Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 09:18 AM GMT

PDB ID	:	3HXJ
Title	:	Crystal Structure of Pyrrolo-quinoline quinone (PQQ_DH) from Methanococcus maripaludis, Northeast Structural Genomics Consortium Target MrR86
Authors	:	Forouhar, F.; Chen, Y.; Seetharaman, J.; Sahdev, S.; Xiao, R.; Ciccosanti, C.; Foote, E.L.; Zhao, L.; Everett, J.K.; Nair, R.; Acton, T.B.; Rost, B.; Montelione, G.T.; Hunt, J.F.; Tong, L.; Northeast Structural Genomics Consortium (NESG)
Deposited on	:	2009-06-20
Resolution	:	2.00 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:

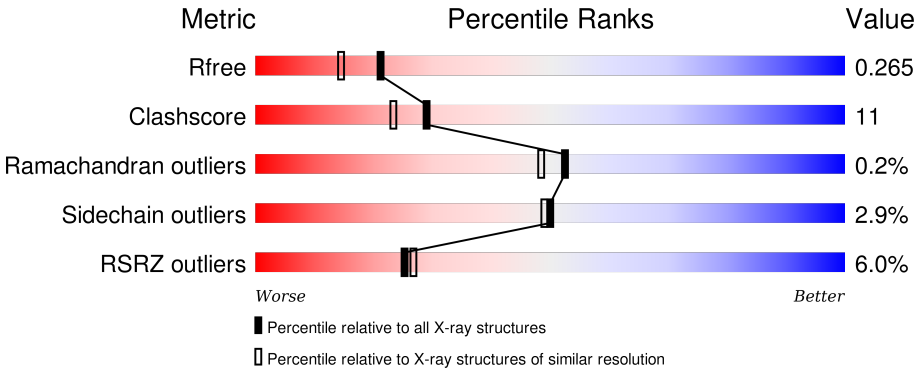
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	6249 (2.00-2.00)
Clashscore	102246	7340 (2.00-2.00)
Ramachandran outliers	100387	7248 (2.00-2.00)
Sidechain outliers	100360	7247 (2.00-2.00)
RSRZ outliers	91569	6262 (2.00-2.00)

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	2% 77% 15% 7%
1	B	330	9% 65% 22% • 11%
1	C	330	5% 68% 17% • 13%
1	D	330	5% 65% 24% • 8%

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	B	351	-	-	-	X

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 10202 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 Pyrrolo-quinoline quinone.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	306	Total	C	N	O	S	Se	0	0	0
			2438	1571	388	477	1	1			
1	B	294	Total	C	N	O	S	Se	0	0	0
			2358	1527	374	455	1	1			
1	C	286	Total	C	N	O	S	Se	0	0	0
			2281	1478	360	441	1	1			
1	D	303	Total	C	N	O	S	Se	0	0	0
			2421	1564	385	470	1	1			

There are 144 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	28	ALA	SER	SEE REMARK 999	UNP A6VIT4
A	33	ILE	VAL	SEE REMARK 999	UNP A6VIT4
A	35	LEU	VAL	SEE REMARK 999	UNP A6VIT4
A	38	SER	GLY	SEE REMARK 999	UNP A6VIT4
A	39	ASN	ASP	SEE REMARK 999	UNP A6VIT4
A	47	THR	PRO	SEE REMARK 999	UNP A6VIT4
A	54	PHE	SER	SEE REMARK 999	UNP A6VIT4
A	58	GLY	ASP	SEE REMARK 999	UNP A6VIT4
A	64	ARG	LYS	SEE REMARK 999	UNP A6VIT4
A	92	ARG	LYS	SEE REMARK 999	UNP A6VIT4
A	94	ASP	GLY	SEE REMARK 999	UNP A6VIT4
A	100	VAL	ALA	SEE REMARK 999	UNP A6VIT4
A	109	ILE	VAL	SEE REMARK 999	UNP A6VIT4
A	115	MSE	LEU	SEE REMARK 999	UNP A6VIT4
A	118	HIS	TYR	SEE REMARK 999	UNP A6VIT4
A	124	THR	PRO	SEE REMARK 999	UNP A6VIT4
A	135	LYS	ASN	SEE REMARK 999	UNP A6VIT4
A	136	LYS	ARG	SEE REMARK 999	UNP A6VIT4
A	177	ALA	THR	SEE REMARK 999	UNP A6VIT4
A	182	ALA	VAL	SEE REMARK 999	UNP A6VIT4
A	209	ASN	LYS	SEE REMARK 999	UNP A6VIT4

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Chain	Residue	Modelled	Actual	Comment	Reference
A	216	THR	ILE	SEE REMARK 999	UNP A6VIT4
A	236	HIS	TYR	SEE REMARK 999	UNP A6VIT4
A	253	GLY	ASP	SEE REMARK 999	UNP A6VIT4
A	266	ASP	GLY	SEE REMARK 999	UNP A6VIT4
A	291	GLU	GLN	SEE REMARK 999	UNP A6VIT4
A	301	VAL	THR	SEE REMARK 999	UNP A6VIT4
A	304	GLU	LYS	SEE REMARK 999	UNP A6VIT4
A	323	LEU	-	EXPRESSION TAG	UNP A6VIT4
A	324	GLU	-	EXPRESSION TAG	UNP A6VIT4
A	325	HIS	-	EXPRESSION TAG	UNP A6VIT4
A	326	HIS	-	EXPRESSION TAG	UNP A6VIT4
A	327	HIS	-	EXPRESSION TAG	UNP A6VIT4
A	328	HIS	-	EXPRESSION TAG	UNP A6VIT4
A	329	HIS	-	EXPRESSION TAG	UNP A6VIT4
A	330	HIS	-	EXPRESSION TAG	UNP A6VIT4
B	28	ALA	SER	SEE REMARK 999	UNP A6VIT4
B	33	ILE	VAL	SEE REMARK 999	UNP A6VIT4
B	35	LEU	VAL	SEE REMARK 999	UNP A6VIT4
B	38	SER	GLY	SEE REMARK 999	UNP A6VIT4
B	39	ASN	ASP	SEE REMARK 999	UNP A6VIT4
B	47	THR	PRO	SEE REMARK 999	UNP A6VIT4
B	54	PHE	SER	SEE REMARK 999	UNP A6VIT4
B	58	GLY	ASP	SEE REMARK 999	UNP A6VIT4
B	64	ARG	LYS	SEE REMARK 999	UNP A6VIT4
B	92	ARG	LYS	SEE REMARK 999	UNP A6VIT4
B	94	ASP	GLY	SEE REMARK 999	UNP A6VIT4
B	100	VAL	ALA	SEE REMARK 999	UNP A6VIT4
B	109	ILE	VAL	SEE REMARK 999	UNP A6VIT4
B	115	MSE	LEU	SEE REMARK 999	UNP A6VIT4
B	118	HIS	TYR	SEE REMARK 999	UNP A6VIT4
B	124	THR	PRO	SEE REMARK 999	UNP A6VIT4
B	135	LYS	ASN	SEE REMARK 999	UNP A6VIT4
B	136	LYS	ARG	SEE REMARK 999	UNP A6VIT4
B	177	ALA	THR	SEE REMARK 999	UNP A6VIT4
B	182	ALA	VAL	SEE REMARK 999	UNP A6VIT4
B	209	ASN	LYS	SEE REMARK 999	UNP A6VIT4
B	216	THR	ILE	SEE REMARK 999	UNP A6VIT4
B	236	HIS	TYR	SEE REMARK 999	UNP A6VIT4
B	253	GLY	ASP	SEE REMARK 999	UNP A6VIT4
B	266	ASP	GLY	SEE REMARK 999	UNP A6VIT4
B	291	GLU	GLN	SEE REMARK 999	UNP A6VIT4
B	301	VAL	THR	SEE REMARK 999	UNP A6VIT4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	304	GLU	LYS	SEE REMARK 999	UNP A6VIT4
B	323	LEU	-	EXPRESSION TAG	UNP A6VIT4
B	324	GLU	-	EXPRESSION TAG	UNP A6VIT4
B	325	HIS	-	EXPRESSION TAG	UNP A6VIT4
B	326	HIS	-	EXPRESSION TAG	UNP A6VIT4
B	327	HIS	-	EXPRESSION TAG	UNP A6VIT4
B	328	HIS	-	EXPRESSION TAG	UNP A6VIT4
B	329	HIS	-	EXPRESSION TAG	UNP A6VIT4
B	330	HIS	-	EXPRESSION TAG	UNP A6VIT4
C	28	ALA	SER	SEE REMARK 999	UNP A6VIT4
C	33	ILE	VAL	SEE REMARK 999	UNP A6VIT4
C	35	LEU	VAL	SEE REMARK 999	UNP A6VIT4
C	38	SER	GLY	SEE REMARK 999	UNP A6VIT4
C	39	ASN	ASP	SEE REMARK 999	UNP A6VIT4
C	47	THR	PRO	SEE REMARK 999	UNP A6VIT4
C	54	PHE	SER	SEE REMARK 999	UNP A6VIT4
C	58	GLY	ASP	SEE REMARK 999	UNP A6VIT4
C	64	ARG	LYS	SEE REMARK 999	UNP A6VIT4
C	92	ARG	LYS	SEE REMARK 999	UNP A6VIT4
C	94	ASP	GLY	SEE REMARK 999	UNP A6VIT4
C	100	VAL	ALA	SEE REMARK 999	UNP A6VIT4
C	109	ILE	VAL	SEE REMARK 999	UNP A6VIT4
C	115	MSE	LEU	SEE REMARK 999	UNP A6VIT4
C	118	HIS	TYR	SEE REMARK 999	UNP A6VIT4
C	124	THR	PRO	SEE REMARK 999	UNP A6VIT4
C	135	LYS	ASN	SEE REMARK 999	UNP A6VIT4
C	136	LYS	ARG	SEE REMARK 999	UNP A6VIT4
C	177	ALA	THR	SEE REMARK 999	UNP A6VIT4
C	182	ALA	VAL	SEE REMARK 999	UNP A6VIT4
C	209	ASN	LYS	SEE REMARK 999	UNP A6VIT4
C	216	THR	ILE	SEE REMARK 999	UNP A6VIT4
C	236	HIS	TYR	SEE REMARK 999	UNP A6VIT4
C	253	GLY	ASP	SEE REMARK 999	UNP A6VIT4
C	266	ASP	GLY	SEE REMARK 999	UNP A6VIT4
C	291	GLU	GLN	SEE REMARK 999	UNP A6VIT4
C	301	VAL	THR	SEE REMARK 999	UNP A6VIT4
C	304	GLU	LYS	SEE REMARK 999	UNP A6VIT4
C	323	LEU	-	EXPRESSION TAG	UNP A6VIT4
C	324	GLU	-	EXPRESSION TAG	UNP A6VIT4
C	325	HIS	-	EXPRESSION TAG	UNP A6VIT4
C	326	HIS	-	EXPRESSION TAG	UNP A6VIT4
C	327	HIS	-	EXPRESSION TAG	UNP A6VIT4

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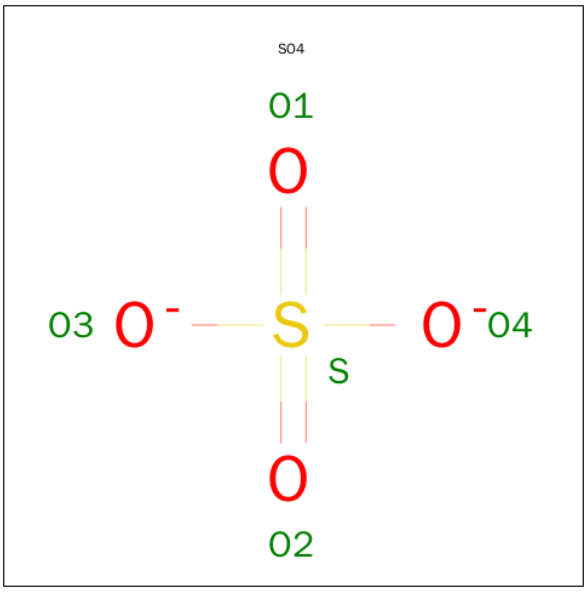
Chain	Residue	Modelled	Actual	Comment	Reference
C	328	HIS	-	EXPRESSION TAG	UNP A6VIT4
C	329	HIS	-	EXPRESSION TAG	UNP A6VIT4
C	330	HIS	-	EXPRESSION TAG	UNP A6VIT4
D	28	ALA	SER	SEE REMARK 999	UNP A6VIT4
D	33	ILE	VAL	SEE REMARK 999	UNP A6VIT4
D	35	LEU	VAL	SEE REMARK 999	UNP A6VIT4
D	38	SER	GLY	SEE REMARK 999	UNP A6VIT4
D	39	ASN	ASP	SEE REMARK 999	UNP A6VIT4
D	47	THR	PRO	SEE REMARK 999	UNP A6VIT4
D	54	PHE	SER	SEE REMARK 999	UNP A6VIT4
D	58	GLY	ASP	SEE REMARK 999	UNP A6VIT4
D	64	ARG	LYS	SEE REMARK 999	UNP A6VIT4
D	92	ARG	LYS	SEE REMARK 999	UNP A6VIT4
D	94	ASP	GLY	SEE REMARK 999	UNP A6VIT4
D	100	VAL	ALA	SEE REMARK 999	UNP A6VIT4
D	109	ILE	VAL	SEE REMARK 999	UNP A6VIT4
D	115	MSE	LEU	SEE REMARK 999	UNP A6VIT4
D	118	HIS	TYR	SEE REMARK 999	UNP A6VIT4
D	124	THR	PRO	SEE REMARK 999	UNP A6VIT4
D	135	LYS	ASN	SEE REMARK 999	UNP A6VIT4
D	136	LYS	ARG	SEE REMARK 999	UNP A6VIT4
D	177	ALA	THR	SEE REMARK 999	UNP A6VIT4
D	182	ALA	VAL	SEE REMARK 999	UNP A6VIT4
D	209	ASN	LYS	SEE REMARK 999	UNP A6VIT4
D	216	THR	ILE	SEE REMARK 999	UNP A6VIT4
D	236	HIS	TYR	SEE REMARK 999	UNP A6VIT4
D	253	GLY	ASP	SEE REMARK 999	UNP A6VIT4
D	266	ASP	GLY	SEE REMARK 999	UNP A6VIT4
D	291	GLU	GLN	SEE REMARK 999	UNP A6VIT4
D	301	VAL	THR	SEE REMARK 999	UNP A6VIT4
D	304	GLU	LYS	SEE REMARK 999	UNP A6VIT4
D	323	LEU	-	EXPRESSION TAG	UNP A6VIT4
D	324	GLU	-	EXPRESSION TAG	UNP A6VIT4
D	325	HIS	-	EXPRESSION TAG	UNP A6VIT4
D	326	HIS	-	EXPRESSION TAG	UNP A6VIT4
D	327	HIS	-	EXPRESSION TAG	UNP A6VIT4
D	328	HIS	-	EXPRESSION TAG	UNP A6VIT4
D	329	HIS	-	EXPRESSION TAG	UNP A6VIT4
D	330	HIS	-	EXPRESSION TAG	UNP A6VIT4

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



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

- Molecule 3 is water.

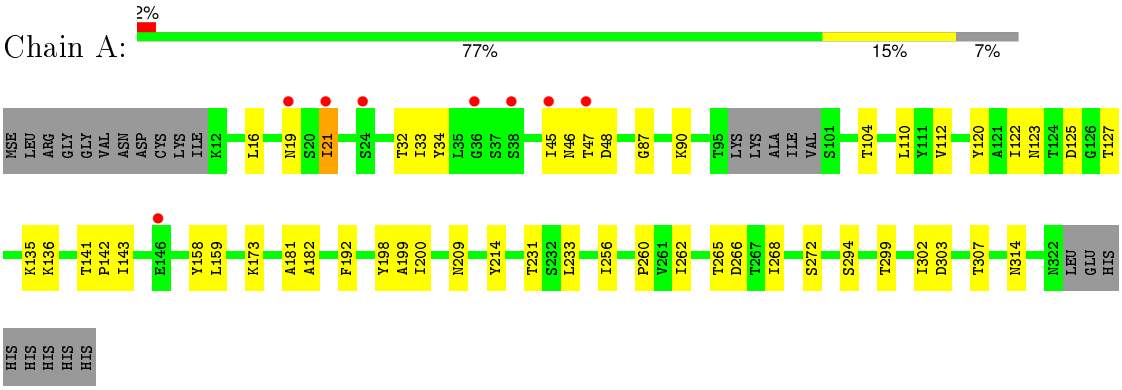
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	190	Total O 190 190	0	0
3	B	139	Total O 139 139	0	0
3	C	205	Total O 205 205	0	0
3	D	135	Total O 135 135	0	0

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.

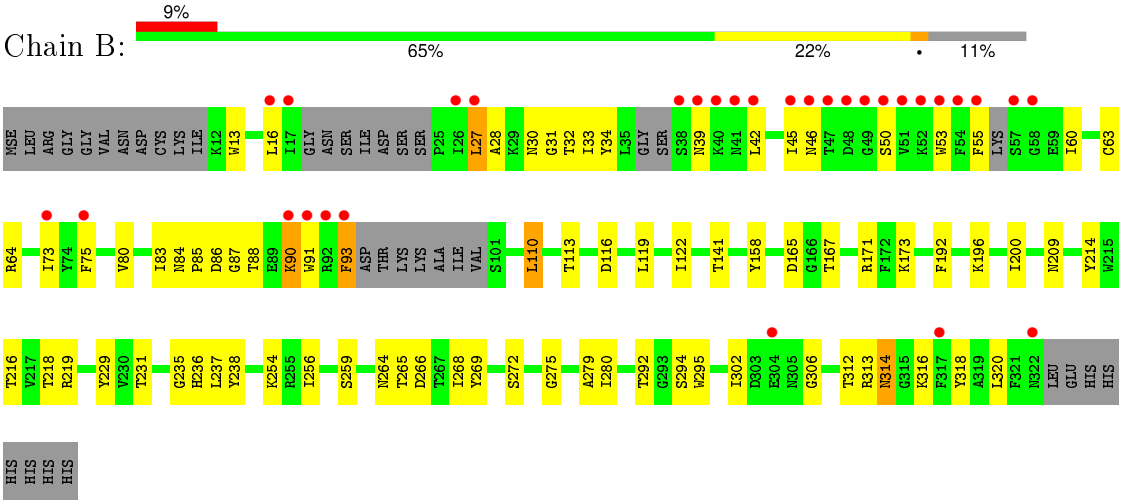
- Molecule 1: Pyrrolo-quinoline quinone

Chain A:



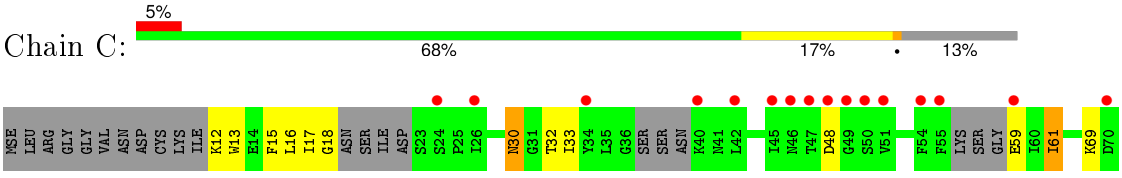
- Molecule 1: Pyrrolo-quinoline quinone

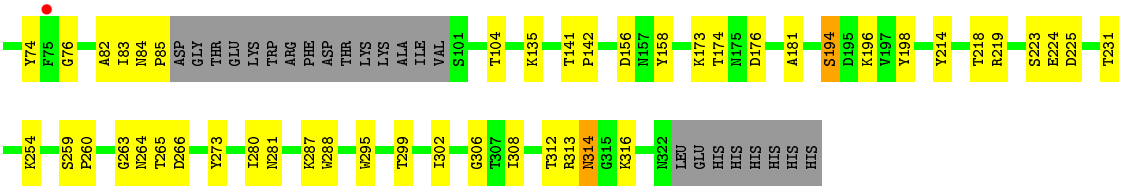
Chain B:



- Molecule 1: Pyrrolo-quinoline quinone

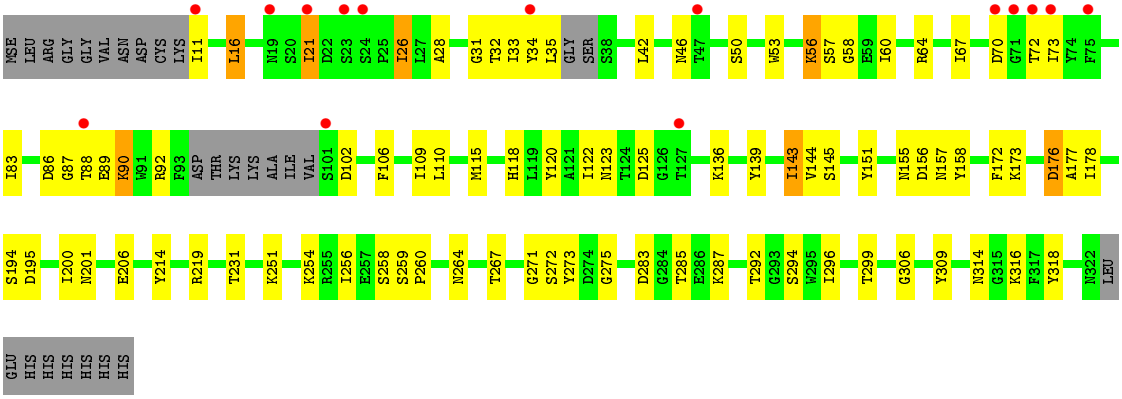
Chain C:





- Molecule 1: Pyrrolo-quinoline quinone

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	99.22Å 66.96Å 112.08Å 90.00° 115.29° 90.00°	Depositor
Resolution (Å)	19.98 – 2.00 29.90 – 2.00	Depositor EDS
% Data completeness (in resolution range)	86.0 (19.98-2.00) 97.8 (29.90-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	3.08 (at 2.00Å)	Xtriage
Refinement program	CNS 1.2 & XtalView	Depositor
R, R_{free}	0.195 , 0.242 0.214 , 0.265	Depositor DCC
R_{free} test set	4373 reflections (4.97%)	DCC
Wilson B-factor (Å^2)	20.2	Xtriage
Anisotropy	0.201	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 52.2	EDS
Estimated twinning fraction	0.012 for h,-k,-h-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	0 of 173941 reflections	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	10202	wwPDB-VP
Average B, all atoms (Å^2)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.16% 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, 0.375 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: 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	0.38	0/2507	0.61	0/3407
1	B	0.37	0/2424	0.57	0/3290
1	C	0.36	0/2344	0.60	0/3183
1	D	0.36	0/2489	0.58	0/3381
All	All	0.37	0/9764	0.59	0/13261

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	2438	0	2309	43	0
1	B	2358	0	2236	58	0
1	C	2281	0	2167	50	0
1	D	2421	0	2300	72	0
2	B	5	0	0	0	0
2	C	20	0	0	0	0
2	D	10	0	0	0	0
3	A	190	0	0	2	0
3	B	139	0	0	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	205	0	0	3	0
3	D	135	0	0	7	0
All	All	10202	0	9012	211	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 11.

All (211) 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:C:219:ARG:HH22	1:C:299:THR:HG21	1.30	0.96
1:D:264:ASN:HD21	1:D:306:GLY:HA3	1.36	0.91
1:D:21:ILE:H	1:D:21:ILE:HD13	1.47	0.79
1:B:302:ILE:HD11	1:B:306:GLY:HA2	1.65	0.78
1:B:27:LEU:HD12	1:B:33:ILE:HD12	1.65	0.78
1:A:21:ILE:HD13	1:A:21:ILE:H	1.47	0.78
1:D:143:ILE:HD13	1:D:144:VAL:N	2.00	0.76
1:C:16:LEU:HG	1:C:17:ILE:HG13	1.68	0.76
1:B:63:CYS:HB2	1:B:80:VAL:HG23	1.69	0.74
1:B:39:ASN:HA	1:B:42:LEU:HD23	1.70	0.72
1:C:219:ARG:NH2	1:C:299:THR:HG21	2.03	0.72
1:B:237:LEU:HD21	1:B:268:ILE:HD13	1.73	0.71
1:C:61:ILE:HD13	1:C:61:ILE:H	1.55	0.71
1:A:125:ASP:OD2	1:A:127:THR:HG22	1.91	0.71
1:C:33:ILE:HG12	1:C:219:ARG:NH2	2.07	0.69
1:D:178:ILE:HD13	1:D:194:SER:HB3	1.74	0.69
1:D:283:ASP:OD2	1:D:285:THR:HG22	1.93	0.69
1:B:55:PHE:HB2	1:B:60:ILE:HD11	1.76	0.68
1:B:30:ASN:OD1	1:B:32:THR:HG22	1.93	0.68
1:A:87:GLY:HA2	1:A:90:LYS:HD3	1.76	0.66
1:C:265:THR:O	1:C:266:ASP:HB2	1.95	0.66
1:D:110:LEU:HD23	1:D:122:ILE:HD11	1.79	0.65
1:B:27:LEU:H	1:B:27:LEU:HD22	1.61	0.65
1:C:219:ARG:HH22	1:C:299:THR:CG2	2.08	0.65
1:D:26:ILE:H	1:D:26:ILE:HD13	1.63	0.64
1:C:13:TRP:HB3	1:C:16:LEU:HD21	1.79	0.63
1:C:61:ILE:N	1:C:61:ILE:HD13	2.13	0.63
1:D:56:LYS:HZ1	1:D:58:GLY:HA3	1.63	0.63
1:D:254:LYS:HD2	1:D:273:TYR:HE1	1.65	0.62
1:C:302:ILE:HG22	1:C:308:ILE:HG12	1.82	0.62
1:C:265:THR:HG21	3:C:494:HOH:O	1.99	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:264:ASN:ND2	1:D:306:GLY:HA3	2.11	0.61
1:C:280:ILE:HD12	1:C:280:ILE:N	2.16	0.61
1:D:46:ASN:HD22	1:D:50:SER:HB3	1.67	0.60
1:A:120:TYR:HB3	1:A:122:ILE:HD11	1.82	0.59
1:D:42:LEU:HD21	1:D:92:ARG:O	2.03	0.58
1:D:231:THR:HG23	1:D:260:PRO:HD3	1.85	0.58
1:B:46:ASN:HD22	1:B:50:SER:HB3	1.69	0.58
1:B:292:THR:HG22	1:B:294:SER:H	1.68	0.57
1:A:46:ASN:HA	1:D:56:LYS:HG2	1.87	0.57
1:D:21:ILE:H	1:D:21:ILE:CD1	2.17	0.56
1:A:16:LEU:HD12	1:C:313:ARG:HD3	1.87	0.55
1:C:158:TYR:CE1	1:C:173:LYS:HB2	2.42	0.55
1:D:254:LYS:HD2	1:D:273:TYR:CE1	2.41	0.54
1:D:26:ILE:HD13	1:D:26:ILE:N	2.22	0.54
1:C:33:ILE:HG12	1:C:219:ARG:HH21	1.72	0.54
1:B:275:GLY:O	1:B:292:THR:HB	2.07	0.54
1:D:83:ILE:HD12	1:D:83:ILE:N	2.23	0.54
1:D:32:THR:HG22	1:D:33:ILE:N	2.23	0.54
1:C:83:ILE:HG22	1:C:85:PRO:HD3	1.89	0.54
1:C:141:THR:HB	1:C:181:ALA:HB2	1.90	0.54
1:D:88:THR:HG23	1:D:89:GLU:HG2	1.90	0.54
1:A:21:ILE:H	1:A:21:ILE:CD1	2.18	0.54
1:B:60:ILE:N	1:B:60:ILE:HD12	2.22	0.54
1:C:30:ASN:ND2	1:C:32:THR:H	2.05	0.54
1:D:67:ILE:HB	1:D:72:THR:OG1	2.08	0.53
1:D:110:LEU:HD23	1:D:122:ILE:CD1	2.38	0.53
1:D:176:ASP:HB2	1:D:195:ASP:HB3	1.90	0.53
1:B:312:THR:OG1	1:B:314:ASN:ND2	2.41	0.53
1:A:45:ILE:HG22	3:A:388:HOH:O	2.06	0.53
1:B:27:LEU:HD22	1:B:27:LEU:N	2.23	0.53
1:C:254:LYS:HD2	1:C:273:TYR:HE2	1.74	0.53
1:D:21:ILE:N	1:D:21:ILE:HD13	2.20	0.53
1:A:198:TYR:HB3	1:A:200:ILE:HD11	1.90	0.53
1:D:144:VAL:HG12	3:D:638:HOH:O	2.08	0.53
1:B:165:ASP:OD1	1:B:167:THR:HB	2.10	0.52
1:C:176:ASP:OD1	1:D:136:LYS:HE3	2.09	0.52
1:B:196:LYS:HD2	1:B:209:ASN:HB2	1.90	0.52
1:B:113:THR:HG22	1:B:119:LEU:HD23	1.92	0.52
1:A:158:TYR:CE1	1:A:173:LYS:HB2	2.45	0.52
1:A:141:THR:HB	1:A:181:ALA:HB2	1.92	0.52
1:D:200:ILE:HG22	1:D:201:ASN:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:219:ARG:HH12	1:C:299:THR:HG21	1.75	0.51
1:A:47:THR:H	1:D:56:LYS:HD3	1.75	0.51
1:B:84:ASN:HD22	1:B:316:LYS:HD3	1.75	0.51
1:A:21:ILE:HD13	1:A:21:ILE:N	2.21	0.51
1:A:110:LEU:HD22	1:D:16:LEU:HD12	1.92	0.51
1:D:314:ASN:OD1	1:D:316:LYS:HG2	2.10	0.51
1:C:312:THR:OG1	1:C:314:ASN:ND2	2.44	0.51
1:D:109:ILE:HD12	3:D:360:HOH:O	2.11	0.50
1:D:178:ILE:CD1	1:D:194:SER:HB3	2.39	0.50
1:C:287:LYS:HG2	1:C:288:TRP:HD1	1.76	0.50
1:B:292:THR:HG22	1:B:294:SER:N	2.25	0.50
1:A:198:TYR:HB3	1:A:200:ILE:CD1	2.42	0.50
1:D:56:LYS:HD2	1:D:57:SER:N	2.26	0.50
1:B:110:LEU:HB3	1:B:122:ILE:HB	1.93	0.50
1:A:46:ASN:HA	1:D:56:LYS:HD3	1.94	0.49
1:D:56:LYS:NZ	1:D:58:GLY:HA3	2.27	0.49
1:A:265:THR:O	1:A:266:ASP:HB2	2.12	0.49
1:D:251:LYS:HG3	3:D:346:HOH:O	2.11	0.49
1:D:106:PHE:HB2	1:D:144:VAL:HG11	1.94	0.49
1:C:263:GLY:C	1:C:265:THR:H	2.16	0.49
1:C:264:ASN:HD21	1:C:306:GLY:HA3	1.77	0.49
1:C:84:ASN:ND2	1:C:316:LYS:HE3	2.27	0.49
1:A:256:ILE:HD13	1:A:272:SER:HA	1.93	0.49
1:D:70:ASP:HB2	1:D:72:THR:HG23	1.95	0.49
1:B:93:PHE:CD2	1:B:93:PHE:N	2.81	0.49
1:D:64:ARG:HB3	3:D:541:HOH:O	2.13	0.49
1:A:199:ALA:C	1:A:200:ILE:HD12	2.34	0.48
1:B:219:ARG:HD3	3:B:599:HOH:O	2.13	0.48
1:B:314:ASN:HD22	1:B:314:ASN:C	2.16	0.48
1:A:104:THR:HG22	1:A:142:PRO:HG2	1.96	0.48
1:A:112:VAL:HG12	1:A:122:ILE:HD13	1.96	0.48
1:A:19:ASN:HD22	1:D:11:ILE:HD11	1.79	0.48
1:A:32:THR:HG22	1:A:33:ILE:N	2.28	0.48
1:C:314:ASN:HD22	1:C:314:ASN:C	2.17	0.48
1:C:281:ASN:OD1	1:C:287:LYS:HE3	2.13	0.47
1:C:74:TYR:CZ	1:C:76:GLY:HA3	2.49	0.47
1:A:233:LEU:HD13	1:B:116:ASP:HA	1.96	0.47
1:B:83:ILE:HG22	1:B:85:PRO:HD3	1.96	0.47
1:B:63:CYS:HB2	1:B:80:VAL:CG2	2.43	0.47
1:C:254:LYS:HD2	1:C:273:TYR:CE2	2.50	0.47
1:D:200:ILE:HD12	1:D:200:ILE:N	2.30	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:196:LYS:HA	3:C:337:HOH:O	2.14	0.47
1:C:295:TRP:CH2	1:D:122:ILE:HD13	2.50	0.46
1:A:46:ASN:HA	1:D:56:LYS:CG	2.45	0.46
1:B:28:ALA:HB2	1:B:34:TYR:HE1	1.81	0.46
1:C:104:THR:HG22	1:C:142:PRO:HG2	1.97	0.46
1:A:47:THR:HG23	1:A:48:ASP:N	2.30	0.46
1:D:115:MSE:HG2	1:D:139:TYR:CE1	2.51	0.46
1:D:86:ASP:OD1	1:D:88:THR:HG22	2.15	0.46
1:B:86:ASP:OD1	1:B:88:THR:HG22	2.15	0.46
1:A:256:ILE:HD13	1:A:272:SER:HB3	1.96	0.46
1:B:158:TYR:CD2	1:B:171:ARG:HD2	2.50	0.46
1:B:279:ALA:C	1:B:280:ILE:HD12	2.35	0.46
1:C:18:GLY:HA3	1:D:314:ASN:O	2.16	0.46
1:B:280:ILE:HD12	1:B:280:ILE:N	2.31	0.46
1:C:231:THR:HG23	1:C:260:PRO:HD3	1.98	0.46
1:A:122:ILE:N	1:A:122:ILE:HD12	2.31	0.45
1:C:196:LYS:HG2	1:C:198:TYR:CE1	2.50	0.45
1:B:229:TYR:CG	1:B:268:ILE:HD12	2.52	0.45
1:D:53:TRP:HB2	1:D:60:ILE:HD13	1.98	0.45
1:A:159:LEU:HD22	1:A:192:PHE:CE1	2.51	0.45
1:C:135:LYS:HB2	1:C:156:ASP:CB	2.46	0.45
1:D:87:GLY:HA2	1:D:90:LYS:HE3	1.98	0.45
1:D:172:PHE:CE2	1:D:206:GLU:HB2	2.51	0.45
1:D:42:LEU:HD23	3:D:355:HOH:O	2.16	0.45
1:D:28:ALA:HB2	1:D:34:TYR:CD1	2.52	0.45
1:A:299:THR:HB	3:A:668:HOH:O	2.16	0.45
1:B:295:TRP:CB	1:B:313:ARG:HD2	2.47	0.45
1:C:13:TRP:HB3	1:C:16:LEU:CD2	2.44	0.45
1:A:123:ASN:HB2	1:A:127:THR:HG22	1.98	0.45
1:C:223:SER:OG	1:C:225:ASP:OD1	2.35	0.44
1:C:135:LYS:HB2	1:C:156:ASP:HB2	2.00	0.44
1:B:269:TYR:CD2	1:B:320:LEU:HD23	2.52	0.44
1:B:31:GLY:HA2	1:B:219:ARG:CZ	2.47	0.44
1:D:31:GLY:HA2	1:D:219:ARG:CZ	2.47	0.44
1:D:56:LYS:HD2	1:D:58:GLY:H	1.83	0.44
1:C:287:LYS:HG2	1:C:288:TRP:CD1	2.53	0.44
1:B:13:TRP:CZ3	1:B:110:LEU:HB2	2.53	0.44
1:D:259:SER:H	1:D:299:THR:HG22	1.83	0.44
1:D:73:ILE:HD12	1:D:73:ILE:N	2.33	0.44
1:B:292:THR:CG2	1:B:294:SER:HB2	2.48	0.44
1:A:200:ILE:HD12	1:A:200:ILE:N	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:219:ARG:HD3	3:D:431:HOH:O	2.17	0.44
1:A:231:THR:HG23	1:A:260:PRO:HD3	2.00	0.44
1:C:30:ASN:HD22	1:C:30:ASN:C	2.21	0.44
1:C:280:ILE:HG22	1:C:281:ASN:O	2.18	0.43
1:D:158:TYR:CE2	1:D:173:LYS:HB2	2.53	0.43
1:A:294:SER:CB	1:A:314:ASN:HD21	2.32	0.43
1:D:156:ASP:O	1:D:157:ASN:HB2	2.17	0.43
1:A:120:TYR:HB3	1:A:122:ILE:CD1	2.48	0.43
1:B:268:ILE:HG22	1:B:280:ILE:O	2.18	0.43
1:D:275:GLY:HA3	1:D:294:SER:O	2.18	0.42
1:A:122:ILE:HG22	1:A:123:ASN:O	2.19	0.42
1:B:171:ARG:NH2	3:B:354:HOH:O	2.50	0.42
1:B:158:TYR:CE2	1:B:173:LYS:HB2	2.54	0.42
1:D:267:THR:HG21	1:D:287:LYS:HE2	2.01	0.42
1:B:42:LEU:N	1:B:42:LEU:HD22	2.34	0.42
1:D:32:THR:HG22	1:D:33:ILE:H	1.82	0.42
1:A:143:ILE:HD13	1:A:182:ALA:O	2.19	0.42
1:B:275:GLY:HA3	1:B:294:SER:O	2.19	0.42
1:C:219:ARG:NH1	1:C:299:THR:HG21	2.34	0.42
1:B:292:THR:HG23	1:B:318:TYR:CZ	2.54	0.42
1:D:271:GLY:HA3	1:D:296:ILE:HD11	2.01	0.42
1:A:303:ASP:OD2	1:A:307:THR:HB	2.20	0.42
1:D:123:ASN:HB2	1:D:125:ASP:OD1	2.20	0.42
1:A:135:LYS:O	1:A:136:LYS:HD2	2.19	0.42
1:A:34:TYR:HA	1:A:302:ILE:O	2.20	0.42
1:B:216:THR:HG23	3:B:495:HOH:O	2.20	0.42
1:B:80:VAL:HG23	1:B:80:VAL:O	2.20	0.41
1:D:155:ASN:HA	1:D:177:ALA:HB1	2.01	0.41
1:D:292:THR:HB	1:D:318:TYR:CZ	2.55	0.41
1:D:145:SER:HB3	1:D:151:TYR:HE2	1.85	0.41
1:C:219:ARG:HG2	1:C:219:ARG:HH11	1.85	0.41
1:B:235:GLY:HA2	1:B:254:LYS:O	2.19	0.41
1:B:256:ILE:HD13	1:B:272:SER:HA	2.02	0.41
1:B:264:ASN:ND2	1:B:306:GLY:HA3	2.35	0.41
1:C:224:GLU:HG2	3:C:434:HOH:O	2.20	0.41
1:B:231:THR:HB	1:B:256:ILE:HG21	2.03	0.41
1:B:265:THR:O	1:B:266:ASP:HB2	2.20	0.41
1:C:15:PHE:CE1	1:C:16:LEU:HD22	2.56	0.41
1:C:61:ILE:HD13	1:C:82:ALA:O	2.20	0.41
1:A:47:THR:CG2	1:D:56:LYS:HZ3	2.34	0.41
1:A:262:ILE:HD12	1:A:268:ILE:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:143:ILE:C	1:D:143:ILE:HD13	2.40	0.41
1:B:53:TRP:CD1	1:B:60:ILE:HG21	2.55	0.41
1:B:295:TRP:HB3	1:B:313:ARG:HD2	2.03	0.41
1:B:218:THR:HB	1:B:259:SER:OG	2.21	0.41
1:D:118:HIS:HB2	1:D:120:TYR:CE1	2.56	0.41
1:D:258:SER:HB2	1:D:299:THR:HG22	2.03	0.41
1:C:174:THR:CB	1:C:194:SER:HG	2.34	0.40
1:B:192:PHE:HE1	1:B:200:ILE:HD11	1.86	0.40
1:D:256:ILE:HD13	1:D:272:SER:HA	2.02	0.40
1:D:35:LEU:HD12	1:D:309:TYR:CE2	2.56	0.40
1:B:64:ARG:CG	1:B:73:ILE:HD11	2.51	0.40
1:B:87:GLY:HA3	3:D:622:HOH:O	2.21	0.40
1:A:159:LEU:HD22	1:A:192:PHE:CD1	2.56	0.40
1:B:236:HIS:HB2	1:B:238:TYR:CE1	2.56	0.40
1:B:90:LYS:HD3	1:B:91:TRP:N	2.36	0.40
1:C:218:THR:HB	1:C:259:SER:OG	2.22	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	302/330 (92%)	290 (96%)	12 (4%)	0	100	100
1	B	284/330 (86%)	273 (96%)	11 (4%)	0	100	100
1	C	276/330 (84%)	266 (96%)	9 (3%)	1 (0%)	39	33
1	D	297/330 (90%)	285 (96%)	11 (4%)	1 (0%)	46	41
All	All	1159/1320 (88%)	1114 (96%)	43 (4%)	2 (0%)	52	48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	102	ASP
1	C	194	SER

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	258/277 (93%)	255 (99%)	3 (1%)	78	81
1	B	248/277 (90%)	238 (96%)	10 (4%)	38	33
1	C	240/277 (87%)	232 (97%)	8 (3%)	45	43
1	D	256/277 (92%)	248 (97%)	8 (3%)	47	46
All	All	1002/1108 (90%)	973 (97%)	29 (3%)	50	49

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	ILE
1	A	209	ASN
1	A	214	TYR
1	B	16	LEU
1	B	27	LEU
1	B	45	ILE
1	B	75	PHE
1	B	90	LYS
1	B	93	PHE
1	B	110	LEU
1	B	141	THR
1	B	214	TYR
1	B	314	ASN
1	C	12	LYS
1	C	30	ASN
1	C	48	ASP
1	C	59	GLU
1	C	61	ILE
1	C	69	LYS
1	C	214	TYR

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Mol	Chain	Res	Type
1	C	314	ASN
1	D	16	LEU
1	D	21	ILE
1	D	26	ILE
1	D	56	LYS
1	D	90	LYS
1	D	143	ILE
1	D	176	ASP
1	D	214	TYR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	46	ASN
1	A	209	ASN
1	A	264	ASN
1	A	305	ASN
1	B	41	ASN
1	B	46	ASN
1	B	84	ASN
1	B	201	ASN
1	B	241	ASN
1	B	264	ASN
1	B	314	ASN
1	C	30	ASN
1	C	46	ASN
1	C	123	ASN
1	C	163	ASN
1	C	241	ASN
1	C	264	ASN
1	C	314	ASN
1	D	41	ASN
1	D	46	ASN
1	D	123	ASN
1	D	209	ASN
1	D	241	ASN
1	D	264	ASN
1	D	305	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 carbohydrates in this entry.

5.6 Ligand geometry

7 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	351	-	4,4,4	0.22	0	6,6,6	0.09	0
2	SO4	C	331	-	4,4,4	0.26	0	6,6,6	0.08	0
2	SO4	C	351	-	4,4,4	0.21	0	6,6,6	0.07	0
2	SO4	C	352	-	4,4,4	0.18	0	6,6,6	0.07	0
2	SO4	C	353	-	4,4,4	0.22	0	6,6,6	0.10	0
2	SO4	D	351	-	4,4,4	0.21	0	6,6,6	0.07	0
2	SO4	D	352	-	4,4,4	0.22	0	6,6,6	0.07	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	B	351	-	-	0/0/0/0	0/0/0/0
2	SO4	C	331	-	-	0/0/0/0	0/0/0/0
2	SO4	C	351	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	C	352	-	-	0/0/0/0	0/0/0/0
2	SO4	C	353	-	-	0/0/0/0	0/0/0/0
2	SO4	D	351	-	-	0/0/0/0	0/0/0/0
2	SO4	D	352	-	-	0/0/0/0	0/0/0/0

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

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	305/330 (92%)	-0.13	8 (2%) 59 60	8, 19, 46, 63	0
1	B	293/330 (88%)	0.37	31 (10%) 8 9	9, 25, 62, 78	0
1	C	285/330 (86%)	0.08	17 (5%) 25 27	9, 21, 54, 74	0
1	D	302/330 (91%)	0.05	15 (4%) 32 34	12, 26, 47, 57	0
All	All	1185/1320 (89%)	0.09	71 (5%) 25 27	8, 23, 54, 78	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	36	GLY	9.2
1	B	47	THR	7.5
1	C	47	THR	7.4
1	B	49	GLY	6.6
1	B	75	PHE	6.3
1	B	48	ASP	6.2
1	C	45	ILE	6.1
1	B	45	ILE	5.9
1	B	51	VAL	5.2
1	C	55	PHE	5.0
1	B	54	PHE	4.8
1	B	50	SER	4.6
1	B	73	ILE	4.6
1	B	322	ASN	4.4
1	B	41	ASN	4.3
1	C	48	ASP	4.3
1	B	38	SER	4.2
1	B	40	LYS	4.0
1	A	47	THR	4.0
1	B	46	ASN	3.9
1	D	73	ILE	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	40	LYS	3.9
1	C	46	ASN	3.7
1	C	51	VAL	3.6
1	B	93	PHE	3.6
1	D	47	THR	3.5
1	B	55	PHE	3.4
1	B	42	LEU	3.4
1	C	42	LEU	3.4
1	B	27	LEU	3.3
1	D	34	TYR	3.3
1	B	52	LYS	3.3
1	B	17	ILE	3.2
1	B	58	GLY	3.1
1	B	90	LYS	3.1
1	C	50	SER	3.0
1	A	38	SER	3.0
1	D	11	ILE	2.8
1	B	16	LEU	2.8
1	A	21	ILE	2.8
1	C	49	GLY	2.8
1	C	75	PHE	2.7
1	B	26	ILE	2.7
1	D	75	PHE	2.7
1	C	70	ASP	2.6
1	B	39	ASN	2.6
1	B	53	TRP	2.6
1	C	54	PHE	2.6
1	B	91	TRP	2.6
1	C	24	SER	2.6
1	D	24	SER	2.5
1	B	92	ARG	2.5
1	D	88	THR	2.5
1	D	71	GLY	2.5
1	C	26	ILE	2.5
1	B	57	SER	2.4
1	A	24	SER	2.4
1	D	70	ASP	2.4
1	D	101	SER	2.4
1	D	23	SER	2.4
1	C	34	TYR	2.3
1	D	21	ILE	2.3
1	A	45	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	304	GLU	2.2
1	C	59	GLU	2.2
1	D	127	THR	2.1
1	D	19	ASN	2.1
1	B	317	PHE	2.1
1	A	146	GLU	2.1
1	D	72	THR	2.1
1	A	19	ASN	2.1

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, 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
2	SO4	B	351	5/5	0.86	0.17	3.20	58,66,70,72	0
2	SO4	D	352	5/5	0.94	0.17	-	77,77,80,82	0
2	SO4	C	353	5/5	0.96	0.17	-	43,47,57,66	0
2	SO4	C	331	5/5	0.96	0.10	-	42,43,47,50	0
2	SO4	C	352	5/5	0.94	0.13	-	43,48,56,61	0
2	SO4	C	351	5/5	0.97	0.16	-	47,52,55,56	0
2	SO4	D	351	5/5	0.97	0.15	-	51,53,58,60	0

6.5 Other polymers (i)

There are no such residues in this entry.