Full wwPDB X-ray Structure Validation Report ⓘ

Jun 16, 2024 – 05:31 AM EDT

PDB ID	:	2HO4
Title	:	Crystal Structure of Protein from Mouse Mm.236127
Authors	:	McCoy, J.G.; Wesenberg, G.E.; Bitto, E.; Phillips Jr., G.N.; Bingman, C.A.; Center for Eukaryotic Structural Genomics (CESG)
Deposited on	:	2006-07-13
Resolution	:	2.20 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 ⓘ 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 ⓘ) were used in the production of this report:

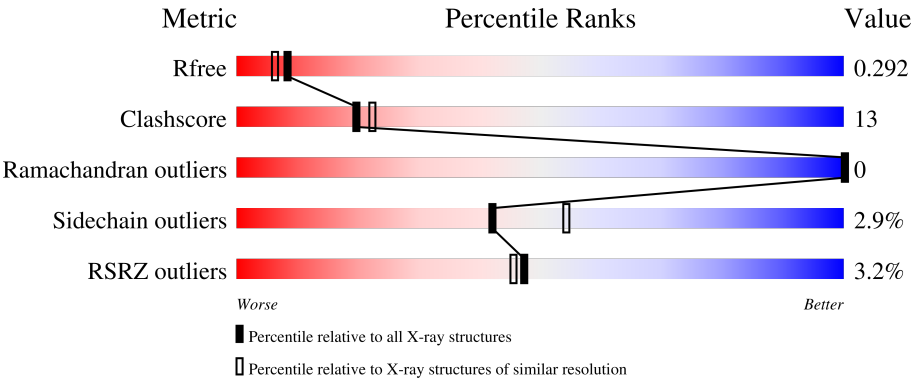
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, 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

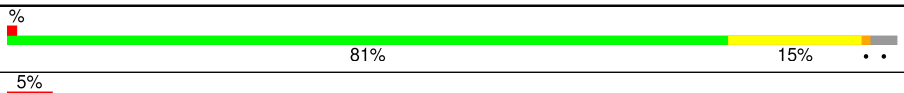
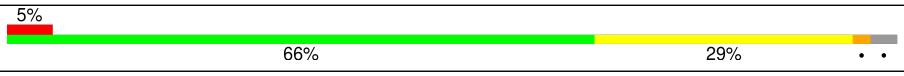
The reported resolution of this entry is 2.20 Å.

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	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)

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	259	
1	B	259	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4103 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 Haloacid dehalogenase-like hydrolase domain containing 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	Se	0	1	0
			1965	1254	335	368	3	5			
1	B	252	Total	C	N	O	S	Se	0	1	0
			1973	1258	337	370	3	5			

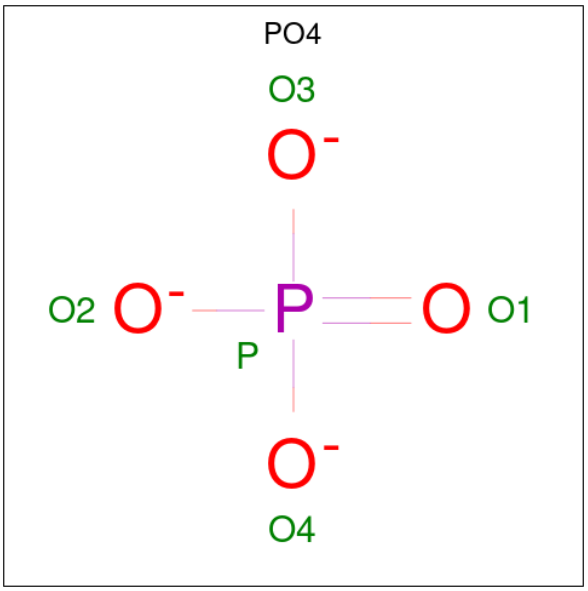
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	SER	-	CLONING ARTIFACT	UNP Q6PEB2
A	41	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
A	91	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
A	94	LEU	VAL	ENGINEERED MUTATION	UNP Q6PEB2
A	175	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
A	201	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
A	218	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
B	1	SER	-	CLONING ARTIFACT	UNP Q6PEB2
B	41	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
B	91	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
B	94	LEU	VAL	ENGINEERED MUTATION	UNP Q6PEB2
B	175	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
B	201	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2
B	218	MSE	MET	MODIFIED RESIDUE	UNP Q6PEB2

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0

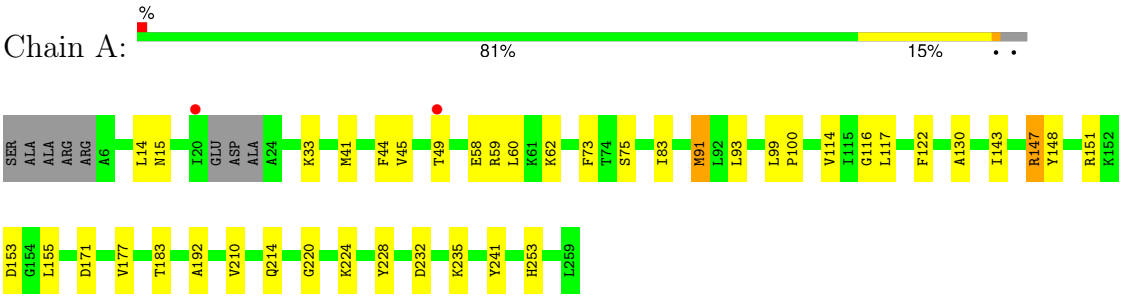
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	77	Total O 77 77	0	0
4	B	56	Total O 56 56	0	0

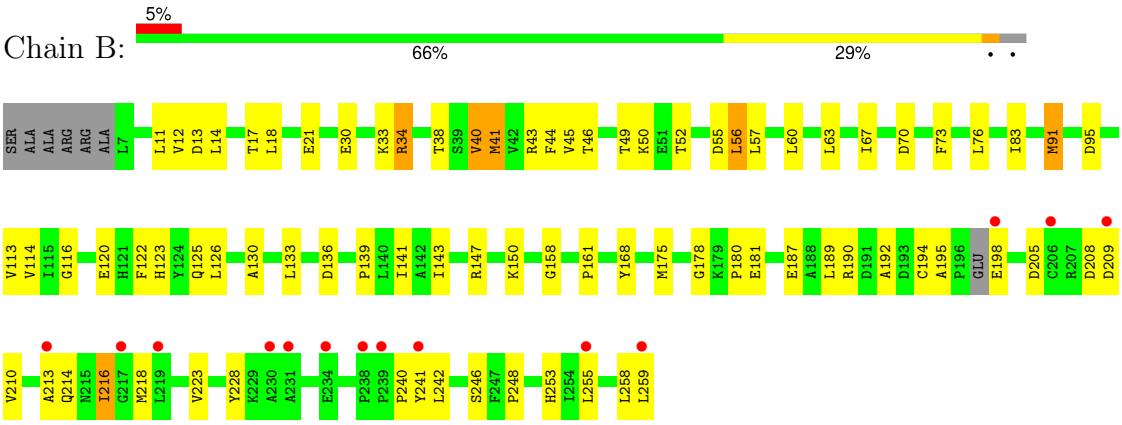
3 Residue-property plots (i)

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: Haloacid dehalogenase-like hydrolase domain containing 2



• Molecule 1: Haloacid dehalogenase-like hydrolase domain containing 2



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	46.59Å 68.08Å 190.98Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.50 – 2.20 46.50 – 2.20	Depositor EDS
% Data completeness (in resolution range)	96.0 (46.50-2.20) 96.1 (46.50-2.20)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.77 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.224 , 0.282 0.248 , 0.292	Depositor DCC
R_{free} test set	1546 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	43.3	Xtriage
Anisotropy	0.239	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 35.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	4103	wwPDB-VP
Average B, all atoms (Å^2)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.81% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, MG

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	0.88	1/1998 (0.1%)	0.81	1/2697 (0.0%)
1	B	0.80	1/2006 (0.0%)	0.81	2/2708 (0.1%)
All	All	0.84	2/4004 (0.0%)	0.81	3/5405 (0.1%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	91	MSE	SE-CE	-5.08	1.65	1.95
1	B	91	MSE	SE-CE	-5.07	1.65	1.95

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	147	ARG	NE-CZ-NH1	5.65	123.13	120.30
1	B	56	LEU	CA-CB-CG	5.59	128.16	115.30
1	B	34	ARG	NE-CZ-NH2	-5.40	117.60	120.30

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	1965	0	2005	37	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1973	0	2011	66	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	15	0	0	0	0
3	B	15	0	0	1	0
4	A	77	0	0	1	0
4	B	56	0	0	3	0
All	All	4103	0	4016	101	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 13.

All (101) 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:91:MSE:HE1	1:A:130:ALA:HB2	1.29	1.09
1:B:91:MSE:CE	1:B:133:LEU:HD12	1.94	0.98
1:B:91:MSE:HE1	1:B:130:ALA:HA	1.52	0.91
1:A:49:THR:HG21	1:A:117:LEU:H	1.35	0.90
1:A:91:MSE:HE3	1:A:93:LEU:CD1	2.03	0.89
1:B:189:LEU:HD21	1:B:218:MSE:HE2	1.54	0.89
1:B:125:GLN:HG3	4:B:433:HOH:O	1.72	0.88
1:A:91:MSE:HE3	1:A:93:LEU:HD11	1.53	0.88
1:B:91:MSE:HE2	1:B:133:LEU:CD1	2.08	0.84
1:A:91:MSE:HE1	1:A:130:ALA:CB	2.10	0.80
1:A:49:THR:HG21	1:A:117:LEU:N	1.96	0.79
1:B:91:MSE:HE2	1:B:133:LEU:HD12	1.65	0.76
1:A:91:MSE:CE	1:A:130:ALA:HB2	2.13	0.76
1:B:189:LEU:HD11	1:B:218:MSE:HE2	1.67	0.75
1:A:214:GLN:HE22	1:A:241:TYR:H	1.32	0.75
1:B:180:PRO:HB3	1:B:208:ASP:HA	1.71	0.73
1:A:210:VAL:O	1:A:214:GLN:HG3	1.90	0.71
1:B:40:VAL:HG13	1:B:259:LEU:HD21	1.73	0.71
1:A:14:LEU:HD21	1:A:44:PHE:HB3	1.73	0.71
1:B:30:GLU:HA	1:B:33:LYS:HE2	1.71	0.70
1:A:59:ARG:HA	1:A:62:LYS:HD2	1.73	0.70
1:B:91:MSE:HE3	1:B:113:VAL:HG22	1.74	0.70
1:B:34:ARG:NH2	4:B:454:HOH:O	2.26	0.69
1:B:41:MSE:HE2	1:B:192:ALA:HB2	1.76	0.68
1:B:50:LYS:HD2	1:B:95:ASP:OD2	1.93	0.68
1:B:189:LEU:HD11	1:B:218:MSE:CE	2.24	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:91:MSE:HE2	1:B:133:LEU:HD11	1.78	0.66
1:B:83:ILE:HD11	1:B:114:VAL:HG21	1.77	0.65
1:B:241:TYR:OH	1:B:258:LEU:HD21	1.97	0.65
1:B:141:ILE:HG12	1:B:175:MSE:HE3	1.79	0.65
1:A:214:GLN:HE21	1:A:220:GLY:H	1.46	0.64
1:A:75:SER:HB3	1:A:143:ILE:HG23	1.80	0.64
1:B:13:ASP:O	1:B:17:THR:HB	1.98	0.64
1:B:189:LEU:CD2	1:B:218:MSE:HE2	2.27	0.63
1:B:139:PRO:HB2	1:B:175:MSE:HE2	1.80	0.62
1:B:205:ASP:O	1:B:209:ASP:HB2	1.99	0.62
1:B:139:PRO:HB2	1:B:175:MSE:CE	2.32	0.59
1:B:195:ALA:O	1:B:198:GLU:HB2	2.03	0.59
1:A:75:SER:HB3	1:A:143:ILE:CG2	2.31	0.59
1:A:177:VAL:HG12	1:A:183:THR:HG21	1.85	0.58
1:A:214:GLN:NE2	1:A:241:TYR:H	2.00	0.58
1:B:52:THR:OG1	1:B:55:ASP:OD1	2.16	0.58
1:A:91:MSE:HE3	1:A:93:LEU:HD13	1.85	0.56
1:B:91:MSE:CE	1:B:133:LEU:CD1	2.68	0.55
1:B:216:ILE:HD11	1:B:218:MSE:HE3	1.89	0.55
1:B:189:LEU:CD1	1:B:218:MSE:HE2	2.36	0.54
1:A:83:ILE:HD11	1:A:114:VAL:HG21	1.91	0.53
1:A:58:GLU:O	1:A:62:LYS:HG3	2.07	0.53
1:A:171:ASP:HB2	1:B:147:ARG:NH1	2.24	0.53
1:A:14:LEU:HD22	1:A:60:LEU:HD11	1.91	0.53
1:B:213:ALA:HB1	1:B:218:MSE:SE	2.59	0.53
1:A:232:ASP:O	1:A:235:LYS:HG2	2.09	0.52
1:B:189:LEU:HD21	1:B:218:MSE:CE	2.35	0.52
1:B:91:MSE:HE3	1:B:133:LEU:HD12	1.89	0.51
1:B:38:THR:HG21	1:B:255:LEU:CD2	2.40	0.51
1:B:123:HIS:NE2	1:B:126:LEU:HD12	2.27	0.50
1:B:175:MSE:HB3	4:B:443:HOH:O	2.11	0.49
1:B:40:VAL:CG1	1:B:259:LEU:HD21	2.39	0.49
1:B:242:LEU:HD22	1:B:253:HIS:CD2	2.47	0.49
1:B:214:GLN:HE22	1:B:241:TYR:H	1.61	0.49
1:B:46:THR:OG1	3:B:401:PO4:O3	2.22	0.49
1:A:49:THR:CG2	1:A:117:LEU:H	2.15	0.48
1:B:223:VAL:HG13	1:B:246:SER:HA	1.93	0.48
1:A:241:TYR:OH	1:A:253:HIS:HE1	1.95	0.48
1:A:151:ARG:HG3	1:A:153:ASP:OD1	2.14	0.48
1:A:148:TYR:CD1	1:A:155:LEU:HD22	2.49	0.47
1:B:14:LEU:HD21	1:B:44:PHE:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:228:TYR:CD1	1:B:228:TYR:C	2.88	0.47
1:B:141:ILE:CG1	1:B:175:MSE:HE3	2.45	0.47
1:B:14:LEU:HD22	1:B:60:LEU:HD11	1.97	0.46
1:B:189:LEU:CG	1:B:218:MSE:HE2	2.46	0.46
1:B:18:LEU:HD23	1:B:18:LEU:HA	1.72	0.45
1:B:49:THR:HA	1:B:76:LEU:HD21	1.98	0.45
1:A:33:LYS:HD3	4:A:444:HOH:O	2.17	0.45
1:B:40:VAL:HG13	1:B:259:LEU:CD2	2.44	0.45
1:B:11:LEU:CD2	1:B:43:ARG:HB2	2.47	0.44
1:A:49:THR:O	1:A:49:THR:HG22	2.16	0.44
1:A:41:MSE:HE3	1:A:41:MSE:HB2	1.86	0.44
1:B:41:MSE:HE3	1:B:41:MSE:HB3	1.68	0.44
1:B:49:THR:HG22	1:B:143:ILE:HG21	2.00	0.43
1:A:41:MSE:SE	1:A:192:ALA:HB2	2.68	0.43
1:A:147:ARG:NH1	1:B:168:TYR:O	2.51	0.43
1:B:187:GLU:HG2	1:B:190:ARG:NH2	2.33	0.43
1:B:76:LEU:CD2	1:B:143:ILE:HD13	2.48	0.43
1:B:63:LEU:HA	1:B:63:LEU:HD23	1.74	0.43
1:B:116:GLY:O	1:B:122:PHE:HZ	2.00	0.43
1:A:45:VAL:HA	1:A:73:PHE:O	2.19	0.43
1:B:210:VAL:HG11	1:B:240:PRO:HB3	2.00	0.43
1:B:49:THR:HG22	1:B:143:ILE:CG2	2.50	0.42
1:A:116:GLY:O	1:A:122:PHE:CZ	2.73	0.42
1:B:241:TYR:OH	1:B:253:HIS:HE1	2.02	0.42
1:A:214:GLN:HE22	1:A:241:TYR:N	2.08	0.41
1:B:246:SER:OG	1:B:248:PRO:HD2	2.21	0.41
1:B:14:LEU:HD23	1:B:18:LEU:HD12	2.03	0.41
1:A:224:LYS:HA	1:A:228:TYR:CG	2.55	0.41
1:B:57:LEU:HD13	1:B:67:ILE:HG22	2.01	0.41
1:B:178:GLY:O	1:B:181:GLU:HB2	2.20	0.41
1:B:45:VAL:HA	1:B:73:PHE:O	2.21	0.41
1:A:99:LEU:N	1:A:100:PRO:CD	2.84	0.41
1:A:49:THR:CG2	1:A:49:THR:O	2.70	0.40
1:B:158:GLY:O	1:B:161:PRO:HD2	2.21	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	248/259 (96%)	240 (97%)	8 (3%)	0	100	100
1	B	249/259 (96%)	236 (95%)	13 (5%)	0	100	100
All	All	497/518 (96%)	476 (96%)	21 (4%)	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	211/210 (100%)	210 (100%)	1 (0%)	88	94
1	B	212/210 (101%)	201 (95%)	11 (5%)	23	28
All	All	423/420 (101%)	411 (97%)	12 (3%)	42	56

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ASN
1	B	12	VAL
1	B	21	GLU
1	B	40	VAL
1	B	41	MSE
1	B	56	LEU
1	B	70	ASP
1	B	120	GLU

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Mol	Chain	Res	Type
1	B	136	ASP
1	B	150	LYS
1	B	194	CYS
1	B	216	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	121	HIS
1	A	123	HIS
1	A	125	GLN
1	A	214	GLN
1	A	253	HIS
1	A	257	HIS
1	B	214	GLN
1	B	253	HIS

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)

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 for Mogul analysis.

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	$\#\|Z\|>2$
3	PO4	B	403	-	4,4,4	0.87	0	6,6,6	0.52	0
3	PO4	B	401	-	4,4,4	0.82	0	6,6,6	1.39	1 (16%)
3	PO4	A	402	-	4,4,4	1.14	0	6,6,6	1.01	0
3	PO4	A	404	-	4,4,4	1.22	0	6,6,6	0.62	0
3	PO4	A	406	-	4,4,4	0.77	0	6,6,6	0.33	0
3	PO4	B	405	-	4,4,4	0.98	0	6,6,6	0.53	0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	B	401	PO4	O4-P-O2	2.55	115.86	107.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	401	PO4	1	0

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data

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	246/259 (94%)	-0.01	2 (0%)	86	85	15, 23, 32, 39	0
1	B	247/259 (95%)	0.27	14 (5%)	23	22	13, 25, 39, 46	0
All	All	493/518 (95%)	0.13	16 (3%)	47	45	13, 24, 36, 46	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	241	TYR	3.8
1	B	239	PRO	3.8
1	A	20	ILE	3.7
1	B	238	PRO	3.2
1	B	255	LEU	3.1
1	B	213	ALA	3.1
1	B	231	ALA	2.9
1	B	259	LEU	2.8
1	B	219	LEU	2.8
1	B	230	ALA	2.6
1	A	49	THR	2.5
1	B	198	GLU	2.4
1	B	234	GLU	2.4
1	B	217	GLY	2.2
1	B	206	CYS	2.1
1	B	209	ASP	2.1

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 (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, 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	B-factors(Å^2)	Q<0.9
2	MG	B	301	1/1	0.49	0.23	44,44,44,44	0
2	MG	A	260	1/1	0.56	0.28	43,43,43,43	1
3	PO4	A	402	5/5	0.87	0.42	37,38,40,42	5
3	PO4	A	406	5/5	0.87	0.35	47,48,50,50	5
3	PO4	B	401	5/5	0.87	0.20	47,48,50,52	5
3	PO4	A	404	5/5	0.91	0.31	41,42,43,43	5
3	PO4	B	403	5/5	0.91	0.26	56,56,56,56	5
3	PO4	B	405	5/5	0.92	0.48	46,47,48,48	5

6.5 Other polymers (i)

There are no such residues in this entry.