:ALA:C	2.57	0.42
1:A:218:TYR:C	1:A:218:TYR:CD1	2.93	0.41
1:A:246:LEU:O	1:A:247:GLY:C	2.58	0.41
1:A:249:LEU:HB2	1:A:272:LEU:HD13	2.02	0.41
1:A:141:PRO:HG2	1:A:144:PHE:HB2	2.01	0.41
1:B:1313:ILE:HB	1:B:1326:TYR:HB3	2.01	0.41
1:B:1249:LEU:HB3	1:B:1272:LEU:HD13	2.03	0.41
1:A:142:HIS:O	1:A:145:PHE:HB2	2.20	0.41
1:B:1156:ASN:HD22	1:B:1156:ASN:H	1.68	0.41
1:A:272:LEU:HD11	1:A:287:MSE:CE	2.47	0.41
1:B:1082:MSE:HE1	1:B:1118:LEU:HD22	2.03	0.41
1:B:1096:ILE:HB	1:B:1104:LEU:HD22	2.03	0.40
1:A:253:GLU:HG3	1:A:253:GLU:H	1.64	0.40
1:A:9:GLU:HG2	1:B:1074:LYS:NZ	2.35	0.40
1:A:174:VAL:O	1:A:269:LEU:HA	2.21	0.40
1:B:1141:PRO:HG2	1:B:1144:PHE:HB2	2.04	0.40
1:A:25:LEU:HA	1:A:25:LEU:HD12	1.91	0.40
1:B:1146:GLU:OE1	1:B:1161:ILE:CG2	2.69	0.40
1:B:1145:PHE:CZ	1:B:1186:THR:HG22	2.30	0.40
1:A:6:LEU:HD12	1:B:1054:LYS:HZ1	1.85	0.40
1:A:108:LEU:CD2	1:A:114:VAL:HG21	2.51	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	321/330 (97%)	287 (89%)	28 (9%)	6 (2%)	10 32
1	B	321/330 (97%)	288 (90%)	28 (9%)	5 (2%)	12 38
All	All	642/660 (97%)	575 (90%)	56 (9%)	11 (2%)	11 36

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	266	LYS
1	B	1266	LYS
1	A	136	SER
1	A	251	SER
1	B	1251	SER
1	B	1022	GLU
1	A	22	GLU
1	A	254	ALA
1	B	1254	ALA
1	A	15	GLU
1	B	1015	GLU

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	274/287 (96%)	262 (96%)	12 (4%)	35 69
1	B	275/287 (96%)	265 (96%)	10 (4%)	42 76

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	549/574 (96%)	527 (96%)	22 (4%)	38 73

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	ASN
1	A	67	PRO
1	A	110	ASN
1	A	135	PRO
1	A	137	LYS
1	A	140	TYR
1	A	156	ASN
1	A	249	LEU
1	A	250	ARG
1	A	253	GLU
1	A	268	THR
1	A	283	ARG
1	B	1095	THR
1	B	1137	LYS
1	B	1140	TYR
1	B	1156	ASN
1	B	1249	LEU
1	B	1250	ARG
1	B	1253	GLU
1	B	1268	THR
1	B	1283	ARG
1	B	1303	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	44	ASN
1	A	51	ASN
1	A	53	ASN
1	A	61	ASN
1	A	110	ASN
1	A	156	ASN
1	A	159	GLN
1	A	220	GLN
1	A	286	ASN
1	A	291	ASN

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Mol	Chain	Res	Type
1	B	1026	ASN
1	B	1051	ASN
1	B	1061	ASN
1	B	1156	ASN
1	B	1159	GLN
1	B	1220	GLN
1	B	1286	ASN
1	B	1291	ASN
1	B	1318	HIS
1	B	1321	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

3 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	4000	-	4,4,4	3.16	2 (50%)	6,6,6	0.94	0
3	2PE	B	2000	-	27,27,27	1.03	1 (3%)	26,26,26	1.26	2 (7%)
2	SO4	B	5000	-	4,4,4	3.26	2 (50%)	6,6,6	0.93	0

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
2	SO4	A	4000	-	-	0/0/0/0	0/0/0/0
3	2PE	B	2000	-	-	0/25/25/25	0/0/0/0
2	SO4	B	5000	-	-	0/0/0/0	0/0/0/0

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	4000	SO4	O3-S	-4.32	1.31	1.47
2	B	5000	SO4	O3-S	-4.29	1.32	1.47
3	B	2000	2PE	O22-C23	2.07	1.50	1.42
2	A	4000	SO4	O1-S	4.57	1.62	1.47
2	B	5000	SO4	O1-S	4.86	1.63	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	2000	2PE	C11-O10-C9	2.65	124.71	113.31
3	B	2000	2PE	O10-C11-C12	3.02	123.78	110.36

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	2000	2PE	5	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, 95^{th} 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	317/330 (96%)	-0.16	3 (0%)	85	79	13, 30, 47, 53	0
1	B	317/330 (96%)	-0.15	2 (0%)	90	86	9, 32, 50, 62	0
All	All	634/660 (96%)	-0.16	5 (0%)	87	81	9, 30, 49, 62	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	319	HIS	2.7
1	A	6	LEU	2.6
1	B	1250	ARG	2.4
1	B	1292	SER	2.2
1	A	25	LEU	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

There are no carbohydrates in this entry.

6.4 Ligands

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
3	2PE	B	2000	28/28	0.88	0.20	0.18	34,40,43,44	0
2	SO4	B	5000	5/5	0.98	0.14	-0.43	32,32,33,35	0
2	SO4	A	4000	5/5	0.97	0.13	-1.19	22,23,25,27	0

6.5 Other polymers (i)

There are no such residues in this entry.