W O R L D W I D E

wwPDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 09:23 AM GMT

PDB ID	:	3I94
Title	:	Crystal structure of PcyA-biliverdin XIII alpha complex
Authors	:	Hagiwara, Y.; Sugishima, M.; Fukuyama, K.
Deposited on	:	2009-07-10
Resolution	:	1.04 Å(reported)

The following versions of software and data (see references (i)) 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
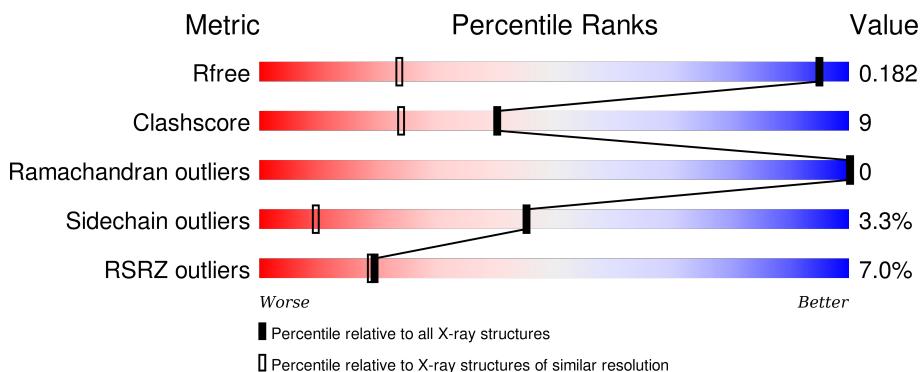
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION
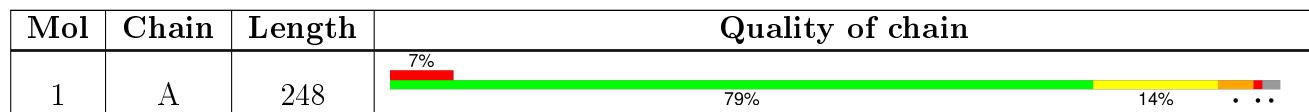
The reported resolution of this entry is 1.04 Å.

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	1032 (1.10-0.98)
Clashscore	102246	1109 (1.10-0.98)
Ramachandran outliers	100387	1041 (1.10-0.98)
Sidechain outliers	100360	1039 (1.10-0.98)
RSRZ outliers	91569	1034 (1.10-0.98)

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	248	

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
3	SO4	A	6610	-	X	X	-

2 Entry composition (i)
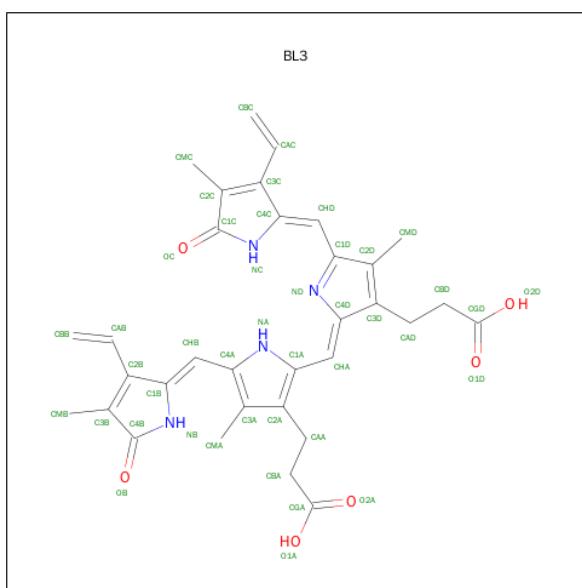
There are 4 unique types of molecules in this entry. The entry contains 3895 atoms, of which 1360 are hydrogens and 0 are deuteriums.

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 Phycocyanobilin:ferredoxin oxidoreductase.
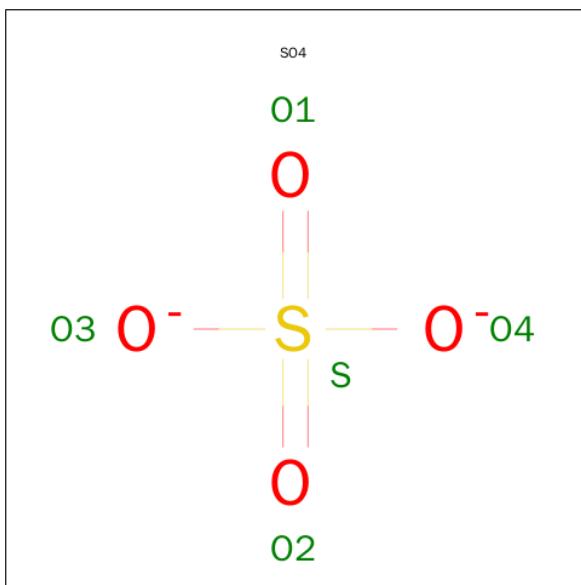
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	243	Total 3471	C 1343	H 1360	N 361	O 392	S 15	0	37	0

- Molecule 2 is 3-[2-[(Z)-[3-(2-CARBOXYETHYL)-5-[(Z)-(3-ETHENYL-4-METHYL-5-OXO -PYRROL-2-YLIDENE)METHYL]-4-METHYL-PYRROL-2-YLIDENE]METHYL]-5-[(Z)-(3-ETHENYL-4-METHYL-5-OXO-PYRROL-2-YLIDENE)METHYL]-4-METHYL-1H-PYR ROL-3-YL]PROPANOIC ACID (three-letter code: BL3) (formula: $C_{33}H_{34}N_4O_6$).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 43	C 33	N 4	O 6	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 5	O 4	S 1	0	0
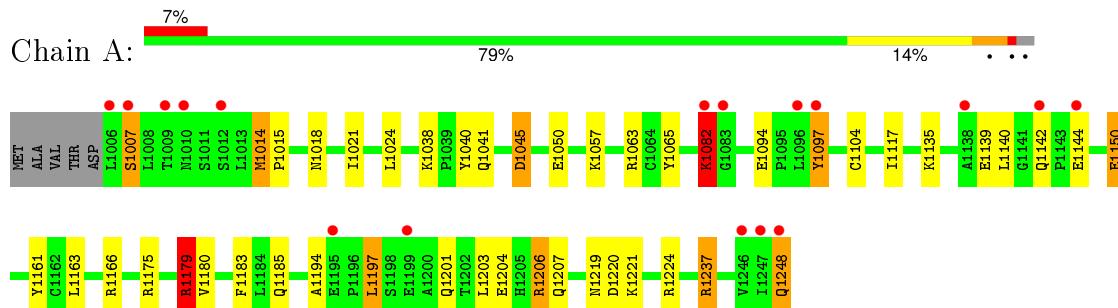
• Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	375	Total 376	O 376	0	1

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: Phycocyanobilin:ferredoxin oxidoreductase

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	70.78Å 94.80Å 42.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.94 – 1.04 28.94 – 1.05	Depositor EDS
% Data completeness (in resolution range)	(Not available) (28.94-1.04) 98.7 (28.94-1.05)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.01 (at 1.05Å)	Xtriage
Refinement program	SHELXL	Depositor
R, R_{free}	0.125 , 0.148 0.176 , 0.182	Depositor DCC
R_{free} test set	6739 reflections (5.29%)	DCC
Wilson B-factor (Å^2)	12.5	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.39 , 59.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.32$	Xtriage
Outliers	1 of 134093 reflections (0.001%)	Xtriage
F_o,F_c correlation	0.98	EDS
Total number of atoms	3895	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.25% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, BL3

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	0.80	0/2296	1.50	41/3103 (1.3%)

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 (41) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	1206	ARG	CD-NE-CZ	21.16	153.22	123.60
1	A	1206	ARG	NE-CZ-NH2	16.00	128.30	120.30
1	A	1166	ARG	NE-CZ-NH1	-13.51	113.55	120.30
1	A	1179[A]	ARG	NE-CZ-NH1	12.63	126.61	120.30
1	A	1179[B]	ARG	NE-CZ-NH1	12.63	126.61	120.30
1	A	1166	ARG	NE-CZ-NH2	12.52	126.56	120.30
1	A	1237[A]	ARG	NE-CZ-NH1	-9.45	115.58	120.30
1	A	1237[B]	ARG	NE-CZ-NH1	-9.45	115.58	120.30
1	A	1065	TYR	CG-CD2-CE2	9.15	128.62	121.30
1	A	1014	MET	CG-SD-CE	-8.79	86.14	100.20
1	A	1104[A]	CYS	CA-CB-SG	8.08	128.54	114.00
1	A	1104[B]	CYS	CA-CB-SG	8.08	128.54	114.00
1	A	1063[A]	ARG	NE-CZ-NH1	7.89	124.25	120.30
1	A	1063[B]	ARG	NE-CZ-NH1	7.89	124.25	120.30
1	A	1175	ARG	NE-CZ-NH2	-7.82	116.39	120.30
1	A	1183	PHE	CB-CG-CD1	7.33	125.93	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1040	TYR	CB-CG-CD2	7.04	125.23	121.00
1	A	1082	LYS	C-N-CA	-7.03	107.55	122.30
1	A	1065	TYR	CZ-CE2-CD2	-6.74	113.73	119.80
1	A	1135	LYS	CA-CB-CG	6.64	128.02	113.40
1	A	1045[A]	ASP	CB-CG-OD1	-6.50	112.45	118.30
1	A	1045[B]	ASP	CB-CG-OD1	-6.50	112.45	118.30
1	A	1150	GLU	OE1-CD-OE2	-6.32	115.72	123.30
1	A	1007	SER	N-CA-CB	6.21	119.82	110.50
1	A	1097	TYR	CG-CD2-CE2	6.09	126.17	121.30
1	A	1204	GLU	OE1-CD-OE2	-6.02	116.08	123.30
1	A	1063[A]	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	A	1063[B]	ARG	NE-CZ-NH2	-5.69	117.46	120.30
1	A	1179[A]	ARG	NH1-CZ-NH2	-5.59	113.25	119.40
1	A	1179[B]	ARG	NH1-CZ-NH2	-5.59	113.25	119.40
1	A	1237[A]	ARG	NH1-CZ-NH2	5.59	125.55	119.40
1	A	1237[B]	ARG	NH1-CZ-NH2	5.59	125.55	119.40
1	A	1161[A]	TYR	CG-CD1-CE1	5.56	125.75	121.30
1	A	1161[B]	TYR	CG-CD1-CE1	5.56	125.75	121.30
1	A	1206	ARG	NE-CZ-NH1	-5.41	117.60	120.30
1	A	1220[A]	ASP	CB-CG-OD2	5.39	123.16	118.30
1	A	1220[B]	ASP	CB-CG-OD2	5.39	123.16	118.30
1	A	1224	ARG	NE-CZ-NH1	5.35	122.97	120.30
1	A	1097	TYR	CB-CG-CD2	5.32	124.19	121.00
1	A	1197[A]	LEU	C-N-CA	5.24	134.79	121.70
1	A	1197[B]	LEU	C-N-CA	5.24	134.79	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1082	LYS	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	2111	1360	2088	36	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	43	0	32	1	0
3	A	5	0	0	3	0
4	A	376	0	0	12	0
All	All	2535	1360	2120	38	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 (38) 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:1057[B]:LYS:HE3	4:A:9182:HOH:O	1.35	1.24
3:A:6610:SO4:S	3:A:6610:SO4:O1	1.99	1.19
1:A:1094[B]:GLU:HG3	4:A:9089:HOH:O	1.82	0.79
1:A:1057[B]:LYS:HB2	1:A:1057[B]:LYS:HZ3	1.49	0.78
1:A:1057[B]:LYS:HD3	3:A:6610:SO4:O2	1.87	0.75
1:A:1024[B]:LEU:HD11	1:A:1180:VAL:HG11	1.70	0.73
1:A:1082:LYS:NZ	1:A:1082:LYS:H	1.85	0.73
1:A:1179[A]:ARG:NH2	4:A:9277:HOH:O	2.13	0.67
1:A:1082:LYS:HZ1	1:A:1082:LYS:H	1.45	0.62
1:A:1197[A]:LEU:HB3	1:A:1201:GLN:NE2	2.16	0.60
1:A:1248:GLN:HA	4:A:9345:HOH:O	2.03	0.58
1:A:1197[A]:LEU:HB3	1:A:1201:GLN:HE21	1.69	0.57
1:A:1057[B]:LYS:NZ	1:A:1057[B]:LYS:HB2	2.19	0.57
2:A:2130:BL3:HMC	2:A:2130:BL3:HBC	1.86	0.57
1:A:1139:GLU:HG2	4:A:9253:HOH:O	2.05	0.56
1:A:1207[B]:GLN:HG2	4:A:9128:HOH:O	2.06	0.55
1:A:1050:GLU:OE2	1:A:1057[B]:LYS:HG3	2.05	0.55
1:A:1140:LEU:HD13	1:A:1179[A]:ARG:CD	2.41	0.50
1:A:1140:LEU:HB3	1:A:1179[A]:ARG:CZ	2.42	0.50
1:A:1150:GLU:HG2	4:A:9252:HOH:O	2.14	0.47
1:A:1057[B]:LYS:CD	3:A:6610:SO4:O2	2.60	0.46
1:A:1206:ARG:HD3	1:A:1248:GLN:O	2.16	0.46
1:A:1041:GLN:NE2	1:A:1045[B]:ASP:OD2	2.48	0.46
1:A:1117:ILE:HA	1:A:1163:LEU:O	2.18	0.44
1:A:1185[A]:GLN:NE2	4:A:9127:HOH:O	2.49	0.44
1:A:1237[B]:ARG:NH2	4:A:9124:HOH:O	2.47	0.43
1:A:1203:LEU:O	1:A:1207[B]:GLN:HG3	2.18	0.42
1:A:1221[B]:LYS:NZ	4:A:9142:HOH:O	2.50	0.42
1:A:1097:TYR:HB3	1:A:1194[B]:ALA:HB1	2.01	0.42
1:A:1038[A]:LYS:NZ	4:A:9104:HOH:O	2.48	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1018:ASN:HD22	1:A:1021:ILE:H	1.69	0.41
1:A:1248:GLN:OXT	1:A:1248:GLN:NE2	2.54	0.41
1:A:1194[B]:ALA:HB3	4:A:9348[B]:HOH:O	2.19	0.41
1:A:1140:LEU:HD13	1:A:1179[A]:ARG:NE	2.35	0.40
1:A:1014:MET:HB3	1:A:1015:PRO:HD3	2.04	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	278/248 (112%)	271 (98%)	7 (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	247/216 (114%)	239 (97%)	8 (3%)	46 10

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1007	SER

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Mol	Chain	Res	Type
1	A	1082	LYS
1	A	1142	GLN
1	A	1144	GLU
1	A	1179[A]	ARG
1	A	1179[B]	ARG
1	A	1219	ASN
1	A	1248	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1018	ASN
1	A	1023	GLN
1	A	1041	GLN
1	A	1178	GLN
1	A	1201	GLN
1	A	1219	ASN
1	A	1248	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)

2 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	BL3	A	2130	-	34,46,46	1.98	7 (20%)	43,67,67	1.20	3 (6%)
3	SO4	A	6610	-	4,4,4	8.79	3 (75%)	6,6,6	2.39	2 (33%)

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	BL3	A	2130	-	-	0/22/74/74	0/4/4/4
3	SO4	A	6610	-	-	0/0/0/0	0/0/0/0

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	6610	SO4	O4-S	-6.27	1.24	1.47
3	A	6610	SO4	O3-S	-5.92	1.26	1.47
2	A	2130	BL3	C4D-C3D	-5.14	1.36	1.45
2	A	2130	BL3	CAC-C3C	-3.02	1.38	1.47
2	A	2130	BL3	C4B-C3B	-2.20	1.41	1.47
2	A	2130	BL3	OC-C1C	2.10	1.27	1.23
2	A	2130	BL3	C1D-ND	2.21	1.42	1.37
2	A	2130	BL3	CHB-C1B	2.37	1.39	1.34
2	A	2130	BL3	CHA-C4D	7.32	1.41	1.35
3	A	6610	SO4	O1-S	15.32	1.99	1.47

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	6610	SO4	O4-S-O3	-4.22	91.83	108.98
2	A	2130	BL3	CAA-C2A-C1A	-3.74	122.94	127.01
3	A	6610	SO4	O2-S-O1	-3.67	97.85	109.50
2	A	2130	BL3	C1B-NB-C4B	-2.27	107.41	110.73
2	A	2130	BL3	C4D-C3D-C2D	3.08	110.26	106.81

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2130	BL3	1	0
3	A	6610	SO4	3	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(Å²)	Q<0.9
1	A	243/248 (97%)	0.36	17 (6%)	19	19	9, 14, 31, 60	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1248	GLN	9.7
1	A	1007	SER	6.9
1	A	1006	LEU	6.1
1	A	1009	THR	5.7
1	A	1010	ASN	5.6
1	A	1142	GLN	4.0
1	A	1083[A]	GLY	3.8
1	A	1097	TYR	3.4
1	A	1144	GLU	3.2
1	A	1082	LYS	2.9
1	A	1195[A]	GLU	2.8
1	A	1096	LEU	2.6
1	A	1247	ILE	2.4
1	A	1199	GLU	2.2
1	A	1138	ALA	2.1
1	A	1012[A]	SER	2.1
1	A	1246	VAL	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. 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, 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	LLDF	B-factors($Å^2$)	Q<0.9
2	BL3	A	2130	43/43	0.96	0.08	0.48	9,11,15,20	0
3	SO4	A	6610	5/5	0.93	0.10	-0.27	18,19,22,24	5

6.5 Other polymers (i)

There are no such residues in this entry.