



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 09:19 PM EDT

PDB ID : 4KEA / pdb_00004kea
Title : Crystal structure of D196N mutant of Monoglyceride lipase from Bacillus sp. H257 in space group P212121
Authors : Rengachari, S.; Aschauer, P.; Gruber, K.; Dreveny, I.; Oberer, M.
Deposited on : 2013-04-25
Resolution : 1.70 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 ⓘ 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:

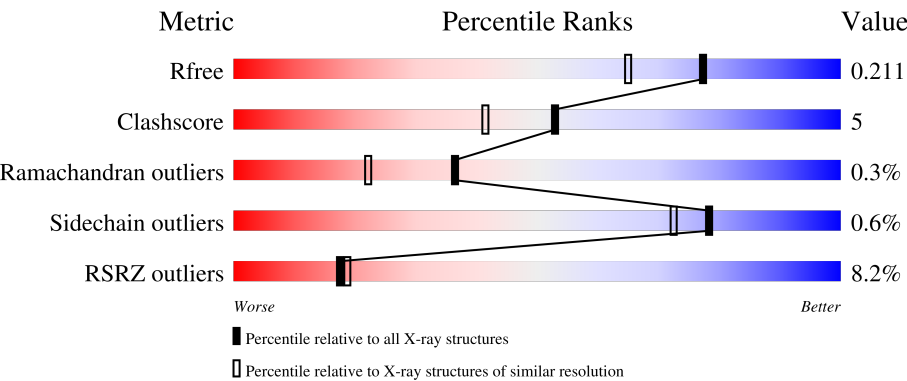
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

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 1.70 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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 $\leq 5\%$. 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	270	3% 85% 7% 8%
1	B	270	4% 82% 7% 10%
1	C	270	7% 81% 9% 9%
1	D	270	6% 85% 6% 10%
1	E	270	7% 85% • 10%

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Mol	Chain	Length	Quality of chain
1	F	270	

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	MPD	C	304	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12656 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 Thermostable monoacylglycerol lipase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	248	Total	C	N	O	S	0	13	0
			1983	1269	331	371	12			
1	B	243	Total	C	N	O	S	0	7	0
			1921	1232	320	359	10			
1	C	245	Total	C	N	O	S	0	10	0
			1957	1254	328	364	11			
1	D	244	Total	C	N	O	S	0	5	0
			1918	1227	322	359	10			
1	E	242	Total	C	N	O	S	0	3	0
			1896	1211	321	355	9			
1	F	240	Total	C	N	O	S	0	4	0
			1885	1208	316	350	11			

There are 126 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP P82597
A	-18	GLY	-	expression tag	UNP P82597
A	-17	SER	-	expression tag	UNP P82597
A	-16	SER	-	expression tag	UNP P82597
A	-15	HIS	-	expression tag	UNP P82597
A	-14	HIS	-	expression tag	UNP P82597
A	-13	HIS	-	expression tag	UNP P82597
A	-12	HIS	-	expression tag	UNP P82597
A	-11	HIS	-	expression tag	UNP P82597
A	-10	HIS	-	expression tag	UNP P82597
A	-9	SER	-	expression tag	UNP P82597
A	-8	SER	-	expression tag	UNP P82597
A	-7	GLY	-	expression tag	UNP P82597
A	-6	LEU	-	expression tag	UNP P82597
A	-5	VAL	-	expression tag	UNP P82597
A	-4	PRO	-	expression tag	UNP P82597
A	-3	ARG	-	expression tag	UNP P82597

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P82597
A	-1	SER	-	expression tag	UNP P82597
A	0	HIS	-	expression tag	UNP P82597
A	196	ASN	ASP	engineered mutation	UNP P82597
B	-19	MET	-	expression tag	UNP P82597
B	-18	GLY	-	expression tag	UNP P82597
B	-17	SER	-	expression tag	UNP P82597
B	-16	SER	-	expression tag	UNP P82597
B	-15	HIS	-	expression tag	UNP P82597
B	-14	HIS	-	expression tag	UNP P82597
B	-13	HIS	-	expression tag	UNP P82597
B	-12	HIS	-	expression tag	UNP P82597
B	-11	HIS	-	expression tag	UNP P82597
B	-10	HIS	-	expression tag	UNP P82597
B	-9	SER	-	expression tag	UNP P82597
B	-8	SER	-	expression tag	UNP P82597
B	-7	GLY	-	expression tag	UNP P82597
B	-6	LEU	-	expression tag	UNP P82597
B	-5	VAL	-	expression tag	UNP P82597
B	-4	PRO	-	expression tag	UNP P82597
B	-3	ARG	-	expression tag	UNP P82597
B	-2	GLY	-	expression tag	UNP P82597
B	-1	SER	-	expression tag	UNP P82597
B	0	HIS	-	expression tag	UNP P82597
B	196	ASN	ASP	engineered mutation	UNP P82597
C	-19	MET	-	expression tag	UNP P82597
C	-18	GLY	-	expression tag	UNP P82597
C	-17	SER	-	expression tag	UNP P82597
C	-16	SER	-	expression tag	UNP P82597
C	-15	HIS	-	expression tag	UNP P82597
C	-14	HIS	-	expression tag	UNP P82597
C	-13	HIS	-	expression tag	UNP P82597
C	-12	HIS	-	expression tag	UNP P82597
C	-11	HIS	-	expression tag	UNP P82597
C	-10	HIS	-	expression tag	UNP P82597
C	-9	SER	-	expression tag	UNP P82597
C	-8	SER	-	expression tag	UNP P82597
C	-7	GLY	-	expression tag	UNP P82597
C	-6	LEU	-	expression tag	UNP P82597
C	-5	VAL	-	expression tag	UNP P82597
C	-4	PRO	-	expression tag	UNP P82597
C	-3	ARG	-	expression tag	UNP P82597

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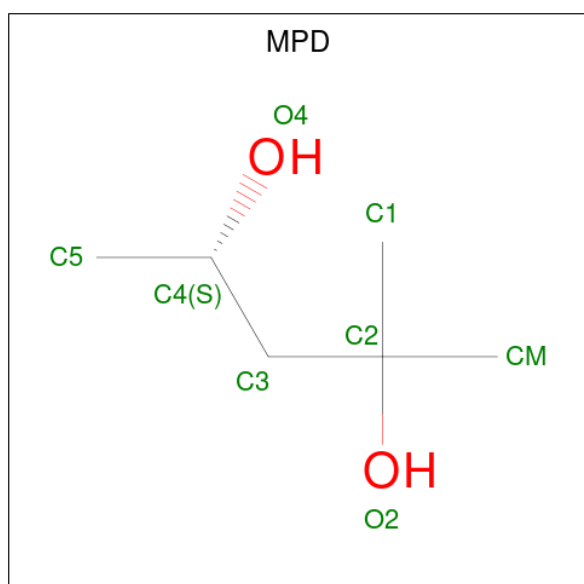
Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	GLY	-	expression tag	UNP P82597
C	-1	SER	-	expression tag	UNP P82597
C	0	HIS	-	expression tag	UNP P82597
C	196	ASN	ASP	engineered mutation	UNP P82597
D	-19	MET	-	expression tag	UNP P82597
D	-18	GLY	-	expression tag	UNP P82597
D	-17	SER	-	expression tag	UNP P82597
D	-16	SER	-	expression tag	UNP P82597
D	-15	HIS	-	expression tag	UNP P82597
D	-14	HIS	-	expression tag	UNP P82597
D	-13	HIS	-	expression tag	UNP P82597
D	-12	HIS	-	expression tag	UNP P82597
D	-11	HIS	-	expression tag	UNP P82597
D	-10	HIS	-	expression tag	UNP P82597
D	-9	SER	-	expression tag	UNP P82597
D	-8	SER	-	expression tag	UNP P82597
D	-7	GLY	-	expression tag	UNP P82597
D	-6	LEU	-	expression tag	UNP P82597
D	-5	VAL	-	expression tag	UNP P82597
D	-4	PRO	-	expression tag	UNP P82597
D	-3	ARG	-	expression tag	UNP P82597
D	-2	GLY	-	expression tag	UNP P82597
D	-1	SER	-	expression tag	UNP P82597
D	0	HIS	-	expression tag	UNP P82597
D	196	ASN	ASP	engineered mutation	UNP P82597
E	-19	MET	-	expression tag	UNP P82597
E	-18	GLY	-	expression tag	UNP P82597
E	-17	SER	-	expression tag	UNP P82597
E	-16	SER	-	expression tag	UNP P82597
E	-15	HIS	-	expression tag	UNP P82597
E	-14	HIS	-	expression tag	UNP P82597
E	-13	HIS	-	expression tag	UNP P82597
E	-12	HIS	-	expression tag	UNP P82597
E	-11	HIS	-	expression tag	UNP P82597
E	-10	HIS	-	expression tag	UNP P82597
E	-9	SER	-	expression tag	UNP P82597
E	-8	SER	-	expression tag	UNP P82597
E	-7	GLY	-	expression tag	UNP P82597
E	-6	LEU	-	expression tag	UNP P82597
E	-5	VAL	-	expression tag	UNP P82597
E	-4	PRO	-	expression tag	UNP P82597
E	-3	ARG	-	expression tag	UNP P82597

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-2	GLY	-	expression tag	UNP P82597
E	-1	SER	-	expression tag	UNP P82597
E	0	HIS	-	expression tag	UNP P82597
E	196	ASN	ASP	engineered mutation	UNP P82597
F	-19	MET	-	expression tag	UNP P82597
F	-18	GLY	-	expression tag	UNP P82597
F	-17	SER	-	expression tag	UNP P82597
F	-16	SER	-	expression tag	UNP P82597
F	-15	HIS	-	expression tag	UNP P82597
F	-14	HIS	-	expression tag	UNP P82597
F	-13	HIS	-	expression tag	UNP P82597
F	-12	HIS	-	expression tag	UNP P82597
F	-11	HIS	-	expression tag	UNP P82597
F	-10	HIS	-	expression tag	UNP P82597
F	-9	SER	-	expression tag	UNP P82597
F	-8	SER	-	expression tag	UNP P82597
F	-7	GLY	-	expression tag	UNP P82597
F	-6	LEU	-	expression tag	UNP P82597
F	-5	VAL	-	expression tag	UNP P82597
F	-4	PRO	-	expression tag	UNP P82597
F	-3	ARG	-	expression tag	UNP P82597
F	-2	GLY	-	expression tag	UNP P82597
F	-1	SER	-	expression tag	UNP P82597
F	0	HIS	-	expression tag	UNP P82597
F	196	ASN	ASP	engineered mutation	UNP P82597

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	A	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	C	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	D	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	E	1	Total	C	O	0	0
			8	6	2		
2	F	1	Total	C	O	0	0
			8	6	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	F	1	Total	C	O	0	0
			8	6	2		
2	F	1	Total	C	O	0	0
			8	6	2		

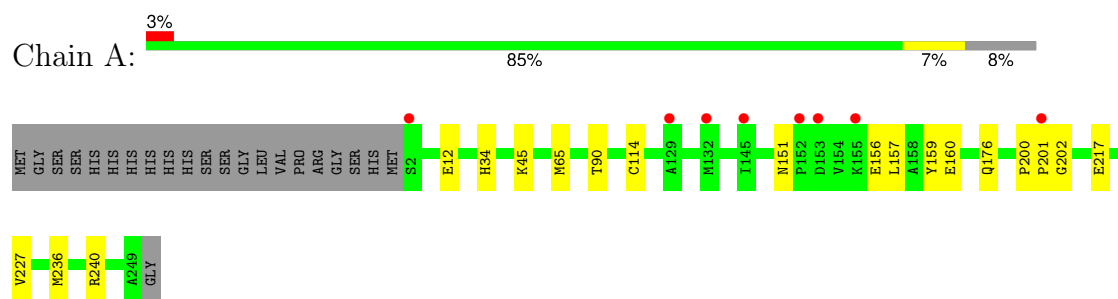
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	207	Total	O	0	0
			207	207		
3	B	188	Total	O	0	0
			188	188		
3	C	123	Total	O	0	0
			123	123		
3	D	125	Total	O	0	0
			125	125		
3	E	153	Total	O	0	0
			153	153		
3	F	108	Total	O	0	0
			108	108		

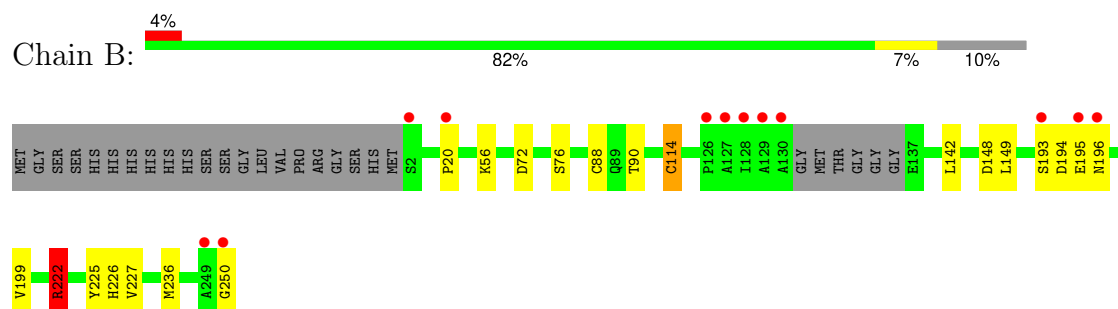
3 Residue-property plots [i](#)

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.

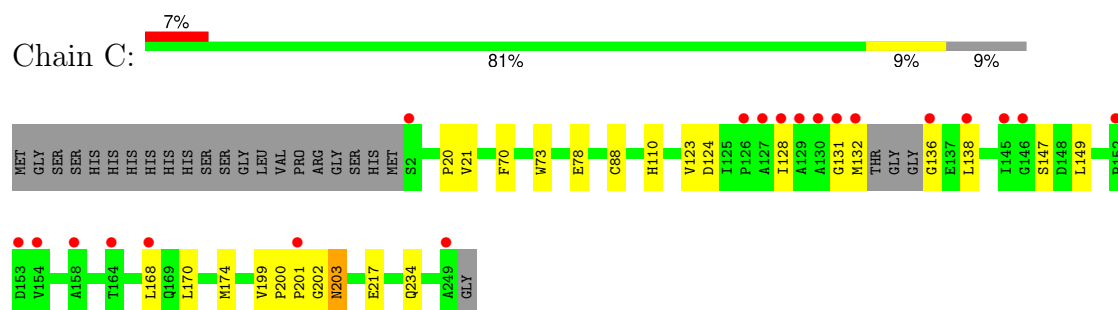
• Molecule 1: Thermostable monoacylglycerol lipase



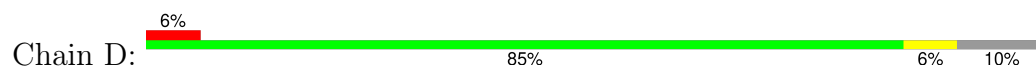
• Molecule 1: Thermostable monoacylglycerol lipase

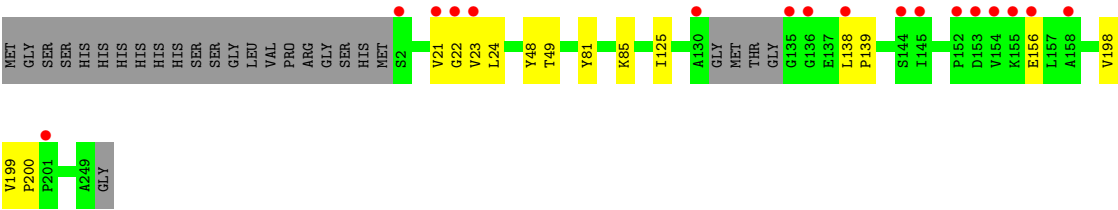


• Molecule 1: Thermostable monoacylglycerol lipase

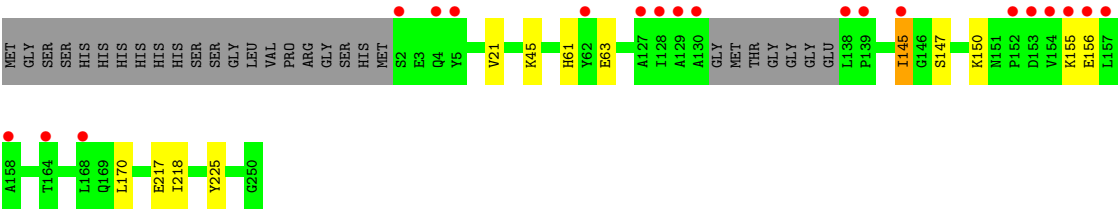
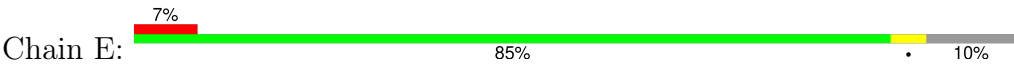


• Molecule 1: Thermostable monoacylglycerol lipase

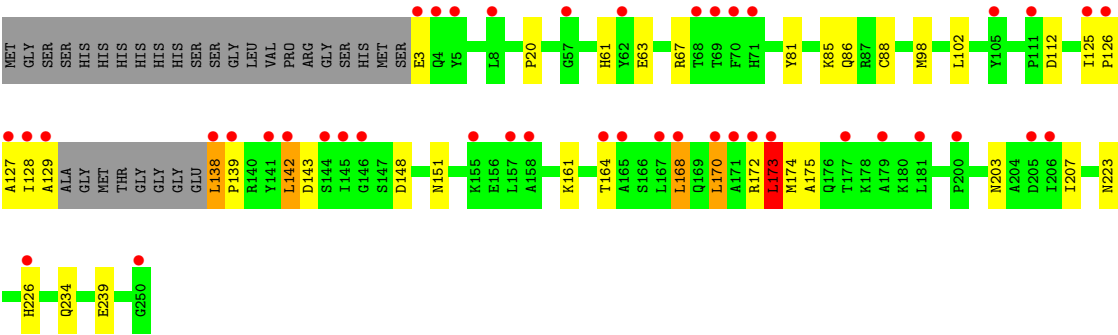
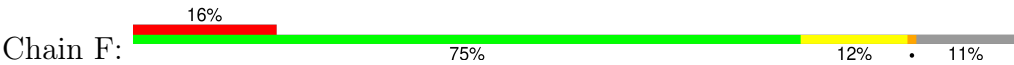




● Molecule 1: Thermostable monoacylglycerol lipase



● Molecule 1: Thermostable monoacylglycerol lipase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	39.16Å 183.13Å 244.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.88 – 1.70 19.88 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.88-1.70) 98.8 (19.88-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.70 (at 1.70Å)	Xtriage
Refinement program	PHENIX 1.8_1069, REFMAC	Depositor
R, R_{free}	0.191 , 0.211 0.191 , 0.211	Depositor DCC
R_{free} test set	9832 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	20.6	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	12656	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.46% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

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	0.47	3/2057 (0.1%)	0.71	2/2799 (0.1%)
1	B	0.41	4/1986 (0.2%)	0.70	0/2701
1	C	0.47	3/2021 (0.1%)	0.73	0/2750
1	D	0.40	2/1977 (0.1%)	0.71	2/2688 (0.1%)
1	E	0.38	1/1949 (0.1%)	0.75	1/2651 (0.0%)
1	F	0.50	1/1941 (0.1%)	0.75	0/2640
All	All	0.44	14/11931 (0.1%)	0.73	5/16229 (0.0%)

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	199	VAL	C-O	-6.98	1.16	1.24
1	A	65	MET	C-O	-6.87	1.16	1.24
1	C	203[A]	ASN	C-O	-5.93	1.17	1.24
1	C	203[B]	ASN	C-O	-5.93	1.17	1.24
1	D	200	PRO	C-O	-5.58	1.18	1.24
1	B	114[A]	CYS	C-O	-5.22	1.17	1.24
1	B	114[B]	CYS	C-O	-5.22	1.17	1.24
1	F	223	ASN	C-N	5.15	1.40	1.33
1	B	236	MET	C-O	-5.14	1.18	1.24
1	E	217	GLU	C-O	-5.14	1.17	1.23
1	A	12	GLU	C-O	-5.09	1.17	1.23
1	A	159	TYR	C-O	-5.05	1.17	1.23
1	B	222	ARG	C-O	-5.04	1.17	1.24
1	C	21	VAL	C-O	-5.03	1.18	1.24

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	125	ILE	CA-C-N	5.59	125.25	119.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	125	ILE	C-N-CA	5.59	125.25	119.05
1	E	218	ILE	O-C-N	5.25	128.85	123.18
1	A	151	ASN	CA-C-N	5.20	124.81	119.56
1	A	151	ASN	C-N-CA	5.20	124.81	119.56

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	1983	0	1978	16	0
1	B	1921	0	1916	19	0
1	C	1957	0	1947	22	0
1	D	1918	0	1902	8	0
1	E	1896	0	1874	10	0
1	F	1885	0	1872	34	0
2	A	48	0	83	6	0
2	B	32	0	56	4	0
2	C	32	0	55	7	0
2	D	24	0	42	2	0
2	E	32	0	56	5	0
2	F	24	0	42	3	0
3	A	207	0	0	5	0
3	B	188	0	0	0	0
3	C	123	0	0	3	0
3	D	125	0	0	0	0
3	E	153	0	0	0	0
3	F	108	0	0	4	0
All	All	12656	0	11823	118	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 (118) 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)
2:C:304:MPD:H12	2:C:304:MPD:C5	1.62	1.25
2:C:304:MPD:H52	2:C:304:MPD:C1	1.69	1.14
1:B:222:ARG:HH11	1:B:222:ARG:HG2	1.27	0.99
2:C:304:MPD:C5	2:C:304:MPD:C1	2.30	0.97
1:F:170:LEU:C	1:F:170:LEU:HD13	1.98	0.88
1:C:234:GLN:HB3	2:C:303:MPD:H51	1.57	0.85
1:E:156:GLU:OE2	2:E:302:MPD:O4	1.96	0.83
2:C:304:MPD:H12	2:C:304:MPD:H52	0.82	0.79
1:F:172:ARG:O	1:F:173:LEU:C	2.25	0.78
1:C:124:ASP:H	1:C:203[B]:ASN:HD21	1.33	0.73
1:A:34:HIS:HD2	1:A:156[B]:GLU:OE2	1.71	0.73
1:B:149[B]:LEU:HD23	1:B:227:VAL:HB	1.70	0.73
1:C:123:VAL:H	1:C:203[B]:ASN:ND2	1.86	0.73
1:F:81:TYR:CE2	1:F:85:LYS:HD2	2.24	0.72
1:C:123:VAL:H	1:C:203[B]:ASN:HD22	1.35	0.72
1:A:217:GLU:HB3	1:C:217:GLU:HB3	1.73	0.69
1:F:98:MET:SD	1:F:170:LEU:HD23	2.33	0.68
1:C:200[B]:PRO:HB3	1:C:201[B]:PRO:HD2	1.77	0.66
1:B:222:ARG:HG2	1:B:222:ARG:NH1	2.07	0.66
1:F:170:LEU:C	1:F:170:LEU:CD1	2.70	0.64
1:F:170:LEU:HD11	1:F:174:MET:SD	2.38	0.64
1:A:45[B]:LYS:CD	3:A:605:HOH:O	2.45	0.64
2:C:304:MPD:HM1	3:C:519:HOH:O	1.98	0.64
1:F:148:ASP:HB3	1:F:226:HIS:HB3	1.80	0.64
1:D:22:GLY:HA2	1:D:49:THR:O	1.98	0.63
2:B:304:MPD:O4	2:B:304:MPD:O2	2.11	0.63
1:B:250:GLY:OXT	1:E:45:LYS:NZ	2.31	0.62
1:B:193:SER:O	1:B:195:GLU:N	2.33	0.62
1:A:45[B]:LYS:HD3	3:A:605:HOH:O	2.00	0.62
1:F:3:GLU:OE2	1:F:67:ARG:NH2	2.34	0.60
1:E:21:VAL:HG21	2:E:303:MPD:H12	1.83	0.59
1:F:85:LYS:NZ	1:F:112:ASP:OD2	2.33	0.59
1:F:172:ARG:O	1:F:175:ALA:N	2.35	0.58
1:B:193:SER:C	1:B:195:GLU:H	2.12	0.58
1:B:193:SER:C	1:B:195:GLU:N	2.62	0.57
2:C:304:MPD:C1	2:C:304:MPD:H53	2.31	0.57
1:B:195:GLU:O	1:B:225:TYR:HA	2.04	0.57
1:D:21:VAL:O	1:D:48:TYR:HD1	1.88	0.56
2:E:302:MPD:O4	2:E:302:MPD:O2	2.20	0.55
2:B:303:MPD:HM1	2:B:304:MPD:H51	1.89	0.55
1:E:170:LEU:HD21	2:E:301:MPD:H11	1.89	0.55
1:F:139:PRO:O	1:F:164:THR:HG21	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:170:LEU:HD13	1:F:170:LEU:O	2.06	0.54
2:A:304:MPD:H52	2:A:304:MPD:O2	2.07	0.54
1:A:90:THR:HG23	1:A:114[B]:CYS:SG	2.48	0.54
1:F:3:GLU:CD	3:F:508:HOH:O	2.51	0.54
1:C:78:GLU:OE2	1:C:110:HIS:NE2	2.25	0.53
1:C:136:GLY:N	3:C:484:HOH:O	2.41	0.53
1:E:147:SER:OG	1:E:156:GLU:OE1	2.18	0.53
1:E:156:GLU:CD	2:E:302:MPD:HO4	2.10	0.52
1:B:56[B]:LYS:HD2	1:B:72:ASP:HB3	1.92	0.52
1:C:124:ASP:H	1:C:203[B]:ASN:ND2	2.04	0.52
2:F:303:MPD:O4	2:F:303:MPD:O2	2.16	0.52
1:B:90:THR:HG23	1:B:114[B]:CYS:SG	2.51	0.51
2:A:306:MPD:O4	2:A:306:MPD:O2	2.26	0.51
1:F:20:PRO:O	1:F:88:CYS:HB3	2.11	0.51
1:D:156:GLU:OE2	2:D:301:MPD:O4	2.28	0.50
1:E:150:LYS:HE3	1:E:225:TYR:CE1	2.45	0.50
1:F:168:LEU:O	1:F:172:ARG:HG3	2.10	0.50
1:B:20:PRO:O	1:B:88:CYS:HB3	2.11	0.50
1:D:198:VAL:HG13	2:D:302:MPD:H11	1.92	0.50
1:A:240:ARG:HH12	2:A:303:MPD:H12	1.77	0.50
1:C:147:SER:HB3	1:C:149:LEU:HD12	1.95	0.49
1:F:234:GLN:HB3	2:F:303:MPD:HM2	1.95	0.49
1:F:3:GLU:CG	3:F:508:HOH:O	2.60	0.49
1:F:172:ARG:O	1:F:174:MET:N	2.46	0.48
1:B:56[A]:LYS:HG3	1:B:76:SER:OG	2.12	0.48
1:F:170:LEU:CD1	1:F:174:MET:SD	3.02	0.47
1:F:203:ASN:O	1:F:207[A]:ILE:HG12	2.14	0.47
1:B:56[A]:LYS:HD2	1:B:72:ASP:HB3	1.96	0.47
1:F:142:LEU:CD2	1:F:164:THR:HG22	2.44	0.47
1:A:176:GLN:NE2	3:A:517:HOH:O	2.33	0.46
1:F:138:LEU:HB2	1:F:139:PRO:HD2	1.98	0.46
1:F:142:LEU:HD22	1:F:164:THR:HG22	1.98	0.46
1:B:222:ARG:HH11	1:B:222:ARG:CG	2.06	0.46
1:D:81:TYR:CZ	1:D:85:LYS:HD2	2.51	0.46
1:F:61:HIS:CE1	1:F:63:GLU:HG3	2.50	0.46
1:F:172:ARG:C	1:F:174:MET:N	2.71	0.46
1:A:157:LEU:HG	2:A:306:MPD:H4	1.98	0.45
1:F:143:ASP:OD1	1:F:161:LYS:NZ	2.39	0.45
1:F:151:ASN:HD22	2:F:303:MPD:C5	2.29	0.45
1:E:61:HIS:CE1	1:E:63:GLU:HG3	2.52	0.45
1:A:45[B]:LYS:NZ	3:A:605:HOH:O	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:GLU:CB	1:C:217:GLU:HB3	2.44	0.45
1:C:20:PRO:O	1:C:88:CYS:HB3	2.17	0.44
1:C:128:ILE:O	1:C:132:MET:HG3	2.18	0.44
1:E:145:ILE:H	1:E:145:ILE:HG13	1.60	0.44
1:F:148:ASP:HB3	1:F:226:HIS:CB	2.46	0.44
1:C:200[B]:PRO:CB	1:C:201[B]:PRO:HD2	2.30	0.43
1:A:200[B]:PRO:CB	1:A:201[B]:PRO:HD2	2.47	0.43
1:A:227:VAL:HG22	2:A:301:MPD:H53	2.00	0.43
1:B:142:LEU:HB3	2:B:304:MPD:H53	2.01	0.43
1:B:196:ASN:HB3	1:B:199:VAL:O	2.18	0.43
1:D:22:GLY:CA	1:D:49:THR:O	2.66	0.43
1:C:201[B]:PRO:HA	1:C:202[B]:GLY:HA2	1.83	0.43
1:A:201[B]:PRO:HA	1:A:202[B]:GLY:HA2	1.59	0.43
1:A:236[A]:MET:HE1	3:A:465:HOH:O	2.17	0.43
1:F:102:LEU:HD21	1:F:173:LEU:HD21	2.01	0.42
1:E:155:LYS:HD2	1:E:155:LYS:HA	1.81	0.42
1:B:222:ARG:NH1	1:B:222:ARG:CG	2.73	0.41
1:B:148:ASP:HB3	1:B:226:HIS:HB3	2.02	0.41
1:C:70:PHE:HA	1:C:73:TRP:CE3	2.55	0.41
1:F:86:GLN:NE2	3:F:498:HOH:O	2.46	0.41
1:A:160:GLU:HG3	2:A:306:MPD:C1	2.51	0.41
1:D:138:LEU:HA	1:D:139:PRO:HD3	1.93	0.41
1:C:201[B]:PRO:O	1:C:201[B]:PRO:HG2	2.20	0.41
1:F:128:ILE:HG13	1:F:129:ALA:N	2.35	0.41
1:C:132:MET:HE1	1:C:168[B]:LEU:HB2	2.02	0.41
1:C:199[B]:VAL:HA	1:C:200[B]:PRO:HD3	1.94	0.41
1:D:23:VAL:HG12	1:D:24:LEU:N	2.35	0.41
1:F:239:GLU:OE2	3:F:505:HOH:O	2.22	0.41
1:C:217:GLU:OE1	3:C:463:HOH:O	2.22	0.41
1:B:142:LEU:HD13	2:B:304:MPD:H32	2.04	0.40
1:C:138:LEU:HD23	1:C:138:LEU:HA	1.93	0.40
1:C:170:LEU:HG	1:C:174:MET:HE2	2.03	0.40
1:F:125:ILE:HA	1:F:126:PRO:HD3	1.80	0.40
1:F:173:LEU:HD12	1:F:173:LEU:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	259/270 (96%)	250 (96%)	9 (4%)	0	100	100
1	B	246/270 (91%)	238 (97%)	7 (3%)	1 (0%)	30	16
1	C	251/270 (93%)	238 (95%)	12 (5%)	1 (0%)	30	16
1	D	245/270 (91%)	237 (97%)	8 (3%)	0	100	100
1	E	241/270 (89%)	232 (96%)	9 (4%)	0	100	100
1	F	240/270 (89%)	228 (95%)	10 (4%)	2 (1%)	16	5
All	All	1482/1620 (92%)	1423 (96%)	55 (4%)	4 (0%)	36	22

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	194	ASP
1	C	131	GLY
1	F	127	ALA
1	F	173	LEU

5.3.2 Protein sidechains

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	216/222 (97%)	216 (100%)	0	100	100
1	B	209/222 (94%)	208 (100%)	1 (0%)	81	76
1	C	212/222 (96%)	212 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	207/222 (93%)	207 (100%)	0	100	100
1	E	204/222 (92%)	203 (100%)	1 (0%)	81	76
1	F	204/222 (92%)	199 (98%)	5 (2%)	42	24
All	All	1252/1332 (94%)	1245 (99%)	7 (1%)	78	72

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	222	ARG
1	E	145	ILE
1	F	138	LEU
1	F	142	LEU
1	F	168	LEU
1	F	170	LEU
1	F	173	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	HIS
1	A	176	GLN
1	A	209	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry

24 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	MPD	B	301	-	7,7,7	0.29	0	9,10,10	0.40	0
2	MPD	A	305	-	7,7,7	0.29	0	9,10,10	0.20	0
2	MPD	A	301	-	7,7,7	0.29	0	9,10,10	0.53	0
2	MPD	D	302	-	7,7,7	0.26	0	9,10,10	0.31	0
2	MPD	D	303	-	7,7,7	0.31	0	9,10,10	0.30	0
2	MPD	A	306	-	7,7,7	0.29	0	9,10,10	0.25	0
2	MPD	E	304	-	7,7,7	0.26	0	9,10,10	0.39	0
2	MPD	A	303	-	7,7,7	0.31	0	9,10,10	0.24	0
2	MPD	C	301	-	7,7,7	0.30	0	9,10,10	0.27	0
2	MPD	B	302	-	7,7,7	0.27	0	9,10,10	0.26	0
2	MPD	D	301	-	7,7,7	0.31	0	9,10,10	0.45	0
2	MPD	F	302	-	7,7,7	0.31	0	9,10,10	0.58	0
2	MPD	F	303	-	7,7,7	0.29	0	9,10,10	0.18	0
2	MPD	E	303	-	7,7,7	0.26	0	9,10,10	0.36	0
2	MPD	A	302	-	7,7,7	0.28	0	9,10,10	0.45	0
2	MPD	B	304	-	7,7,7	0.27	0	9,10,10	0.24	0
2	MPD	E	301	-	7,7,7	0.28	0	9,10,10	0.58	0
2	MPD	C	302	-	7,7,7	1.10	0	9,10,10	1.12	1 (11%)
2	MPD	C	303	-	7,7,7	0.27	0	9,10,10	0.62	0
2	MPD	A	304	-	7,7,7	1.61	1 (14%)	9,10,10	0.76	0
2	MPD	B	303	-	7,7,7	0.29	0	9,10,10	0.32	0
2	MPD	F	301	-	7,7,7	0.24	0	9,10,10	0.47	0
2	MPD	C	304	-	7,7,7	0.86	0	9,10,10	0.91	0
2	MPD	E	302	-	7,7,7	0.28	0	9,10,10	0.29	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	MPD	B	301	-	-	2/5/5/5	-
2	MPD	A	305	-	-	4/5/5/5	-
2	MPD	A	301	-	-	1/5/5/5	-
2	MPD	D	302	-	-	4/5/5/5	-
2	MPD	D	303	-	-	4/5/5/5	-
2	MPD	A	306	-	-	5/5/5/5	-
2	MPD	E	304	-	-	5/5/5/5	-
2	MPD	A	303	-	-	0/5/5/5	-
2	MPD	C	301	-	-	0/5/5/5	-
2	MPD	B	302	-	-	0/5/5/5	-
2	MPD	D	301	-	-	3/5/5/5	-
2	MPD	F	302	-	-	1/5/5/5	-
2	MPD	F	303	-	-	4/5/5/5	-
2	MPD	E	303	-	-	1/5/5/5	-
2	MPD	A	302	-	-	0/5/5/5	-
2	MPD	B	304	-	-	3/5/5/5	-
2	MPD	E	301	-	-	3/5/5/5	-
2	MPD	C	302	-	-	2/5/5/5	-
2	MPD	C	303	-	-	1/5/5/5	-
2	MPD	A	304	-	-	2/5/5/5	-
2	MPD	B	303	-	-	2/5/5/5	-
2	MPD	F	301	-	-	3/5/5/5	-
2	MPD	C	304	-	-	2/5/5/5	-
2	MPD	E	302	-	-	1/5/5/5	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	304	MPD	O2-C2	-3.49	1.36	1.44

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	302	MPD	O4-C4-C5	-2.00	100.83	109.45

There are no chirality outliers.

All (53) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	MPD	C2-C3-C4-C5
2	A	306	MPD	C2-C3-C4-C5
2	B	301	MPD	C2-C3-C4-O4
2	B	301	MPD	C2-C3-C4-C5
2	C	302	MPD	C2-C3-C4-O4
2	C	304	MPD	C2-C3-C4-O4
2	D	302	MPD	C2-C3-C4-O4
2	D	302	MPD	C2-C3-C4-C5
2	D	303	MPD	C2-C3-C4-O4
2	D	303	MPD	C2-C3-C4-C5
2	E	301	MPD	O2-C2-C3-C4
2	E	301	MPD	CM-C2-C3-C4
2	E	304	MPD	C1-C2-C3-C4
2	E	304	MPD	O2-C2-C3-C4
2	F	301	MPD	C2-C3-C4-C5
2	F	302	MPD	C2-C3-C4-C5
2	B	304	MPD	C2-C3-C4-O4
2	F	303	MPD	C2-C3-C4-O4
2	A	304	MPD	C1-C2-C3-C4
2	A	305	MPD	CM-C2-C3-C4
2	A	306	MPD	C1-C2-C3-C4
2	A	306	MPD	CM-C2-C3-C4
2	B	303	MPD	CM-C2-C3-C4
2	B	304	MPD	CM-C2-C3-C4
2	D	301	MPD	CM-C2-C3-C4
2	D	303	MPD	C1-C2-C3-C4
2	E	301	MPD	C1-C2-C3-C4
2	E	304	MPD	CM-C2-C3-C4
2	F	301	MPD	C1-C2-C3-C4
2	A	305	MPD	C2-C3-C4-C5
2	C	302	MPD	C2-C3-C4-C5
2	C	303	MPD	C2-C3-C4-C5
2	C	304	MPD	C2-C3-C4-C5
2	E	304	MPD	C2-C3-C4-C5
2	F	303	MPD	C2-C3-C4-C5
2	A	306	MPD	O2-C2-C3-C4
2	D	301	MPD	O2-C2-C3-C4
2	D	302	MPD	O2-C2-C3-C4
2	E	303	MPD	O2-C2-C3-C4
2	F	303	MPD	O2-C2-C3-C4
2	A	305	MPD	C2-C3-C4-O4
2	A	306	MPD	C2-C3-C4-O4
2	E	302	MPD	C2-C3-C4-O4

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Mol	Chain	Res	Type	Atoms
2	E	304	MPD	C2-C3-C4-O4
2	A	304	MPD	CM-C2-C3-C4
2	A	305	MPD	C1-C2-C3-C4
2	B	303	MPD	C1-C2-C3-C4
2	B	304	MPD	C1-C2-C3-C4
2	D	301	MPD	C1-C2-C3-C4
2	D	302	MPD	CM-C2-C3-C4
2	D	303	MPD	CM-C2-C3-C4
2	F	301	MPD	CM-C2-C3-C4
2	F	303	MPD	CM-C2-C3-C4

There are no ring outliers.

14 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	MPD	1	0
2	D	302	MPD	1	0
2	A	306	MPD	3	0
2	A	303	MPD	1	0
2	D	301	MPD	1	0
2	F	303	MPD	3	0
2	E	303	MPD	1	0
2	B	304	MPD	4	0
2	E	301	MPD	1	0
2	C	303	MPD	1	0
2	A	304	MPD	1	0
2	B	303	MPD	1	0
2	C	304	MPD	6	0
2	E	302	MPD	3	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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, 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	248/270 (91%)	-0.20	8 (3%)	50	54	9, 16, 35, 51	13 (5%)
1	B	243/270 (90%)	-0.01	12 (4%)	35	38	7, 19, 41, 72	7 (2%)
1	C	245/270 (90%)	0.37	20 (8%)	17	19	12, 24, 51, 81	10 (4%)
1	D	244/270 (90%)	0.30	17 (6%)	22	24	8, 25, 51, 66	5 (2%)
1	E	242/270 (89%)	0.30	20 (8%)	17	18	11, 25, 59, 85	3 (1%)
1	F	240/270 (88%)	1.03	43 (17%)	3	3	13, 33, 61, 83	4 (1%)
All	All	1462/1620 (90%)	0.30	120 (8%)	17	19	7, 24, 53, 85	42 (2%)

All (120) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	250	GLY	7.0
1	F	129	ALA	5.6
1	D	23	VAL	4.7
1	F	145	ILE	4.4
1	C	131	GLY	4.2
1	E	130	ALA	4.2
1	D	22	GLY	4.2
1	F	128	ILE	4.2
1	F	138	LEU	4.1
1	E	157	LEU	4.0
1	C	145	ILE	3.9
1	E	139	PRO	3.9
1	D	21	VAL	3.8
1	B	195	GLU	3.7
1	E	129	ALA	3.6
1	D	145	ILE	3.6
1	F	70	PHE	3.6
1	F	127	ALA	3.6
1	E	138	LEU	3.6

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Mol	Chain	Res	Type	RSRZ
1	E	145	ILE	3.5
1	A	201[A]	PRO	3.4
1	D	135	GLY	3.3
1	D	130	ALA	3.2
1	B	126	PRO	3.2
1	F	71	HIS	3.2
1	E	158	ALA	3.2
1	E	156	GLU	3.2
1	F	168	LEU	3.1
1	A	145	ILE	3.1
1	F	69	THR	3.1
1	F	126	PRO	3.0
1	C	126	PRO	3.0
1	D	152	PRO	3.0
1	A	153	ASP	3.0
1	F	177	THR	3.0
1	F	170	LEU	3.0
1	B	129	ALA	2.9
1	F	139	PRO	2.9
1	C	152	PRO	2.8
1	E	154	VAL	2.8
1	F	62	TYR	2.8
1	C	130	ALA	2.7
1	F	158	ALA	2.7
1	B	20	PRO	2.7
1	F	5	TYR	2.7
1	C	164	THR	2.7
1	E	2	SER	2.7
1	F	57	GLY	2.6
1	C	128	ILE	2.6
1	C	201[A]	PRO	2.6
1	D	153	ASP	2.6
1	D	136	GLY	2.6
1	C	154	VAL	2.6
1	F	141	TYR	2.6
1	D	2	SER	2.6
1	F	142	LEU	2.5
1	A	129	ALA	2.5
1	E	152	PRO	2.5
1	F	206	ILE	2.5
1	F	167	LEU	2.5
1	A	152	PRO	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	130	ALA	2.5
1	E	128	ILE	2.5
1	F	125	ILE	2.5
1	B	249	ALA	2.4
1	F	181	LEU	2.4
1	C	127	ALA	2.4
1	F	172	ARG	2.4
1	F	226	HIS	2.4
1	F	173	LEU	2.4
1	A	155	LYS	2.4
1	E	155	LYS	2.3
1	A	2	SER	2.3
1	C	146	GLY	2.3
1	B	127	ALA	2.3
1	C	129	ALA	2.3
1	D	158	ALA	2.3
1	F	171	ALA	2.3
1	C	168[A]	LEU	2.3
1	E	168	LEU	2.3
1	F	144	SER	2.3
1	E	153	ASP	2.3
1	D	201	PRO	2.2
1	F	200	PRO	2.2
1	D	138	LEU	2.2
1	E	5	TYR	2.2
1	F	165	ALA	2.2
1	F	179	ALA	2.2
1	B	193	SER	2.2
1	D	144	SER	2.2
1	F	8	LEU	2.2
1	F	146	GLY	2.2
1	F	250	GLY	2.2
1	B	196	ASN	2.2
1	C	158	ALA	2.2
1	C	138	LEU	2.2
1	F	105	TYR	2.2
1	F	155	LYS	2.2
1	F	68	THR	2.2
1	B	2	SER	2.2
1	C	132	MET	2.1
1	A	132	MET	2.1
1	C	153[A]	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	4	GLN	2.1
1	C	249	ALA	2.1
1	D	155	LYS	2.1
1	D	156	GLU	2.1
1	F	164	THR	2.1
1	B	128	ILE	2.1
1	E	62	TYR	2.1
1	C	136	GLY	2.1
1	F	4	GLN	2.1
1	C	2	SER	2.1
1	F	205	ASP	2.1
1	F	157	LEU	2.1
1	E	164	THR	2.1
1	F	3	GLU	2.0
1	D	154	VAL	2.0
1	F	111	PRO	2.0
1	E	127	ALA	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 oligosaccharides 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($\text{\AA}^2$)	Q<0.9
2	MPD	C	304	8/8	0.53	0.26	55,64,68,71	0
2	MPD	A	303	8/8	0.60	0.20	39,47,59,59	0
2	MPD	A	306	8/8	0.66	0.20	39,45,49,49	0
2	MPD	A	305	8/8	0.66	0.21	35,46,52,55	0
2	MPD	C	303	8/8	0.67	0.24	44,56,73,74	0
2	MPD	E	304	8/8	0.70	0.20	43,49,52,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	MPD	F	303	8/8	0.70	0.18	28,54,63,65	0
2	MPD	F	301	8/8	0.71	0.19	47,53,63,70	0
2	MPD	B	304	8/8	0.76	0.14	33,43,49,49	0
2	MPD	A	304	8/8	0.76	0.15	32,43,45,47	0
2	MPD	D	303	8/8	0.80	0.16	38,44,51,55	0
2	MPD	E	301	8/8	0.81	0.20	44,52,55,55	0
2	MPD	D	301	8/8	0.81	0.15	35,47,48,54	0
2	MPD	D	302	8/8	0.81	0.15	37,47,51,59	0
2	MPD	C	302	8/8	0.81	0.18	39,43,47,52	0
2	MPD	E	302	8/8	0.82	0.14	45,54,60,65	0
2	MPD	A	301	8/8	0.84	0.14	31,37,41,42	0
2	MPD	B	301	8/8	0.86	0.11	30,36,39,40	0
2	MPD	F	302	8/8	0.86	0.13	48,53,56,60	0
2	MPD	B	303	8/8	0.86	0.12	41,44,45,47	0
2	MPD	E	303	8/8	0.87	0.12	19,24,33,35	0
2	MPD	B	302	8/8	0.88	0.12	19,33,38,42	0
2	MPD	C	301	8/8	0.89	0.12	39,43,50,54	0
2	MPD	A	302	8/8	0.89	0.11	29,33,37,42	0

6.5 Other polymers [i](#)

There are no such residues in this entry.