



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:37 AM GMT

PDB ID : 3PK1
Title : Crystal structure of Mcl-1 in complex with the BaxBH3 domain
Authors : Czabotar, P.E.; Colman, P.M.
Deposited on : 2010-11-11
Resolution : 2.49 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) 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

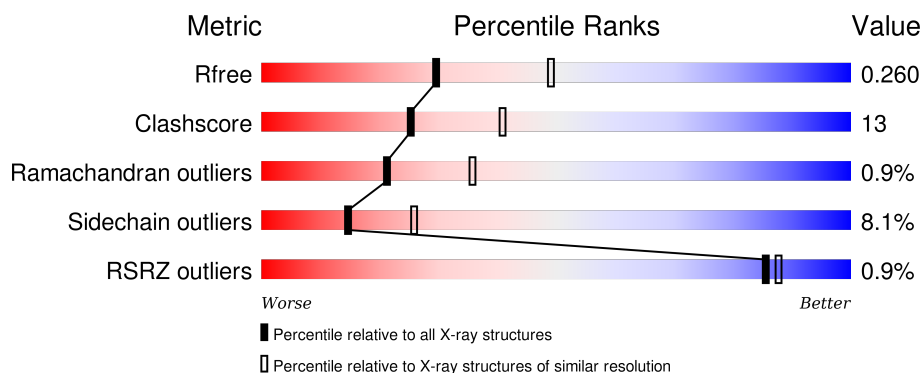
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.49 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	4309 (2.50-2.46)
Clashscore	102246	5050 (2.50-2.46)
Ramachandran outliers	100387	4961 (2.50-2.46)
Sidechain outliers	100360	4963 (2.50-2.46)
RSRZ outliers	91569	4319 (2.50-2.46)

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 $\leq 5\%$. 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	189	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 23%, green 49%, grey 26%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 49% 23% •• 26% </div> </div>
1	C	189	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 24%, green 48%, grey 28%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> % 48% 24% • 28% </div> </div>
2	B	34	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 32%, green 47%, grey 21%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 47% 32% 21% </div> </div>
2	D	34	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, yellow 21%, green 59%, grey 21%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> 59% 21% 21% </div> </div>

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 2740 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 Induced myeloid leukemia cell differentiation protein Mcl-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	140	Total	C	N	O	S	47	0	0
			1133	716	209	205	3			
1	C	137	Total	C	N	O	S	67	0	0
			1114	704	205	202	3			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	138	GLY	-	EXPRESSION TAG	UNP Q07820
A	139	SER	-	EXPRESSION TAG	UNP Q07820
A	140	GLY	-	EXPRESSION TAG	UNP Q07820
A	141	MET	-	EXPRESSION TAG	UNP Q07820
A	142	LYS	-	EXPRESSION TAG	UNP Q07820
A	143	GLU	-	EXPRESSION TAG	UNP Q07820
A	144	THR	-	EXPRESSION TAG	UNP Q07820
A	145	ALA	-	EXPRESSION TAG	UNP Q07820
A	146	ALA	-	EXPRESSION TAG	UNP Q07820
A	147	ALA	-	EXPRESSION TAG	UNP Q07820
A	148	LYS	-	EXPRESSION TAG	UNP Q07820
A	149	PHE	-	EXPRESSION TAG	UNP Q07820
A	150	GLU	-	EXPRESSION TAG	UNP Q07820
A	151	ARG	-	EXPRESSION TAG	UNP Q07820
A	152	GLN	-	EXPRESSION TAG	UNP Q07820
A	153	HIS	-	EXPRESSION TAG	UNP Q07820
A	154	MET	-	EXPRESSION TAG	UNP Q07820
A	155	ASP	-	EXPRESSION TAG	UNP Q07820
A	156	SER	-	EXPRESSION TAG	UNP Q07820
A	157	PRO	-	EXPRESSION TAG	UNP Q07820
A	158	ASP	-	EXPRESSION TAG	UNP Q07820
A	159	LEU	-	EXPRESSION TAG	UNP Q07820
A	160	GLY	-	EXPRESSION TAG	UNP Q07820
A	161	THR	-	EXPRESSION TAG	UNP Q07820
A	162	ASP	-	EXPRESSION TAG	UNP Q07820

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Chain	Residue	Modelled	Actual	Comment	Reference
A	163	ASP	-	EXPRESSION TAG	UNP Q07820
A	164	ASP	-	EXPRESSION TAG	UNP Q07820
A	165	ASP	-	EXPRESSION TAG	UNP Q07820
A	166	LYS	-	EXPRESSION TAG	UNP Q07820
A	167	ALA	-	EXPRESSION TAG	UNP Q07820
A	168	MET	-	EXPRESSION TAG	UNP Q07820
A	169	ALA	-	EXPRESSION TAG	UNP Q07820
A	170	ASP	-	EXPRESSION TAG	UNP Q07820
A	171	ILE	-	EXPRESSION TAG	UNP Q07820
A	172	GLY	-	EXPRESSION TAG	UNP Q07820
A	173	SER	-	EXPRESSION TAG	UNP Q07820
C	138	GLY	-	EXPRESSION TAG	UNP Q07820
C	139	SER	-	EXPRESSION TAG	UNP Q07820
C	140	GLY	-	EXPRESSION TAG	UNP Q07820
C	141	MET	-	EXPRESSION TAG	UNP Q07820
C	142	LYS	-	EXPRESSION TAG	UNP Q07820
C	143	GLU	-	EXPRESSION TAG	UNP Q07820
C	144	THR	-	EXPRESSION TAG	UNP Q07820
C	145	ALA	-	EXPRESSION TAG	UNP Q07820
C	146	ALA	-	EXPRESSION TAG	UNP Q07820
C	147	ALA	-	EXPRESSION TAG	UNP Q07820
C	148	LYS	-	EXPRESSION TAG	UNP Q07820
C	149	PHE	-	EXPRESSION TAG	UNP Q07820
C	150	GLU	-	EXPRESSION TAG	UNP Q07820
C	151	ARG	-	EXPRESSION TAG	UNP Q07820
C	152	GLN	-	EXPRESSION TAG	UNP Q07820
C	153	HIS	-	EXPRESSION TAG	UNP Q07820
C	154	MET	-	EXPRESSION TAG	UNP Q07820
C	155	ASP	-	EXPRESSION TAG	UNP Q07820
C	156	SER	-	EXPRESSION TAG	UNP Q07820
C	157	PRO	-	EXPRESSION TAG	UNP Q07820
C	158	ASP	-	EXPRESSION TAG	UNP Q07820
C	159	LEU	-	EXPRESSION TAG	UNP Q07820
C	160	GLY	-	EXPRESSION TAG	UNP Q07820
C	161	THR	-	EXPRESSION TAG	UNP Q07820
C	162	ASP	-	EXPRESSION TAG	UNP Q07820
C	163	ASP	-	EXPRESSION TAG	UNP Q07820
C	164	ASP	-	EXPRESSION TAG	UNP Q07820
C	165	ASP	-	EXPRESSION TAG	UNP Q07820
C	166	LYS	-	EXPRESSION TAG	UNP Q07820
C	167	ALA	-	EXPRESSION TAG	UNP Q07820
C	168	MET	-	EXPRESSION TAG	UNP Q07820

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Chain	Residue	Modelled	Actual	Comment	Reference
C	169	ALA	-	EXPRESSION TAG	UNP Q07820
C	170	ASP	-	EXPRESSION TAG	UNP Q07820
C	171	ILE	-	EXPRESSION TAG	UNP Q07820
C	172	GLY	-	EXPRESSION TAG	UNP Q07820
C	173	SER	-	EXPRESSION TAG	UNP Q07820

- Molecule 2 is a protein called Apoptosis regulator BAX.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	27	Total	C	N	O	S	24	0	0
			213	129	38	43	3			
2	D	27	Total	C	N	O	S	32	0	0
			213	129	38	43	3			

- Molecule 3 is CADMIUM ION (three-letter code: CD) (formula: Cd).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Cd	0	0
			2	2		
3	A	8	Total	Cd	0	0
			8	8		
3	D	2	Total	Cd	0	0
			2	2		
3	C	6	Total	Cd	0	0
			6	6		

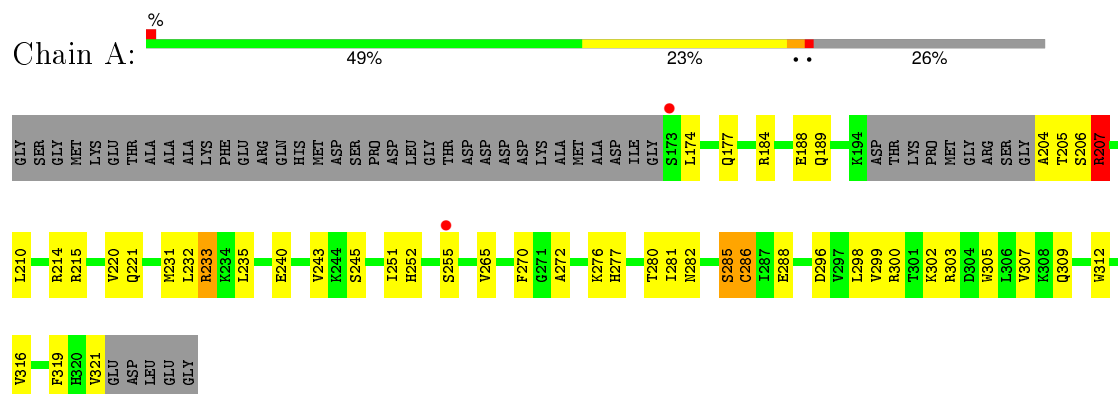
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	20	Total	O	0	0
			20	20		
4	B	6	Total	O	0	0
			6	6		
4	C	21	Total	O	0	0
			21	21		
4	D	2	Total	O	0	0
			2	2		

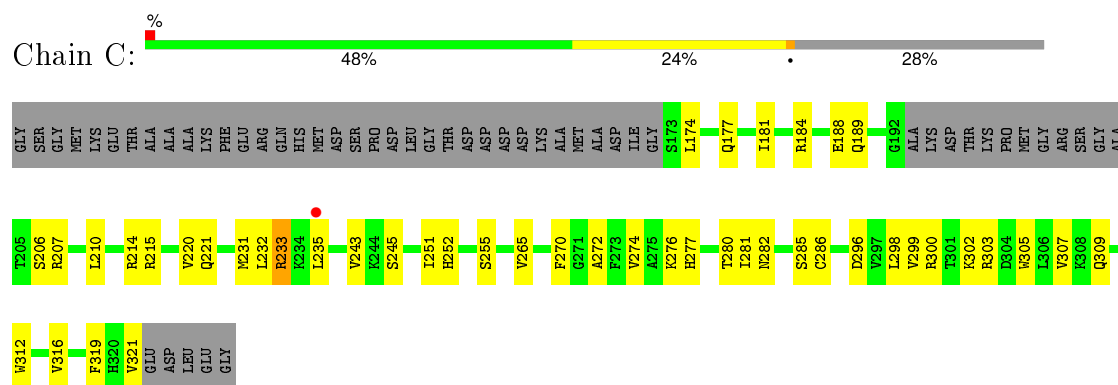
3 Residue-property plots [i](#)

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.

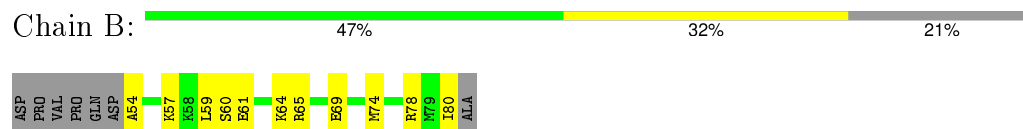
- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1



- Molecule 1: Induced myeloid leukemia cell differentiation protein Mcl-1

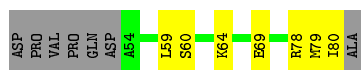


- Molecule 2: Apoptosis regulator BAX



- Molecule 2: Apoptosis regulator BAX





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	97.92Å 81.47Å 57.93Å 90.00° 124.23° 90.00°	Depositor
Resolution (Å)	20.14 – 2.49 20.14 – 2.49	Depositor EDS
% Data completeness (in resolution range)	98.2 (20.14-2.49) 89.4 (20.14-2.49)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.50Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.212 , 0.245 0.221 , 0.260	Depositor DCC
R_{free} test set	650 reflections (4.99%)	DCC
Wilson B-factor (Å ²)	42.8	Xtriage
Anisotropy	0.296	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.5	EDS
Estimated twinning fraction	0.154 for h+2*l,-k,-l 0.004 for k+l,h+l,-l 0.004 for -k+l,-h-l,-l 0.267 for -h-2*l,-k,l	Xtriage
Reported twinning fraction	0.154 for h+2*l,-k,-l	Depositor
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 13062 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	2740	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.86% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ 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: CD

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	0.44	0/1151	0.87	6/1547 (0.4%)
1	C	0.42	0/1132	0.83	6/1522 (0.4%)
2	B	0.43	0/212	0.54	0/279
2	D	0.42	0/212	0.54	0/279
All	All	0.43	0/2707	0.81	12/3627 (0.3%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	207	ARG	NE-CZ-NH2	13.91	127.25	120.30
1	A	207	ARG	NE-CZ-NH1	-13.48	113.56	120.30
1	C	207	ARG	NE-CZ-NH2	-12.03	114.29	120.30
1	C	233	ARG	NE-CZ-NH2	-11.98	114.31	120.30
1	C	207	ARG	NE-CZ-NH1	11.68	126.14	120.30
1	A	233	ARG	NE-CZ-NH1	-11.36	114.62	120.30
1	C	233	ARG	NE-CZ-NH1	11.29	125.94	120.30
1	A	233	ARG	NE-CZ-NH2	10.63	125.61	120.30
1	A	207	ARG	CD-NE-CZ	6.87	133.22	123.60
1	C	207	ARG	CD-NE-CZ	6.38	132.53	123.60
1	C	233	ARG	CD-NE-CZ	5.76	131.66	123.60
1	A	233	ARG	CD-NE-CZ	5.58	131.41	123.60

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	1133	0	1149	30	0
1	C	1114	0	1126	28	0
2	B	213	0	222	7	0
2	D	213	0	222	2	0
3	A	8	0	0	0	0
3	B	2	0	0	0	0
3	C	6	0	0	0	0
3	D	2	0	0	0	0
4	A	20	0	0	1	0
4	B	6	0	0	1	0
4	C	21	0	0	2	0
4	D	2	0	0	0	0
All	All	2740	0	2719	63	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 (63) 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:231:MET:HG2	2:B:59:LEU:HD22	1.64	0.78
1:C:309:GLN:HB3	4:C:328:HOH:O	1.87	0.73
1:C:231:MET:HG2	2:D:59:LEU:HD22	1.69	0.73
2:B:61:GLU:O	2:B:65:ARG:HG3	1.92	0.68
1:C:184:ARG:O	1:C:188:GLU:HG3	1.95	0.66
1:A:204:ALA:O	1:A:207:ARG:HB3	1.95	0.66
1:A:184:ARG:O	1:A:188:GLU:HG3	1.98	0.63
1:C:235:LEU:HD11	1:C:270:PHE:HE2	1.64	0.63
1:A:280:THR:HG22	1:A:281:ILE:HD13	1.80	0.61
1:A:235:LEU:HD11	1:A:270:PHE:HE2	1.64	0.60
1:C:221:GLN:HE22	1:C:276:LYS:HE3	1.66	0.60
1:A:221:GLN:HE22	1:A:276:LYS:HE3	1.67	0.59
1:A:277:HIS:O	1:A:280:THR:HB	2.03	0.58
1:C:177:GLN:HE21	1:C:206:SER:HB3	1.68	0.58
1:A:189:GLN:NE2	1:A:276:LYS:HE2	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:305:TRP:O	1:A:309:GLN:HG2	2.04	0.57
1:C:298:LEU:O	1:C:302:LYS:HB2	2.04	0.57
1:A:312:TRP:O	1:A:316:VAL:HG23	2.04	0.56
1:A:298:LEU:O	1:A:302:LYS:HB2	2.06	0.56
1:C:303:ARG:O	1:C:307:VAL:HG23	2.06	0.56
1:A:303:ARG:O	1:A:307:VAL:HG23	2.06	0.54
1:C:189:GLN:NE2	1:C:276:LYS:HE2	2.22	0.54
2:B:57:LYS:O	2:B:61:GLU:HG3	2.07	0.54
1:A:286:CYS:SG	1:A:288:GLU:OE1	2.66	0.54
1:C:312:TRP:O	1:C:316:VAL:HG23	2.08	0.54
1:A:177:GLN:HE21	1:A:206:SER:HB3	1.74	0.53
1:C:210:LEU:O	1:C:210:LEU:HD12	2.10	0.52
1:C:305:TRP:O	1:C:309:GLN:HG2	2.10	0.52
1:C:277:HIS:O	1:C:280:THR:HB	2.11	0.50
1:C:174:LEU:HD22	1:C:299:VAL:HG13	1.94	0.50
1:A:215:ARG:NH2	1:A:319:PHE:O	2.44	0.50
1:C:215:ARG:NH2	1:C:319:PHE:O	2.45	0.49
2:B:60:SER:O	2:B:64:LYS:HB2	2.12	0.49
1:A:245:SER:HB3	4:A:329:HOH:O	2.11	0.49
1:C:296:ASP:O	1:C:300:ARG:HB2	2.13	0.49
1:A:210:LEU:HD12	1:A:210:LEU:O	2.13	0.48
2:D:60:SER:O	2:D:64:LYS:HB2	2.13	0.48
1:A:282:ASN:ND2	1:A:285:SER:H	2.10	0.48
1:A:296:ASP:O	1:A:300:ARG:HB2	2.15	0.47
1:C:245:SER:HB3	4:C:6:HOH:O	2.13	0.47
1:A:235:LEU:HD11	1:A:270:PHE:CE2	2.47	0.47
1:A:174:LEU:HD22	1:A:299:VAL:HG13	1.97	0.47
1:C:174:LEU:CD2	1:C:299:VAL:HG13	2.45	0.47
1:A:210:LEU:O	1:A:214:ARG:HG3	2.15	0.47
1:C:235:LEU:HD11	1:C:270:PHE:CE2	2.46	0.47
2:B:54:ALA:N	4:B:42:HOH:O	2.48	0.45
1:A:319:PHE:CD2	2:B:74:MET:HG3	2.53	0.44
1:C:174:LEU:HD23	1:C:174:LEU:C	2.37	0.43
1:C:189:GLN:HG3	1:C:272:ALA:HB1	2.00	0.43
1:A:319:PHE:CE2	2:B:74:MET:HG3	2.54	0.43
1:A:174:LEU:CD2	1:A:299:VAL:HG13	2.48	0.43
1:A:240:GLU:HB3	1:A:285:SER:HB2	2.00	0.43
1:A:174:LEU:C	1:A:174:LEU:HD23	2.38	0.43
1:A:302:LYS:HA	1:A:302:LYS:HD3	1.71	0.42
1:A:189:GLN:HG3	1:A:272:ALA:HB1	2.01	0.42
1:C:210:LEU:O	1:C:214:ARG:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:281:ILE:HD13	1:C:281:ILE:N	2.32	0.42
1:C:302:LYS:HA	1:C:302:LYS:HD3	1.75	0.42
1:A:252:HIS:HA	1:A:255:SER:HB3	2.01	0.42
1:C:252:HIS:HA	1:C:255:SER:HB3	2.01	0.42
1:C:270:PHE:O	1:C:274:VAL:HG23	2.19	0.41
1:C:282:ASN:ND2	1:C:285:SER:H	2.18	0.41
1:C:189:GLN:O	1:C:276:LYS:HG2	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	136/189 (72%)	127 (93%)	8 (6%)	1 (1%)	26	43
1	C	133/189 (70%)	123 (92%)	9 (7%)	1 (1%)	24	39
2	B	25/34 (74%)	24 (96%)	1 (4%)	0	100	100
2	D	25/34 (74%)	24 (96%)	0	1 (4%)	4	4
All	All	319/446 (72%)	298 (93%)	18 (6%)	3 (1%)	21	36

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	79	MET
1	A	285	SER
1	C	181	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	123/160 (77%)	113 (92%)	10 (8%)	15	26
1	C	122/160 (76%)	114 (93%)	8 (7%)	21	36
2	B	25/31 (81%)	22 (88%)	3 (12%)	6	11
2	D	25/31 (81%)	22 (88%)	3 (12%)	6	11
All	All	295/382 (77%)	271 (92%)	24 (8%)	15	26

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	205	THR
1	A	207	ARG
1	A	220	VAL
1	A	232	LEU
1	A	233	ARG
1	A	243	VAL
1	A	251	ILE
1	A	265	VAL
1	A	286	CYS
1	A	321	VAL
2	B	69	GLU
2	B	78	ARG
2	B	80	ILE
1	C	220	VAL
1	C	232	LEU
1	C	233	ARG
1	C	243	VAL
1	C	251	ILE
1	C	265	VAL
1	C	286	CYS
1	C	321	VAL
2	D	69	GLU
2	D	78	ARG
2	D	80	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	177	GLN
1	A	189	GLN
1	A	221	GLN
1	A	282	ASN
1	C	177	GLN
1	C	189	GLN
1	C	221	GLN
1	C	282	ASN
1	C	320	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

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 ⓘ

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	140/189 (74%)	-0.22	2 (1%) 78 80	36, 50, 70, 75	15 (10%)
1	C	137/189 (72%)	-0.26	1 (0%) 89 90	35, 49, 69, 75	18 (13%)
2	B	27/34 (79%)	-0.15	0 100 100	38, 51, 78, 85	7 (25%)
2	D	27/34 (79%)	-0.43	0 100 100	38, 51, 77, 85	8 (29%)
All	All	331/446 (74%)	-0.25	3 (0%) 85 88	35, 50, 72, 85	48 (14%)

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	173	SER	2.6
1	A	255	SER	2.4
1	C	235	LEU	2.2

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(\AA^2)	Q<0.9
3	CD	B	7	1/1	0.94	0.15	-0.27	88,88,88,88	1
3	CD	D	9	1/1	0.90	0.08	-	94,94,94,94	1
3	CD	A	13	1/1	0.76	0.07	-	120,120,120,120	0
3	CD	A	18	1/1	0.95	0.08	-	94,94,94,94	0
3	CD	A	1	1/1	1.00	0.14	-	42,42,42,42	0
3	CD	C	4	1/1	0.69	0.08	-	162,162,162,162	0
3	CD	C	10	1/1	0.94	0.09	-	125,125,125,125	0
3	CD	A	12	1/1	0.87	0.14	-	107,107,107,107	0
3	CD	C	16	1/1	0.89	0.05	-	120,120,120,120	0
3	CD	B	8	1/1	0.84	0.15	-	75,75,75,75	1
3	CD	C	15	1/1	0.90	0.13	-	102,102,102,102	0
3	CD	C	11	1/1	0.89	0.16	-	129,129,129,129	0
3	CD	C	3	1/1	0.99	0.10	-	50,50,50,50	0
3	CD	A	14	1/1	0.90	0.20	-	111,111,111,111	0
3	CD	A	2	1/1	0.99	0.15	-	46,46,46,46	0
3	CD	D	6	1/1	0.96	0.14	-	71,71,71,71	1
3	CD	A	17	1/1	0.80	0.13	-	122,122,122,122	0
3	CD	A	5	1/1	0.99	0.10	-	48,48,48,48	0

6.5 Other polymers [i](#)

There are no such residues in this entry.