Full wwPDB X-ray Structure Validation Report (i)

Jun 16, 2024 – 09:13 AM EDT

PDB ID	:	5D5O
Title	:	HcgC from Methanocaldococcus jannaschii
Authors	:	Fujishiro, T.; Ermler, U.; Shima, S.
Deposited on	:	2015-08-11
Resolution	:	2.70 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:

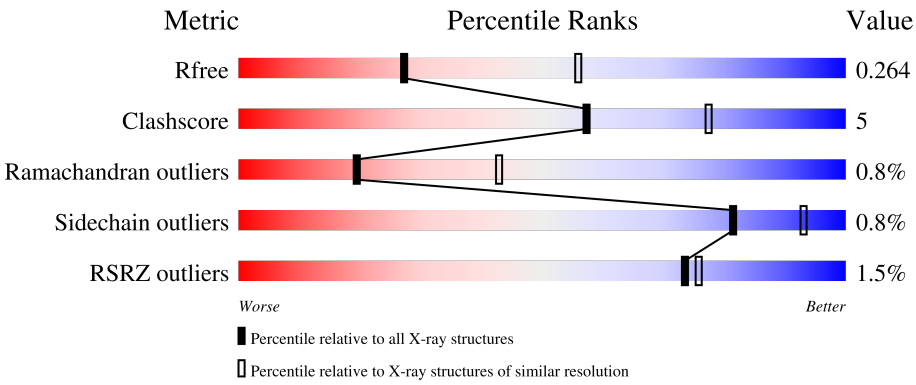
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 2.70 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	268	83% 9% 8%
1	B	268	3% 74% 14% • 9%
1	C	268	% 84% 7% • 9%
1	D	268	82% 10% • 7%
1	E	268	% 83% 9% 8%

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Mol	Chain	Length	Quality of chain
1	F	268	4% 77% 13% • 9%
1	G	268	% 82% 8% • 9%
1	H	268	% 82% 9% • 7%

2 Entry composition (i)

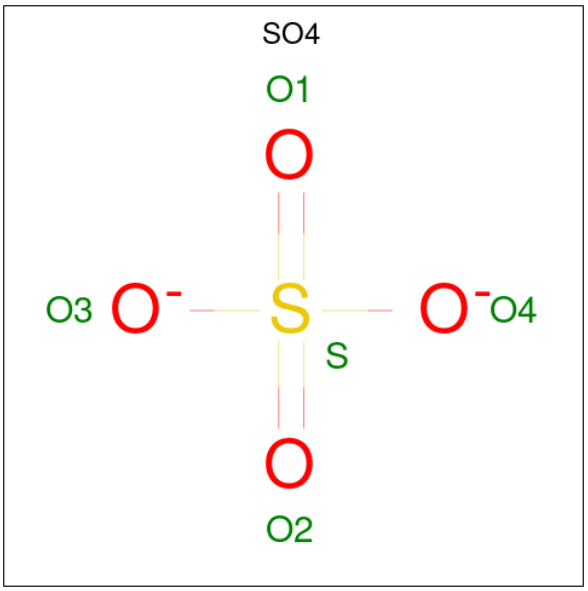
There are 3 unique types of molecules in this entry. The entry contains 15905 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Uncharacterized protein MJ0489.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	246	1985	1287	315	380	3	0	0	0
1	B	244	1967	1277	310	377	3	0	0	0
1	C	245	1977	1283	313	378	3	0	0	0
1	D	248	2001	1295	319	384	3	0	0	0
1	E	247	1993	1291	317	382	3	0	0	0
1	F	243	1961	1274	309	375	3	0	0	0
1	G	245	1977	1283	313	378	3	0	0	0
1	H	248	2001	1295	319	384	3	0	0	0

- 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

- Molecule 3 is water.

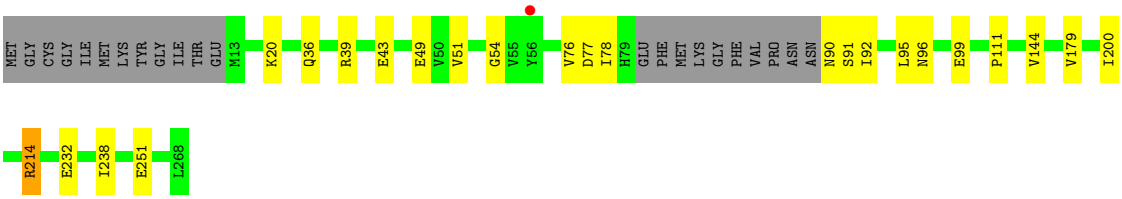
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	8	8	8	0	0
3	B	2	2	2	0	0
3	C	3	3	3	0	0
3	D	3	3	3	0	0
3	E	10	10	10	0	0
3	F	3	3	3	0	0
3	G	5	5	5	0	0
3	H	4	4	4	0	0

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.

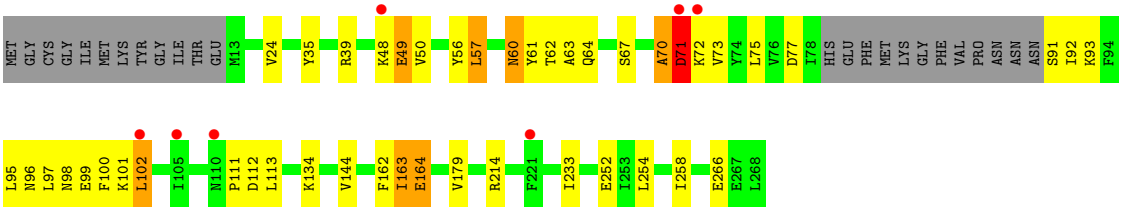
• Molecule 1: Uncharacterized protein MJ0489

Chain A:



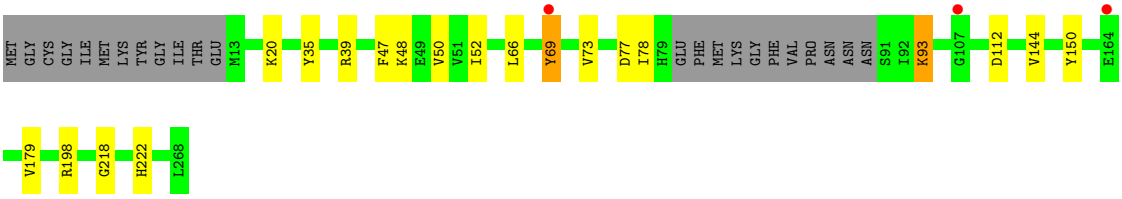
• Molecule 1: Uncharacterized protein MJ0489

Chain B:



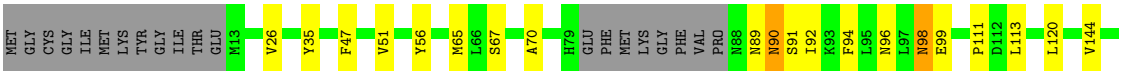
• Molecule 1: Uncharacterized protein MJ0489

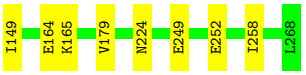
Chain C:



• Molecule 1: Uncharacterized protein MJ0489

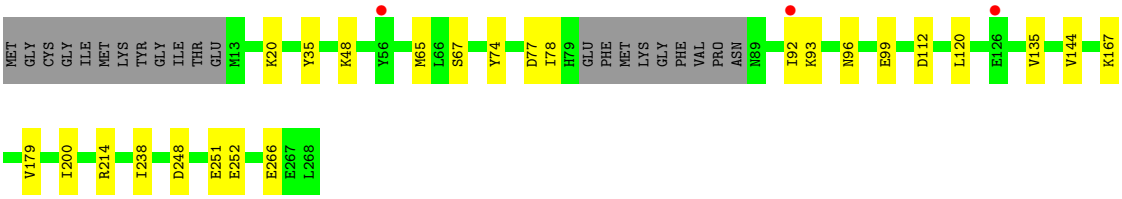
Chain D:





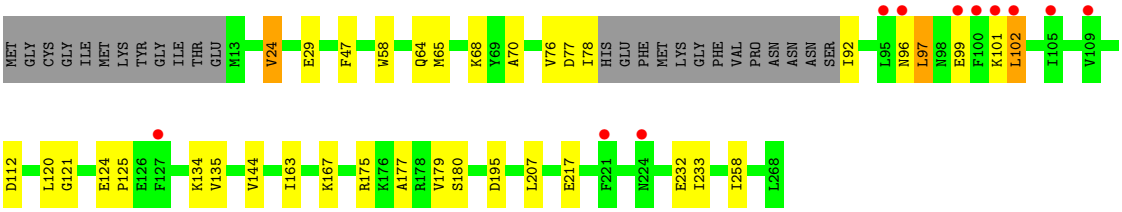
• Molecule 1: Uncharacterized protein MJ0489

Chain E:



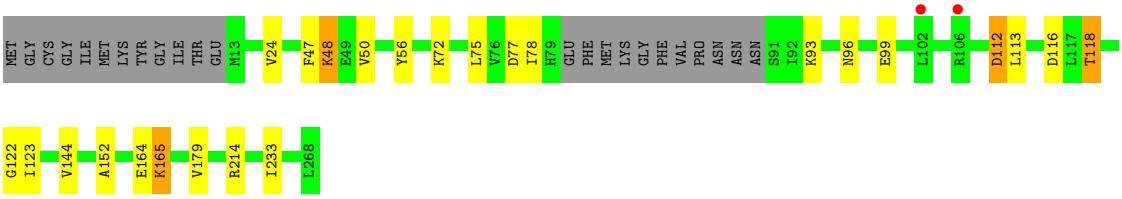
• Molecule 1: Uncharacterized protein MJ0489

Chain F:



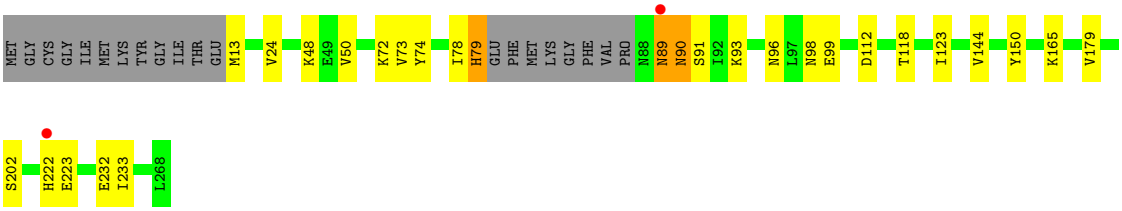
• Molecule 1: Uncharacterized protein MJ0489

Chain G:



• Molecule 1: Uncharacterized protein MJ0489

Chain H:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	142.25Å 143.28Å 148.33Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.33 – 2.70 48.33 – 2.70	Depositor EDS
% Data completeness (in resolution range)	94.5 (48.33-2.70) 94.6 (48.33-2.70)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.28 (at 2.69Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.217 , 0.263 0.218 , 0.264	Depositor DCC
R_{free} test set	4168 reflections (5.26%)	wwPDB-VP
Wilson B-factor (Å^2)	52.9	Xtriage
Anisotropy	0.054	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.32 , 37.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k 0.000 for -l,-k,-h 0.000 for k,h,-l 0.000 for k,l,h 0.000 for l,h,k	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	15905	wwPDB-VP
Average B, all atoms (Å^2)	61.0	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 51.42 % 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 5.6206e-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, 0.333 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	0/2021	0.60	0/2734
1	B	0.47	0/2002	0.71	3/2708 (0.1%)
1	C	0.39	0/2013	0.62	0/2723
1	D	0.40	0/2037	0.62	0/2756
1	E	0.39	0/2029	0.57	0/2745
1	F	0.39	0/1996	0.68	1/2700 (0.0%)
1	G	0.40	0/2013	0.63	0/2723
1	H	0.43	0/2037	0.67	0/2756
All	All	0.41	0/16148	0.64	4/21845 (0.0%)

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	B	0	3
1	F	0	1
1	G	0	1
All	All	0	5

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	71	ASP	CB-CG-OD1	6.44	124.10	118.30
1	F	102	LEU	CA-CB-CG	6.29	129.76	115.30
1	B	71	ASP	OD1-CG-OD2	-5.56	112.73	123.30
1	B	102	LEU	CA-CB-CG	5.37	127.65	115.30

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	163	ILE	Peptide
1	B	70	ALA	Peptide
1	B	71	ASP	Peptide
1	F	163	ILE	Peptide
1	G	164	GLU	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	1985	0	2008	14	0
1	B	1967	0	1995	38	0
1	C	1977	0	2002	16	0
1	D	2001	0	2020	16	0
1	E	1993	0	2014	15	0
1	F	1961	0	1990	25	0
1	G	1977	0	2002	19	0
1	H	2001	0	2020	22	0
2	A	5	0	0	0	0
3	A	8	0	0	0	0
3	B	2	0	0	0	0
3	C	3	0	0	0	0
3	D	3	0	0	0	0
3	E	10	0	0	0	0
3	F	3	0	0	0	0
3	G	5	0	0	0	0
3	H	4	0	0	0	0
All	All	15905	0	16051	155	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 5.

All (155) 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:B:48:LYS:NZ	1:B:71:ASP:HB2	1.85	0.91
1:F:65:MET:SD	1:F:68:LYS:NZ	2.52	0.82
1:D:67:SER:HB3	1:D:92:ILE:HD11	1.63	0.80
1:C:218:GLY:O	1:C:222:HIS:HB3	1.84	0.78
1:D:164:GLU:HG2	1:D:165:LYS:HG3	1.65	0.78
1:F:99:GLU:HA	1:F:102:LEU:HG	1.67	0.77
1:B:48:LYS:HZ2	1:B:71:ASP:HB2	1.46	0.77
1:C:52:ILE:HD11	1:C:66:LEU:HD12	1.69	0.75
1:B:49:GLU:N	1:B:71:ASP:OD1	2.20	0.74
1:H:89:ASN:O	1:H:90:ASN:HB2	1.89	0.73
1:H:72:LYS:HE2	1:H:93:LYS:HZ1	1.55	0.71
1:B:60:ASN:O	1:B:63:ALA:N	2.25	0.69
1:H:144:VAL:HG11	1:H:179:VAL:HG13	1.76	0.68
1:F:29:GLU:HG2	1:F:258:ILE:HG21	1.76	0.67
1:B:97:LEU:HG	1:B:101:LYS:HE3	1.77	0.66
1:F:58:TRP:NE1	1:F:217:GLU:OE2	2.28	0.66
1:D:90:ASN:OD1	1:D:91:SER:N	2.21	0.66
1:B:48:LYS:HZ3	1:B:71:ASP:HB2	1.58	0.66
1:G:118:THR:CG2	1:G:122:GLY:HA3	2.27	0.64
1:B:24:VAL:HG23	1:B:233:ILE:O	1.97	0.64
1:D:98:ASN:H	1:D:98:ASN:HD22	1.45	0.63
1:D:98:ASN:HD22	1:D:98:ASN:N	1.95	0.63
1:F:77:ASP:OD1	1:F:78:ILE:N	2.32	0.62
1:C:48:LYS:N	1:C:112:ASP:OD2	2.31	0.62
1:A:214:ARG:CZ	1:A:232:GLU:OE1	2.48	0.61
1:G:116:ASP:OD1	1:G:118:THR:HB	2.00	0.60
1:B:70:ALA:HB1	1:B:71:ASP:OD2	2.00	0.60
1:G:48:LYS:HG3	1:G:112:ASP:OD2	2.02	0.60
1:A:43:GLU:OE1	1:H:98:ASN:ND2	2.34	0.59
1:E:77:ASP:OD1	1:E:78:ILE:N	2.35	0.59
1:H:96:ASN:OD1	1:H:99:GLU:HG3	2.03	0.58
1:B:48:LYS:HG3	1:B:71:ASP:CB	2.34	0.58
1:B:91:SER:OG	1:B:92:ILE:N	2.34	0.58
1:D:249:GLU:HA	1:D:252:GLU:HG2	1.86	0.58
1:H:72:LYS:HE2	1:H:93:LYS:NZ	2.18	0.58
1:B:67:SER:HA	1:B:73:VAL:HG21	1.85	0.58
1:D:144:VAL:HG11	1:D:179:VAL:HG13	1.86	0.57
1:E:214:ARG:NH2	1:F:232:GLU:OE1	2.29	0.56
1:B:144:VAL:HG11	1:B:179:VAL:HG13	1.87	0.56
1:G:152:ALA:HB1	1:H:13:MET:HE3	1.88	0.55
1:E:67:SER:HB3	1:E:92:ILE:HD11	1.87	0.55
1:E:120:LEU:HD12	1:F:207:LEU:HD21	1.89	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:PHE:O	1:B:164:GLU:N	2.40	0.55
1:B:96:ASN:HD21	1:B:99:GLU:HG3	1.72	0.55
1:E:200:ILE:HD12	1:E:238:ILE:HD13	1.89	0.54
1:A:90:ASN:C	1:A:92:ILE:H	2.10	0.54
1:F:175:ARG:NH2	1:F:195:ASP:OD2	2.35	0.54
1:F:144:VAL:HG11	1:F:179:VAL:HG13	1.89	0.54
1:H:24:VAL:HG23	1:H:233:ILE:O	2.07	0.54
1:G:77:ASP:OD1	1:G:78:ILE:N	2.40	0.53
1:H:222:HIS:CD2	1:H:223:GLU:HG2	2.43	0.53
1:G:118:THR:HG21	1:G:123:ILE:H	1.73	0.53
1:A:36:GLN:HG2	1:A:39:ARG:NH2	2.24	0.53
1:C:144:VAL:HG11	1:C:179:VAL:HG13	1.89	0.53
1:A:200:ILE:HD12	1:A:238:ILE:HD13	1.90	0.53
1:B:97:LEU:O	1:B:101:LYS:HG2	2.09	0.53
1:G:214:ARG:NH1	1:H:232:GLU:OE1	2.41	0.53
1:A:232:GLU:OE2	1:B:214:ARG:NH1	2.42	0.52
1:H:24:VAL:HG22	1:H:233:ILE:HG23	1.91	0.52
1:B:93:LYS:N	1:B:93:LYS:HD3	2.25	0.52
1:B:48:LYS:HG3	1:B:71:ASP:HB2	1.91	0.52
1:B:67:SER:HB3	1:B:92:ILE:HD11	1.91	0.52
1:B:99:GLU:HA	1:B:102:LEU:HG	1.92	0.52
1:G:24:VAL:HG23	1:G:233:ILE:O	2.09	0.51
1:G:50:VAL:HG22	1:G:113:LEU:HB3	1.92	0.51
1:H:78:ILE:N	1:H:79:HIS:HA	2.26	0.51
1:G:72:LYS:HD3	1:G:93:LYS:NZ	2.25	0.51
1:E:96:ASN:OD1	1:E:99:GLU:HG3	2.11	0.51
1:B:64:GLN:O	1:B:67:SER:OG	2.23	0.51
1:B:71:ASP:CG	1:B:72:LYS:N	2.64	0.50
1:G:96:ASN:OD1	1:G:99:GLU:HG3	2.12	0.50
1:A:90:ASN:O	1:A:92:ILE:N	2.43	0.50
1:D:56:TYR:HE1	1:D:94:PHE:CE2	2.30	0.50
1:C:198:ARG:HH11	1:C:198:ARG:HG2	1.76	0.49
1:G:152:ALA:HB1	1:H:13:MET:CE	2.41	0.49
1:H:78:ILE:H	1:H:79:HIS:HA	1.77	0.49
1:E:20:LYS:N	1:E:251:GLU:OE2	2.43	0.49
1:C:35:TYR:HH	1:C:69:TYR:HH	1.61	0.49
1:E:248:ASP:O	1:E:252:GLU:OE1	2.30	0.49
1:A:49:GLU:HB3	1:A:111:PRO:HA	1.93	0.49
1:F:76:VAL:HG12	1:F:97:LEU:CD1	2.42	0.49
1:F:135:VAL:HG22	1:F:167:LYS:HB3	1.94	0.48
1:H:90:ASN:OD1	1:H:91:SER:N	2.32	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:177:ALA:HB1	1:H:202:SER:HB2	1.94	0.48
1:D:120:LEU:HD11	1:D:149:ILE:HG23	1.96	0.48
1:B:96:ASN:ND2	1:B:98:ASN:HB2	2.28	0.48
1:C:77:ASP:OD1	1:C:78:ILE:N	2.47	0.48
1:B:49:GLU:HG3	1:B:111:PRO:HA	1.96	0.47
1:D:47:PHE:CD1	1:D:113:LEU:HB2	2.49	0.47
1:F:78:ILE:HG13	1:F:97:LEU:HD13	1.96	0.47
1:G:144:VAL:HG11	1:G:179:VAL:HG13	1.96	0.47
1:A:96:ASN:OD1	1:A:99:GLU:HG3	2.14	0.47
1:B:266:GLU:OE2	1:C:150:TYR:OH	2.33	0.47
1:B:56:TYR:O	1:B:57:LEU:HB3	2.15	0.47
1:F:96:ASN:OD1	1:F:96:ASN:N	2.48	0.47
1:G:72:LYS:HD3	1:G:93:LYS:HZ3	1.80	0.47
1:C:35:TYR:OH	1:C:69:TYR:OH	2.30	0.46
1:E:35:TYR:CZ	1:E:65:MET:HB3	2.51	0.46
1:A:144:VAL:HG11	1:A:179:VAL:HG13	1.97	0.46
1:C:35:TYR:HE2	1:C:39:ARG:NH1	2.14	0.46
1:B:48:LYS:HA	1:B:71:ASP:CG	2.36	0.46
1:F:24:VAL:HG13	1:F:233:ILE:HG12	1.98	0.46
1:F:175:ARG:HD3	1:F:180:SER:OG	2.16	0.46
1:A:54:GLY:O	1:A:77:ASP:HA	2.16	0.45
1:B:95:LEU:HD23	1:B:100:PHE:HB2	1.98	0.45
1:B:35:TYR:CE2	1:B:39:ARG:HD2	2.51	0.45
1:H:112:ASP:OD1	1:H:112:ASP:N	2.48	0.45
1:C:47:PHE:HD2	1:C:112:ASP:HB2	1.81	0.45
1:H:48:LYS:HE3	1:H:48:LYS:HB2	1.76	0.45
1:H:118:THR:HG21	1:H:123:ILE:HG12	1.99	0.45
1:A:51:VAL:HG23	1:A:111:PRO:HB3	1.98	0.44
1:B:60:ASN:O	1:B:62:THR:N	2.50	0.44
1:D:35:TYR:CZ	1:D:65:MET:HB3	2.52	0.44
1:A:76:VAL:HA	1:A:95:LEU:O	2.18	0.44
1:B:56:TYR:N	1:B:77:ASP:OD1	2.50	0.44
1:B:73:VAL:HB	1:B:92:ILE:HD12	1.98	0.44
1:D:96:ASN:OD1	1:D:99:GLU:HG3	2.16	0.44
1:B:49:GLU:H	1:B:71:ASP:CG	2.18	0.44
1:F:65:MET:O	1:F:68:LYS:HD2	2.18	0.43
1:C:222:HIS:CD2	1:C:222:HIS:O	2.71	0.43
1:D:89:ASN:OD1	1:D:90:ASN:N	2.41	0.43
1:F:65:MET:HA	1:F:68:LYS:NZ	2.33	0.43
1:F:99:GLU:CA	1:F:102:LEU:HG	2.44	0.43
1:G:72:LYS:HE2	1:G:72:LYS:HB2	1.77	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:97:LEU:O	1:F:101:LYS:HG3	2.19	0.43
1:F:124:GLU:HA	1:F:125:PRO:HD3	1.91	0.43
1:E:144:VAL:HG11	1:E:179:VAL:HG13	2.00	0.42
1:F:99:GLU:HA	1:F:102:LEU:CG	2.44	0.42
1:B:50:VAL:HG22	1:B:113:LEU:HB3	2.01	0.42
1:C:93:LYS:HA	1:C:93:LYS:HD2	1.50	0.42
1:H:50:VAL:HB	1:H:73:VAL:HG22	2.00	0.42
1:F:92:ILE:HD12	1:F:92:ILE:N	2.34	0.42
1:E:74:TYR:CE1	1:E:93:LYS:HD2	2.55	0.42
1:D:47:PHE:O	1:D:70:ALA:HA	2.20	0.42
1:G:165:LYS:O	1:G:165:LYS:HG3	2.19	0.42
1:D:26:VAL:HG22	1:D:258:ILE:HD11	2.01	0.42
1:F:47:PHE:O	1:F:70:ALA:HA	2.19	0.41
1:F:112:ASP:O	1:F:134:LYS:N	2.50	0.41
1:B:112:ASP:HB2	1:B:134:LYS:HE2	2.01	0.41
1:B:254:LEU:O	1:B:258:ILE:HG13	2.21	0.41
1:E:135:VAL:HG22	1:E:167:LYS:HB3	2.02	0.41
1:E:266:GLU:OE2	1:H:150:TYR:OH	2.29	0.41
1:B:75:LEU:HD12	1:B:75:LEU:HA	1.87	0.41
1:E:48:LYS:HB3	1:E:48:LYS:HE2	1.86	0.41
1:E:112:ASP:OD1	1:E:112:ASP:N	2.52	0.41
1:G:47:PHE:HD1	1:G:112:ASP:HB2	1.86	0.41
1:D:51:VAL:HG23	1:D:111:PRO:HB3	2.02	0.41
1:C:222:HIS:CD2	1:C:222:HIS:C	2.94	0.41
1:G:56:TYR:HD1	1:G:75:LEU:HD22	1.85	0.41
1:C:50:VAL:CG1	1:C:73:VAL:HG22	2.51	0.41
1:G:24:VAL:CG2	1:G:233:ILE:HG23	2.51	0.41
1:A:20:LYS:N	1:A:251:GLU:OE2	2.52	0.40
1:B:96:ASN:OD1	1:B:96:ASN:N	2.54	0.40
1:C:20:LYS:O	1:C:20:LYS:HD2	2.22	0.40
1:H:74:TYR:CE2	1:H:93:LYS:HD2	2.56	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	242/268 (90%)	237 (98%)	3 (1%)	2 (1%)	19	43
1	B	240/268 (90%)	232 (97%)	1 (0%)	7 (3%)	4	10
1	C	241/268 (90%)	239 (99%)	2 (1%)	0	100	100
1	D	244/268 (91%)	241 (99%)	2 (1%)	1 (0%)	34	60
1	E	243/268 (91%)	240 (99%)	3 (1%)	0	100	100
1	F	239/268 (89%)	231 (97%)	6 (2%)	2 (1%)	19	43
1	G	241/268 (90%)	237 (98%)	4 (2%)	0	100	100
1	H	244/268 (91%)	238 (98%)	3 (1%)	3 (1%)	13	32
All	All	1934/2144 (90%)	1895 (98%)	24 (1%)	15 (1%)	19	43

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	91	SER
1	B	49	GLU
1	B	164	GLU
1	F	97	LEU
1	H	89	ASN
1	H	90	ASN
1	H	165	LYS
1	B	57	LEU
1	B	60	ASN
1	B	61	TYR
1	B	71	ASP
1	B	163	ILE
1	F	121	GLY
1	D	90	ASN
1	A	78	ILE

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	221/239 (92%)	220 (100%)	1 (0%)	88	96
1	B	219/239 (92%)	218 (100%)	1 (0%)	88	96
1	C	220/239 (92%)	218 (99%)	2 (1%)	78	92
1	D	223/239 (93%)	221 (99%)	2 (1%)	78	92
1	E	222/239 (93%)	222 (100%)	0	100	100
1	F	218/239 (91%)	215 (99%)	3 (1%)	67	86
1	G	220/239 (92%)	216 (98%)	4 (2%)	59	83
1	H	223/239 (93%)	222 (100%)	1 (0%)	91	97
All	All	1766/1912 (92%)	1752 (99%)	14 (1%)	81	93

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	214	ARG
1	B	252	GLU
1	C	69	TYR
1	C	93	LYS
1	D	98	ASN
1	D	224	ASN
1	F	24	VAL
1	F	64	GLN
1	F	120	LEU
1	G	48	LYS
1	G	112	ASP
1	G	118	THR
1	G	165	LYS
1	H	79	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	222	HIS
1	D	224	ASN
1	F	110	ASN
1	F	132	ASN

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)

1 ligand is 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	301	-	4,4,4	0.76	0	6,6,6	0.22	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	246/268 (91%)	-0.31	1 (0%)	92	93	32, 52, 83, 109	0
1	B	244/268 (91%)	0.06	7 (2%)	51	52	32, 67, 121, 139	0
1	C	245/268 (91%)	-0.05	3 (1%)	79	80	32, 56, 87, 104	0
1	D	248/268 (92%)	-0.41	0	100	100	31, 49, 77, 103	0
1	E	247/268 (92%)	-0.27	3 (1%)	79	80	35, 56, 91, 128	0
1	F	243/268 (90%)	0.07	11 (4%)	33	31	41, 68, 117, 149	0
1	G	245/268 (91%)	-0.08	2 (0%)	86	87	31, 54, 87, 97	0
1	H	248/268 (92%)	-0.23	2 (0%)	86	87	31, 54, 81, 114	0
All	All	1966/2144 (91%)	-0.15	29 (1%)	73	76	31, 56, 100, 149	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	222	HIS	4.6
1	B	71	ASP	4.1
1	A	56	TYR	3.9
1	F	102	LEU	3.8
1	F	105	ILE	3.5
1	E	56	TYR	3.1
1	C	69	TYR	3.0
1	F	109	VAL	3.0
1	E	126	GLU	3.0
1	F	95	LEU	2.7
1	B	221	PHE	2.6
1	B	102	LEU	2.6
1	H	89	ASN	2.4
1	G	106	ARG	2.4
1	F	127	PHE	2.4
1	B	72	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	100	PHE	2.3
1	F	101	LYS	2.3
1	B	105	ILE	2.3
1	F	221	PHE	2.3
1	C	164	GLU	2.2
1	C	107	GLY	2.2
1	G	102	LEU	2.2
1	B	110	ASN	2.1
1	F	99	GLU	2.1
1	F	96	ASN	2.1
1	F	224	ASN	2.1
1	B	48	LYS	2.0
1	E	92	ILE	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	301	5/5	0.91	0.43	144,144,169,213	0

6.5 Other polymers (i)

There are no such residues in this entry.