



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:11 PM UTC

PDB ID : 5I8U / pdb_00005i8u
Title : Crystal Structure of the RV1700 (MT ADPRASE) E142Q mutant
Authors : Thirawatananond, P.; Kang, L.-W.; Amzel, L.M.; Gabelli, S.B.
Deposited on : 2016-02-19
Resolution : 2.00 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<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:

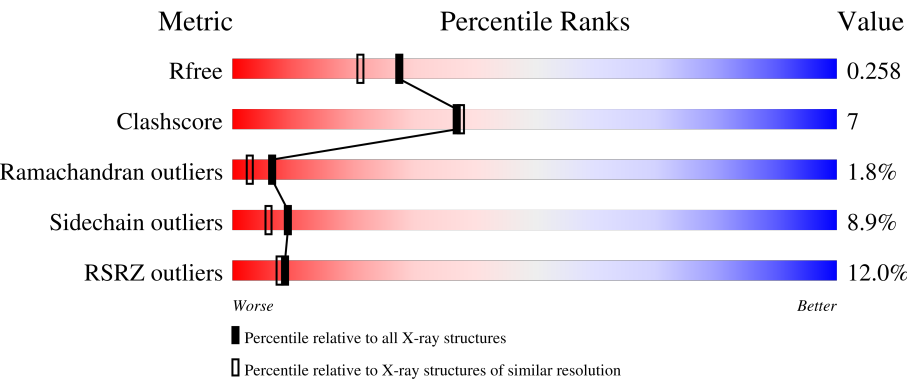
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (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 2.00 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



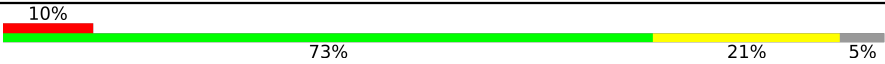
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	207	7% 73% 19% ..
1	B	207	17% 76% 18% ..
1	C	207	9% 68% 24% 5% ..
1	D	207	12% 72% 14% 5% 7%
1	E	207	17% 78% 13% .. 8%

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Mol	Chain	Length	Quality of chain
1	F	207	
1	G	207	

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
4	PEG	A	403	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 11350 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 ADP-ribose pyrophosphatase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	197	Total	C	N	O	S	0	0	0
			1527	962	277	283	5			
1	A	198	Total	C	N	O	S	0	0	0
			1541	968	281	287	5			
1	B	202	Total	C	N	O	S	0	0	0
			1574	989	289	291	5			
1	C	203	Total	C	N	O	S	0	0	0
			1582	993	290	294	5			
1	D	192	Total	C	N	O	S	0	0	0
			1495	943	271	276	5			
1	E	190	Total	C	N	O	S	0	0	0
			1475	933	266	271	5			
1	F	196	Total	C	N	O	S	0	0	0
			1519	958	276	280	5			

There are 7 discrepancies between the modelled and reference sequences:

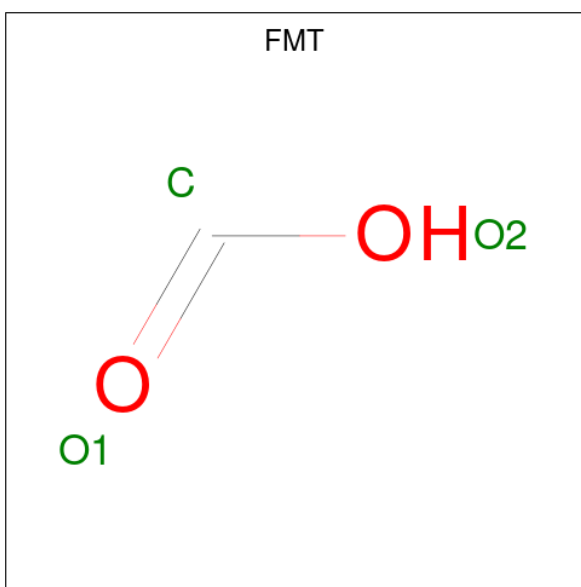
Chain	Residue	Modelled	Actual	Comment	Reference
G	142	GLN	GLU	engineered mutation	UNP A0A045KHE5
A	142	GLN	GLU	engineered mutation	UNP A0A045KHE5
B	142	GLN	GLU	engineered mutation	UNP A0A045KHE5
C	142	GLN	GLU	engineered mutation	UNP A0A045KHE5
D	142	GLN	GLU	engineered mutation	UNP A0A045KHE5
E	142	GLN	GLU	engineered mutation	UNP A0A045KHE5
F	142	GLN	GLU	engineered mutation	UNP A0A045KHE5

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	G	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is FORMIC ACID (CCD ID: FMT) (formula: CH₂O₂).



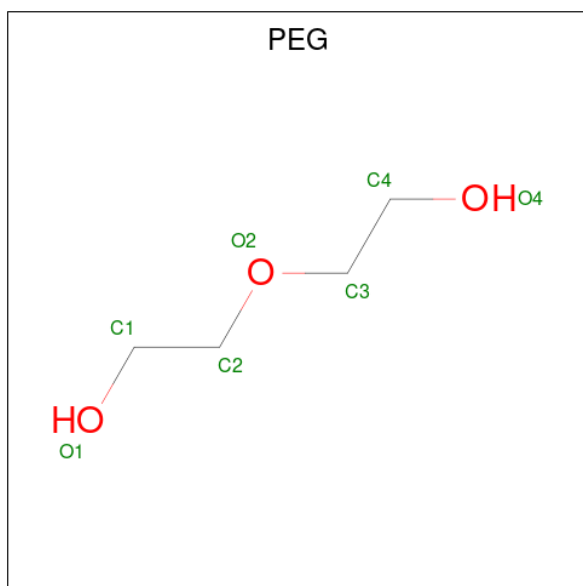
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			3	1	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			3	1	2		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	C	2	Total	Na	0	0
			2	2		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	G	132	Total	O	0	0
			132	132		
6	A	112	Total	O	0	0
			112	112		
6	B	75	Total	O	0	0
			75	75		
6	C	117	Total	O	0	0
			117	117		

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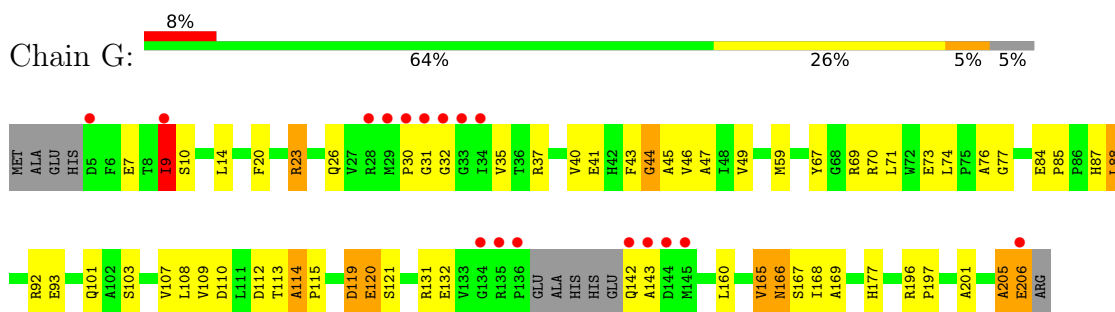
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	44	Total 44	O 44	0	0
6	E	36	Total 36	O 36	0	0
6	F	91	Total 91	O 91	0	0

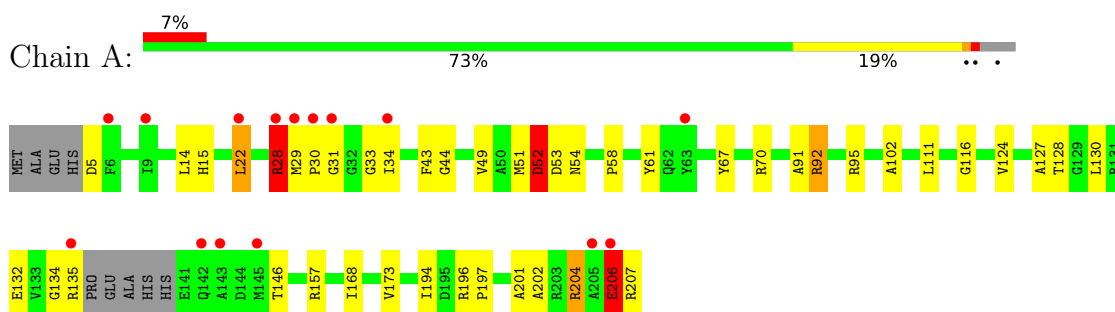
3 Residue-property plots [i](#)

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.

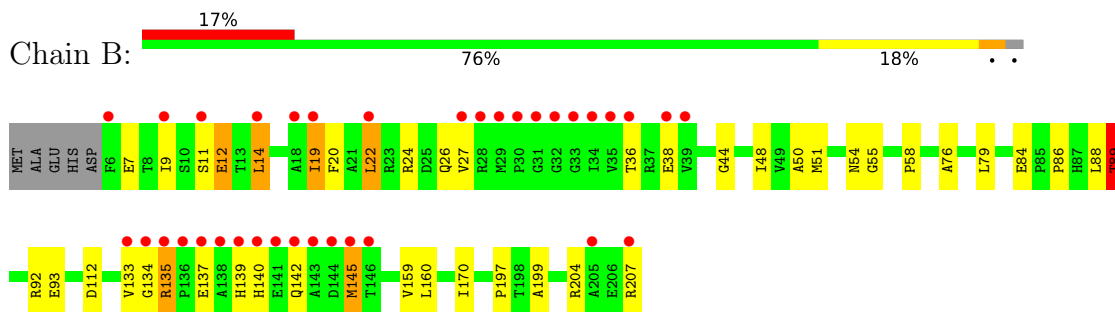
- Molecule 1: ADP-ribose pyrophosphatase



- Molecule 1: ADP-ribose pyrophosphatase

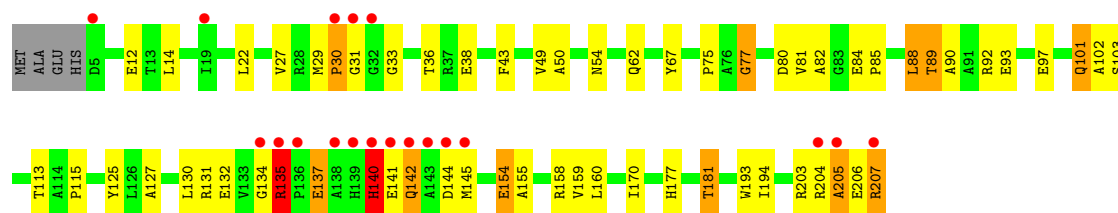


- Molecule 1: ADP-ribose pyrophosphatase

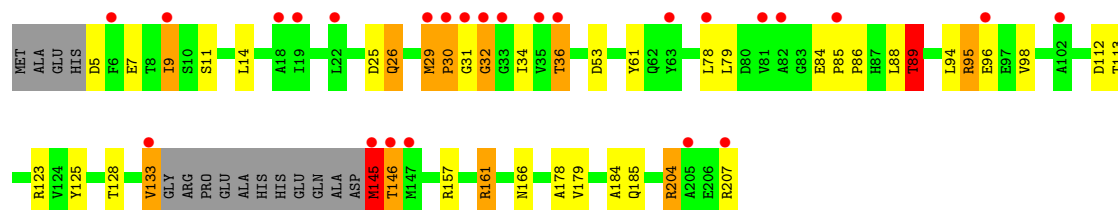
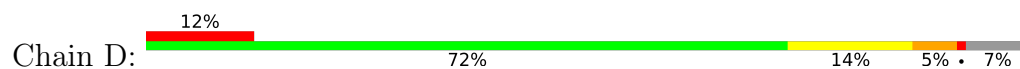


- Molecule 1: ADP-ribose pyrophosphatase

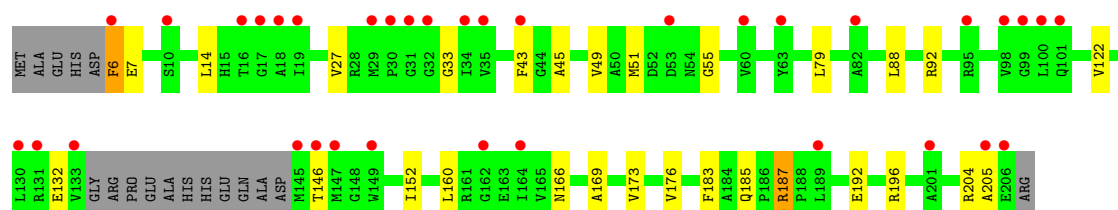
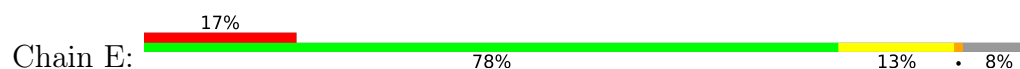




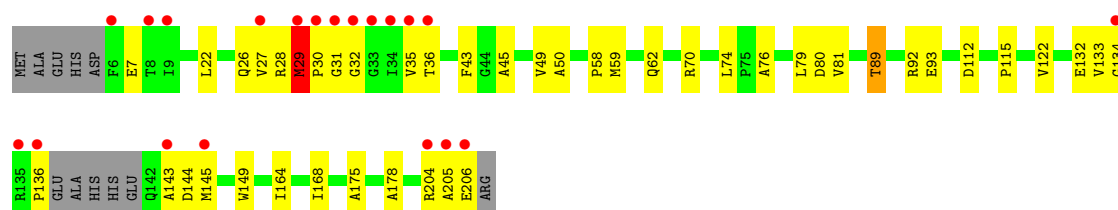
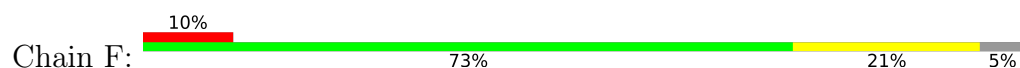
• Molecule 1: ADP-ribose pyrophosphatase



• Molecule 1: ADP-ribose pyrophosphatase



• Molecule 1: ADP-ribose pyrophosphatase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	152.77Å 124.84Å 142.96Å 90.00° 98.50° 90.00°	Depositor
Resolution (Å)	141.42 – 2.00 141.39 – 2.00	Depositor EDS
% Data completeness (in resolution range)	88.2 (141.42-2.00) 88.3 (141.39-2.00)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.07 (at 1.98Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.222 , 0.258 0.222 , 0.258	Depositor DCC
R_{free} test set	8011 reflections (4.41%)	wwPDB-VP
Wilson B-factor (Å ²)	40.5	Xtriage
Anisotropy	0.336	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 57.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11350	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.81% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMT, NA, SO4, PEG

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	1.34	6/1573 (0.4%)	1.36	7/2139 (0.3%)
1	B	1.04	0/1610	1.18	6/2192 (0.3%)
1	C	1.32	8/1618 (0.5%)	1.34	9/2203 (0.4%)
1	D	0.96	0/1527	1.19	6/2078 (0.3%)
1	E	0.91	0/1507	1.11	3/2053 (0.1%)
1	F	1.15	2/1552 (0.1%)	1.24	7/2114 (0.3%)
1	G	1.73	19/1560 (1.2%)	1.67	40/2125 (1.9%)
All	All	1.24	35/10947 (0.3%)	1.31	78/14904 (0.5%)

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	C	0	1
1	D	0	1
1	G	0	1
All	All	0	3

All (35) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	169	ALA	N-CA	12.04	1.61	1.46
1	G	44	GLY	N-CA	11.33	1.56	1.45
1	G	46	VAL	C-O	10.94	1.35	1.23
1	G	76	ALA	N-CA	10.56	1.58	1.46
1	G	67	TYR	CZ-OH	9.10	1.57	1.38
1	G	45	ALA	N-CA	8.40	1.55	1.46
1	G	196	ARG	C-O	7.26	1.33	1.24
1	A	58	PRO	C-O	7.12	1.31	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	167	SER	C-O	6.75	1.32	1.24
1	G	114	ALA	C-O	6.73	1.31	1.24
1	G	49	VAL	N-CA	-6.44	1.38	1.46
1	A	173	VAL	N-CA	6.30	1.53	1.46
1	G	74	LEU	C-O	6.27	1.32	1.23
1	A	52	ASP	CB-CG	-6.17	1.36	1.52
1	A	124	VAL	C-O	6.04	1.31	1.24
1	F	49	VAL	CA-CB	6.02	1.61	1.53
1	G	120	GLU	N-CA	-6.00	1.38	1.46
1	C	77	GLY	C-O	5.99	1.29	1.23
1	G	47	ALA	N-CA	5.95	1.53	1.45
1	C	30	PRO	CA-C	5.87	1.58	1.52
1	G	69	ARG	N-CA	5.72	1.53	1.46
1	G	107	VAL	CA-C	5.70	1.59	1.52
1	G	112	ASP	CG-OD2	5.70	1.36	1.25
1	C	90	ALA	CA-C	5.64	1.59	1.52
1	G	166	ASN	CG-OD1	5.64	1.34	1.23
1	C	50	ALA	N-CA	5.54	1.54	1.46
1	F	112	ASP	C-O	5.43	1.30	1.24
1	G	47	ALA	C-O	-5.42	1.16	1.23
1	A	91	ALA	N-CA	5.35	1.52	1.46
1	A	49	VAL	CA-C	5.25	1.59	1.52
1	C	170	ILE	C-O	-5.25	1.18	1.24
1	G	108	LEU	C-O	5.19	1.29	1.23
1	C	49	VAL	CA-C	5.12	1.58	1.52
1	C	193	TRP	CA-C	5.11	1.59	1.52
1	C	125	TYR	C-O	5.02	1.30	1.23

All (78) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	44	GLY	N-CA-C	-10.72	99.36	112.33
1	F	43	PHE	N-CA-C	9.48	122.80	111.33
1	A	168	ILE	N-CA-C	-9.06	101.12	111.00
1	G	168	ILE	N-CA-C	-8.70	101.52	111.00
1	G	168	ILE	CA-C-N	-7.62	109.47	120.29
1	G	168	ILE	C-N-CA	-7.62	109.47	120.29
1	F	29	MET	CA-C-N	-7.14	110.92	119.84
1	F	29	MET	C-N-CA	-7.14	110.92	119.84
1	G	47	ALA	CA-C-N	-6.82	113.46	122.94
1	G	47	ALA	C-N-CA	-6.82	113.46	122.94
1	G	103	SER	N-CA-C	6.79	118.76	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	134	GLY	N-CA-C	6.69	123.04	115.08
1	G	9	ILE	CB-CA-C	6.61	119.15	111.55
1	G	109	VAL	CA-C-O	-6.48	113.97	120.90
1	F	80	ASP	N-CA-C	6.47	120.18	112.93
1	A	52	ASP	CB-CA-C	-6.47	97.55	110.42
1	G	120	GLU	CB-CA-C	-6.41	99.90	109.90
1	C	194	ILE	N-CA-C	6.38	117.06	110.36
1	A	34	ILE	N-CA-C	6.37	117.88	108.45
1	G	120	GLU	CA-CB-CG	-6.34	101.42	114.10
1	G	205	ALA	CA-C-N	6.30	133.03	121.70
1	G	205	ALA	C-N-CA	6.30	133.03	121.70
1	C	130	LEU	N-CA-C	6.29	119.79	110.48
1	G	44	GLY	CA-C-N	-6.27	111.08	121.80
1	G	44	GLY	C-N-CA	-6.27	111.08	121.80
1	C	31	GLY	N-CA-C	-6.18	98.54	113.18
1	G	113	THR	O-C-N	6.17	128.51	122.09
1	E	183	PHE	N-CA-C	6.14	118.94	111.82
1	G	40	VAL	CB-CA-C	-6.07	104.67	111.23
1	G	113	THR	N-CA-C	6.04	118.35	111.11
1	D	84	GLU	N-CA-C	5.97	117.42	109.83
1	G	9	ILE	N-CA-C	-5.83	106.80	111.81
1	B	145	MET	N-CA-C	5.82	121.04	113.88
1	G	59	MET	CA-C-N	-5.79	114.12	122.45
1	G	59	MET	C-N-CA	-5.79	114.12	122.45
1	G	196	ARG	CA-C-N	-5.77	114.32	120.03
1	G	196	ARG	C-N-CA	-5.77	114.32	120.03
1	G	119	ASP	CA-C-N	-5.70	112.78	120.82
1	G	119	ASP	C-N-CA	-5.70	112.78	120.82
1	A	116	GLY	N-CA-C	5.64	119.71	112.83
1	C	103	SER	CB-CA-C	-5.63	98.90	110.38
1	G	114	ALA	CB-CA-C	-5.62	103.00	111.27
1	B	48	ILE	N-CA-C	5.59	116.17	108.12
1	B	199	ALA	N-CA-C	5.59	117.81	111.11
1	F	133	VAL	N-CA-C	-5.58	100.64	108.80
1	A	194	ILE	N-CA-C	5.54	116.18	110.36
1	A	157	ARG	NE-CZ-NH1	-5.54	115.96	121.50
1	G	23	ARG	N-CA-CB	-5.50	102.30	111.20
1	D	32	GLY	CA-C-N	5.46	125.28	120.10
1	D	32	GLY	C-N-CA	5.46	125.28	120.10
1	G	165	VAL	CB-CA-C	-5.45	105.51	110.63
1	C	205	ALA	CA-C-N	5.43	131.47	121.70
1	C	205	ALA	C-N-CA	5.43	131.47	121.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	7	GLU	N-CA-C	5.38	118.20	109.06
1	D	85	PRO	O-C-N	5.32	123.65	121.15
1	G	201	ALA	N-CA-C	-5.29	105.43	111.14
1	B	20	PHE	N-CA-C	5.27	116.15	108.14
1	C	30	PRO	O-C-N	-5.27	117.81	122.93
1	G	110	ASP	CA-C-N	-5.25	113.70	122.21
1	G	110	ASP	C-N-CA	-5.25	113.70	122.21
1	G	69	ARG	NE-CZ-NH1	-5.25	116.25	121.50
1	G	45	ALA	CA-C-N	-5.24	114.39	122.68
1	G	45	ALA	C-N-CA	-5.24	114.39	122.68
1	G	43	PHE	CA-C-N	-5.24	113.73	122.43
1	G	43	PHE	C-N-CA	-5.24	113.73	122.43
1	C	155	ALA	N-CA-C	-5.24	105.47	111.07
1	E	185	GLN	CA-C-N	5.20	125.93	120.11
1	E	185	GLN	C-N-CA	5.20	125.93	120.11
1	G	114	ALA	CA-C-N	-5.17	113.47	119.47
1	G	114	ALA	C-N-CA	-5.17	113.47	119.47
1	C	27	VAL	N-CA-C	5.15	115.39	107.77
1	F	74	LEU	CA-C-N	-5.07	114.54	119.76
1	F	74	LEU	C-N-CA	-5.07	114.54	119.76
1	G	45	ALA	N-CA-C	-5.05	101.23	108.60
1	G	103	SER	CB-CA-C	-5.05	102.27	110.85
1	D	161	ARG	N-CA-C	-5.04	106.06	113.61
1	B	89	THR	CB-CA-C	5.03	119.13	110.79
1	D	89	THR	CB-CA-C	5.02	119.91	110.63

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	30	PRO	Peptide
1	D	145	MET	Peptide
1	G	205	ALA	Peptide

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	1541	0	1514	35	0
1	B	1574	0	1543	22	0
1	C	1582	0	1547	30	0
1	D	1495	0	1475	25	0
1	E	1475	0	1458	12	0
1	F	1519	0	1498	19	0
1	G	1527	0	1502	21	0
2	A	5	0	0	0	0
2	D	5	0	0	0	0
2	G	5	0	0	0	0
3	A	3	0	1	0	0
3	C	3	0	1	0	0
4	A	7	0	10	9	0
5	C	2	0	0	0	0
6	A	112	0	0	2	0
6	B	75	0	0	0	0
6	C	117	0	0	0	0
6	D	44	0	0	0	0
6	E	36	0	0	2	0
6	F	91	0	0	0	0
6	G	132	0	0	3	0
All	All	11350	0	10549	151	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 7.

All (151) 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:E:187:ARG:HH11	1:E:187:ARG:HG3	1.09	1.10
1:D:29:MET:HB2	1:D:30:PRO:HD3	1.47	0.93
1:G:132:GLU:OE2	1:F:92:ARG:NH1	2.02	0.93
1:E:187:ARG:HG3	1:E:187:ARG:NH1	1.86	0.88
1:A:52:ASP:HB3	1:A:54:ASN:H	1.42	0.85
1:A:128:THR:HB	4:A:403:PEG:H31	1.59	0.84
1:G:9:ILE:HG22	1:G:26:GLN:HB2	1.63	0.78
1:D:29:MET:CB	1:D:30:PRO:HD3	2.14	0.78
1:A:206:GLU:CB	1:A:207:ARG:HA	2.18	0.74
1:A:130:LEU:HG	4:A:403:PEG:H21	1.69	0.73
1:A:130:LEU:H	4:A:403:PEG:H12	1.54	0.72
1:E:166:ASN:ND2	1:F:115:PRO:HG2	2.05	0.70
1:A:204:ARG:HH21	1:A:207:ARG:NH2	1.89	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:51:MET:O	4:A:403:PEG:H32	1.92	0.70
1:D:30:PRO:HB2	1:D:31:GLY:HA3	1.74	0.68
1:D:29:MET:HB2	1:D:30:PRO:CD	2.22	0.68
1:C:29:MET:HE3	1:C:33:GLY:H	1.60	0.67
1:D:86:PRO:HA	1:D:89:THR:HG23	1.77	0.66
1:C:160:LEU:HD23	1:D:184:ALA:HB3	1.77	0.65
1:G:44:GLY:HA3	1:G:197:PRO:HG2	1.78	0.65
1:C:154:GLU:O	1:C:158:ARG:HG3	1.95	0.65
1:A:206:GLU:HB2	1:A:207:ARG:HA	1.78	0.65
1:F:26:GLN:HE22	1:F:36:THR:HG22	1.62	0.63
1:A:204:ARG:HH21	1:A:207:ARG:HH22	1.46	0.63
1:G:84:GLU:OE1	1:G:92:ARG:NH1	2.33	0.62
1:B:139:HIS:HA	1:B:140:HIS:HB2	1.81	0.61
1:D:204:ARG:HA	1:D:207:ARG:HB3	1.81	0.61
1:B:19:ILE:H	1:B:19:ILE:HD13	1.66	0.60
1:A:95:ARG:HH22	1:F:132:GLU:HB3	1.66	0.60
1:A:130:LEU:H	4:A:403:PEG:C1	2.15	0.60
1:B:11:SER:O	1:B:12:GLU:HB2	2.01	0.60
1:G:87:HIS:CE1	1:G:88:LEU:HD13	2.37	0.60
1:G:44:GLY:CA	1:G:197:PRO:HG2	2.33	0.59
1:B:133:VAL:HG23	1:B:133:VAL:O	2.03	0.59
1:A:28:ARG:O	1:A:33:GLY:O	2.21	0.59
1:B:76:ALA:C	1:B:93:GLU:HG2	2.28	0.59
1:G:119:ASP:O	1:G:120:GLU:C	2.42	0.58
1:F:29:MET:C	1:F:31:GLY:HA3	2.28	0.58
1:F:45:ALA:HB3	1:F:122:VAL:HG22	1.86	0.57
1:C:82:ALA:H	1:C:204:ARG:NH2	2.02	0.57
1:G:37:ARG:NH2	6:G:401:HOH:O	2.38	0.56
1:A:132:GLU:OE1	1:C:92:ARG:NH1	2.37	0.56
1:A:202:ALA:C	1:A:204:ARG:H	2.13	0.56
1:F:134:GLY:O	1:F:136:PRO:HD3	2.05	0.56
1:G:206:GLU:N	1:G:206:GLU:CD	2.63	0.56
1:B:14:LEU:HD21	1:B:24:ARG:HB2	1.87	0.55
1:A:52:ASP:HA	4:A:403:PEG:H22	1.89	0.55
1:C:102:ALA:CB	1:C:127:ALA:HB1	2.37	0.55
1:C:160:LEU:HD21	1:D:178:ALA:HB3	1.88	0.55
1:A:43:PHE:HZ	1:A:206:GLU:HG2	1.73	0.54
1:C:29:MET:CE	1:C:33:GLY:H	2.20	0.53
1:D:79:LEU:HD21	1:D:86:PRO:HB3	1.91	0.53
1:D:29:MET:CB	1:D:30:PRO:CD	2.86	0.53
1:G:70:ARG:O	1:G:71:LEU:HD23	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:44:GLY:HA3	1:B:197:PRO:HG2	1.90	0.52
1:F:143:ALA:HB1	1:F:144:ASP:HB2	1.90	0.52
1:C:177:HIS:O	1:C:181:THR:HB	2.09	0.52
1:B:135:ARG:HH12	1:B:139:HIS:CE1	2.28	0.52
1:D:30:PRO:CB	1:D:31:GLY:HA3	2.39	0.52
1:D:157:ARG:O	1:D:161:ARG:HB2	2.10	0.52
1:A:53:ASP:HA	4:A:403:PEG:H42	1.93	0.51
1:F:58:PRO:HD3	1:F:149:TRP:CZ3	2.45	0.51
1:C:115:PRO:HG2	1:D:166:ASN:ND2	2.25	0.51
1:C:134:GLY:O	1:C:135:ARG:HB2	2.10	0.51
1:D:9:ILE:CG1	1:D:26:GLN:HB3	2.41	0.51
1:C:160:LEU:HD21	1:D:178:ALA:CB	2.41	0.51
1:E:33:GLY:HA2	6:E:331:HOH:O	2.11	0.50
1:C:43:PHE:CE1	1:C:80:ASP:HA	2.47	0.50
1:D:94:LEU:HD12	1:D:98:VAL:CG2	2.42	0.50
1:G:20:PHE:HB2	1:G:41:GLU:O	2.12	0.49
1:C:62:GLN:HE22	1:C:142:GLN:HG2	1.76	0.49
1:D:61:TYR:O	1:D:145:MET:HB3	2.12	0.49
1:E:152:ILE:CD1	1:E:176:VAL:HG13	2.42	0.49
1:A:52:ASP:HB3	1:A:54:ASN:N	2.21	0.49
1:C:82:ALA:H	1:C:204:ARG:HH21	1.59	0.49
1:F:206:GLU:OE2	1:F:206:GLU:HA	2.13	0.49
1:A:196:ARG:HD2	6:A:567:HOH:O	2.13	0.48
1:F:29:MET:HB2	1:F:31:GLY:HA3	1.96	0.48
1:A:67:TYR:OH	1:B:112:ASP:HB3	2.14	0.48
1:B:84:GLU:OE1	1:B:92:ARG:NH2	2.37	0.47
1:B:133:VAL:O	1:B:133:VAL:CG2	2.61	0.47
4:A:403:PEG:H41	6:A:502:HOH:O	2.14	0.47
1:C:84:GLU:OE2	1:C:89:THR:CG2	2.62	0.47
1:G:73:GLU:HB3	6:G:411:HOH:O	2.14	0.47
1:B:14:LEU:HD23	1:B:22:LEU:CD1	2.45	0.47
1:A:44:GLY:HA3	1:A:197:PRO:HG2	1.97	0.47
1:A:201:ALA:O	1:A:204:ARG:HA	2.15	0.47
1:C:140:HIS:HB3	1:C:141:GLU:H	1.61	0.47
1:D:95:ARG:HD2	1:D:133:VAL:HG21	1.96	0.46
1:C:62:GLN:HE22	1:C:142:GLN:CG	2.27	0.46
1:E:152:ILE:HD11	1:E:176:VAL:HG13	1.98	0.46
1:F:122:VAL:HG11	1:F:168:ILE:HG12	1.97	0.46
1:G:70:ARG:HG3	1:G:70:ARG:HH11	1.81	0.46
1:E:45:ALA:HB3	1:E:122:VAL:HG22	1.97	0.46
1:F:79:LEU:HD23	1:F:89:THR:HG21	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:77:GLY:HA3	1:G:93:GLU:HG3	1.98	0.45
1:G:85:PRO:HG2	1:G:88:LEU:HD22	1.99	0.45
1:B:50:ALA:O	1:B:58:PRO:HD3	2.17	0.45
1:D:26:GLN:OE1	1:D:36:THR:HB	2.17	0.45
1:G:114:ALA:O	1:G:115:PRO:C	2.56	0.45
1:A:61:TYR:CZ	1:A:70:ARG:HB3	2.51	0.45
1:C:101:GLN:NE2	1:C:131:ARG:HH21	2.15	0.45
1:D:11:SER:HB3	1:D:25:ASP:OD1	2.15	0.45
1:B:84:GLU:OE1	1:B:89:THR:HB	2.16	0.45
1:C:54:ASN:OD1	1:C:54:ASN:C	2.58	0.45
1:C:113:THR:HB	1:D:113:THR:O	2.16	0.45
1:F:62:GLN:O	1:F:70:ARG:HA	2.17	0.45
1:G:23:ARG:HD3	1:G:41:GLU:OE2	2.17	0.44
1:G:30:PRO:HA	1:G:31:GLY:HA2	1.77	0.44
1:B:159:VAL:HG13	1:B:170:ILE:HG12	1.99	0.44
1:C:67:TYR:OH	1:D:112:ASP:HB3	2.18	0.44
1:A:95:ARG:NH2	1:F:132:GLU:OE2	2.51	0.44
1:A:52:ASP:CA	4:A:403:PEG:H22	2.47	0.44
1:E:187:ARG:NH1	1:E:187:ARG:CG	2.62	0.44
1:F:175:ALA:O	1:F:178:ALA:HB3	2.18	0.44
1:A:5:ASP:N	1:A:30:PRO:HB3	2.32	0.44
1:F:50:ALA:O	1:F:58:PRO:HD2	2.17	0.44
1:G:177:HIS:HE1	6:G:518:HOH:O	1.99	0.44
1:A:92:ARG:HG3	1:A:92:ARG:HH11	1.83	0.44
1:A:102:ALA:CB	1:A:127:ALA:HB1	2.48	0.44
1:E:6:PHE:N	6:E:303:HOH:O	2.51	0.43
1:C:85:PRO:HB2	1:C:88:LEU:HD22	2.00	0.43
1:E:49:VAL:HG11	1:E:176:VAL:HG11	1.99	0.43
1:B:44:GLY:CA	1:B:197:PRO:HG2	2.48	0.43
1:B:86:PRO:HA	1:B:89:THR:HG23	2.00	0.43
1:D:30:PRO:HB2	1:D:31:GLY:CA	2.46	0.43
1:A:204:ARG:NH2	1:A:207:ARG:NH2	2.61	0.43
1:D:123:ARG:HG2	1:D:125:TYR:CZ	2.54	0.43
1:A:67:TYR:CZ	1:B:112:ASP:HB3	2.54	0.42
1:E:51:MET:SD	1:E:55:GLY:HA2	2.59	0.42
1:F:59:MET:HE1	1:F:164:ILE:HD13	2.01	0.42
1:B:84:GLU:HG2	1:B:89:THR:HG22	2.01	0.42
1:B:14:LEU:CD2	1:B:24:ARG:HB2	2.49	0.42
1:A:44:GLY:CA	1:A:197:PRO:HG2	2.49	0.42
1:C:159:VAL:HG12	1:C:160:LEU:HD12	2.01	0.42
1:A:61:TYR:CE1	1:A:70:ARG:HB3	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:77:GLY:HA3	1:C:93:GLU:HG3	2.01	0.42
1:F:76:ALA:C	1:F:93:GLU:HG2	2.45	0.42
1:B:160:LEU:HD13	1:B:160:LEU:HA	1.88	0.41
1:A:146:THR:HG21	1:C:205:ALA:HB3	2.02	0.41
1:C:102:ALA:HB3	1:C:127:ALA:HB1	2.02	0.41
1:B:51:MET:HE3	1:B:55:GLY:HA2	2.03	0.41
1:D:179:VAL:HA	1:D:184:ALA:O	2.21	0.41
1:A:201:ALA:O	1:A:204:ARG:N	2.54	0.41
1:G:73:GLU:OE2	1:G:166:ASN:ND2	2.53	0.41
1:E:169:ALA:O	1:E:173:VAL:HG23	2.19	0.41
1:C:22:LEU:HD11	1:C:38:GLU:HG2	2.02	0.41
1:C:75:PRO:HA	1:C:97:GLU:OE1	2.21	0.41
1:G:121:SER:HB3	1:G:197:PRO:HD3	2.04	0.40
1:A:15:HIS:HB3	1:A:22:LEU:HB2	2.03	0.40
1:C:203:ARG:O	1:C:207:ARG:HB2	2.20	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	194/207 (94%)	179 (92%)	10 (5%)	5 (3%)	4	1
1	B	200/207 (97%)	180 (90%)	15 (8%)	5 (2%)	4	1
1	C	201/207 (97%)	188 (94%)	10 (5%)	3 (2%)	8	4
1	D	188/207 (91%)	171 (91%)	12 (6%)	5 (3%)	4	1
1	E	186/207 (90%)	171 (92%)	14 (8%)	1 (0%)	24	21
1	F	192/207 (93%)	176 (92%)	13 (7%)	3 (2%)	7	3
1	G	193/207 (93%)	181 (94%)	10 (5%)	2 (1%)	12	8
All	All	1354/1449 (93%)	1246 (92%)	84 (6%)	24 (2%)	6	3

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	12	GLU
1	C	135	ARG
1	C	140	HIS
1	D	29	MET
1	D	146	THR
1	E	205	ALA
1	A	52	ASP
1	A	206	GLU
1	B	134	GLY
1	F	205	ALA
1	A	31	GLY
1	D	30	PRO
1	D	32	GLY
1	D	53	ASP
1	F	30	PRO
1	A	28	ARG
1	A	29	MET
1	B	79	LEU
1	G	143	ALA
1	C	137	GLU
1	B	142	GLN
1	G	32	GLY
1	B	9	ILE
1	F	32	GLY

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	156/163 (96%)	147 (94%)	9 (6%)	18	15
1	B	159/163 (98%)	144 (91%)	15 (9%)	8	5
1	C	160/163 (98%)	142 (89%)	18 (11%)	5	3
1	D	152/163 (93%)	134 (88%)	18 (12%)	5	3
1	E	150/163 (92%)	135 (90%)	15 (10%)	7	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	F	154/163 (94%)	144 (94%)	10 (6%)	15	12
1	G	155/163 (95%)	143 (92%)	12 (8%)	12	8
All	All	1086/1141 (95%)	989 (91%)	97 (9%)	9	6

All (97) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	7	GLU
1	G	9	ILE
1	G	10	SER
1	G	14	LEU
1	G	35	VAL
1	G	88	LEU
1	G	101	GLN
1	G	131	ARG
1	G	142	GLN
1	G	160	LEU
1	G	165	VAL
1	G	206	GLU
1	A	14	LEU
1	A	22	LEU
1	A	28	ARG
1	A	52	ASP
1	A	92	ARG
1	A	111	LEU
1	A	135	ARG
1	A	204	ARG
1	A	206	GLU
1	B	14	LEU
1	B	19	ILE
1	B	22	LEU
1	B	26	GLN
1	B	27	VAL
1	B	36	THR
1	B	38	GLU
1	B	54	ASN
1	B	88	LEU
1	B	89	THR
1	B	135	ARG
1	B	137	GLU
1	B	145	MET

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Mol	Chain	Res	Type
1	B	204	ARG
1	B	207	ARG
1	C	12	GLU
1	C	14	LEU
1	C	36	THR
1	C	81	VAL
1	C	88	LEU
1	C	89	THR
1	C	101	GLN
1	C	132	GLU
1	C	135	ARG
1	C	137	GLU
1	C	140	HIS
1	C	142	GLN
1	C	144	ASP
1	C	145	MET
1	C	154	GLU
1	C	181	THR
1	C	206	GLU
1	C	207	ARG
1	D	5	ASP
1	D	7	GLU
1	D	9	ILE
1	D	14	LEU
1	D	26	GLN
1	D	34	ILE
1	D	36	THR
1	D	78	LEU
1	D	88	LEU
1	D	89	THR
1	D	95	ARG
1	D	96	GLU
1	D	128	THR
1	D	133	VAL
1	D	145	MET
1	D	146	THR
1	D	185	GLN
1	D	204	ARG
1	E	6	PHE
1	E	7	GLU
1	E	14	LEU
1	E	27	VAL

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Mol	Chain	Res	Type
1	E	43	PHE
1	E	79	LEU
1	E	88	LEU
1	E	92	ARG
1	E	132	GLU
1	E	146	THR
1	E	160	LEU
1	E	187	ARG
1	E	192	GLU
1	E	196	ARG
1	E	204	ARG
1	F	7	GLU
1	F	22	LEU
1	F	27	VAL
1	F	28	ARG
1	F	29	MET
1	F	35	VAL
1	F	81	VAL
1	F	89	THR
1	F	145	MET
1	F	204	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	G	142	GLN
1	A	56	ASN
1	B	26	GLN
1	B	54	ASN
1	C	62	GLN
1	C	101	GLN
1	C	140	HIS
1	D	101	GLN
1	D	185	GLN
1	E	106	GLN
1	E	177	HIS
1	F	26	GLN
1	F	142	GLN

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 oligosaccharides 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	FMT	A	401	-	2,2,2	0.84	0	1,1,1	0.80	0
2	SO4	G	301	-	4,4,4	0.59	0	6,6,6	0.41	0
3	FMT	C	401	-	2,2,2	0.63	0	1,1,1	0.82	0
2	SO4	D	301	-	4,4,4	0.52	0	6,6,6	0.22	0
2	SO4	A	402	-	4,4,4	0.51	0	6,6,6	0.32	0
4	PEG	A	403	-	6,6,6	0.77	0	5,5,5	1.29	1 (20%)

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
4	PEG	A	403	-	-	3/4/4/4	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	403	PEG	C3-O2-C2	2.36	123.58	113.26

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	403	PEG	O1-C1-C2-O2
4	A	403	PEG	O2-C3-C4-O4
4	A	403	PEG	C4-C3-O2-C2

There are no ring outliers.

1 monomer is involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	403	PEG	9	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	198/207 (95%)	0.37	15 (7%) 20 18	28, 46, 114, 162	0
1	B	202/207 (97%)	1.01	35 (17%) 4 3	40, 62, 149, 194	0
1	C	203/207 (98%)	0.21	19 (9%) 14 13	26, 46, 112, 183	0
1	D	192/207 (92%)	0.96	25 (13%) 7 6	44, 70, 119, 154	0
1	E	190/207 (91%)	1.28	35 (18%) 3 3	44, 78, 127, 153	0
1	F	196/207 (94%)	0.42	20 (10%) 12 11	33, 51, 134, 162	0
1	G	197/207 (95%)	0.17	17 (8%) 16 15	18, 38, 95, 145	0
All	All	1378/1449 (95%)	0.63	166 (12%) 9 8	18, 57, 124, 194	0

All (166) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	136	PRO	9.2
1	A	143	ALA	7.5
1	E	133	VAL	7.4
1	B	138	ALA	6.7
1	C	136	PRO	6.6
1	E	30	PRO	6.5
1	F	143	ALA	6.1
1	B	134	GLY	6.0
1	A	205	ALA	5.9
1	C	138	ALA	5.9
1	B	19	ILE	5.9
1	B	136	PRO	5.8
1	F	136	PRO	5.6
1	G	143	ALA	5.6
1	D	146	THR	5.5
1	C	143	ALA	5.4
1	D	145	MET	5.2

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Mol	Chain	Res	Type	RSRZ
1	B	30	PRO	5.1
1	E	35	VAL	5.1
1	F	32	GLY	4.9
1	B	143	ALA	4.7
1	B	6	PHE	4.6
1	D	30	PRO	4.6
1	F	33	GLY	4.5
1	B	35	VAL	4.5
1	D	9	ILE	4.5
1	B	29	MET	4.4
1	E	34	ILE	4.4
1	E	29	MET	4.4
1	F	34	ILE	4.3
1	A	29	MET	4.3
1	B	145	MET	4.3
1	F	6	PHE	4.3
1	B	34	ILE	4.2
1	E	145	MET	4.2
1	D	133	VAL	4.2
1	E	6	PHE	4.1
1	C	140	HIS	4.0
1	D	29	MET	3.9
1	G	9	ILE	3.9
1	A	30	PRO	3.8
1	A	135	ARG	3.8
1	C	205	ALA	3.7
1	G	144	ASP	3.7
1	F	134	GLY	3.7
1	F	135	ARG	3.7
1	C	145	MET	3.6
1	A	9	ILE	3.6
1	B	22	LEU	3.6
1	C	142	GLN	3.6
1	E	205	ALA	3.5
1	E	53	ASP	3.4
1	F	204	ARG	3.4
1	B	137	GLU	3.4
1	F	145	MET	3.4
1	G	135	ARG	3.3
1	F	206	GLU	3.3
1	D	31	GLY	3.3
1	G	34	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	31	GLY	3.3
1	E	31	GLY	3.2
1	F	35	VAL	3.2
1	D	19	ILE	3.2
1	B	144	ASP	3.2
1	A	142	GLN	3.2
1	B	139	HIS	3.1
1	G	33	GLY	3.1
1	D	6	PHE	3.1
1	C	204	ARG	3.1
1	B	207	ARG	3.1
1	A	145	MET	3.1
1	B	133	VAL	3.0
1	F	30	PRO	3.0
1	D	205	ALA	3.0
1	B	205	ALA	2.9
1	B	32	GLY	2.9
1	C	141	GLU	2.9
1	G	142	GLN	2.9
1	F	29	MET	2.9
1	E	95	ARG	2.9
1	C	144	ASP	2.9
1	A	206	GLU	2.8
1	D	35	VAL	2.8
1	F	9	ILE	2.8
1	B	14	LEU	2.8
1	B	36	THR	2.8
1	G	28	ARG	2.7
1	B	135	ARG	2.7
1	D	207	ARG	2.7
1	G	29	MET	2.7
1	B	31	GLY	2.7
1	G	145	MET	2.7
1	G	32	GLY	2.7
1	D	63	TYR	2.7
1	B	9	ILE	2.7
1	F	27	VAL	2.7
1	C	32	GLY	2.7
1	C	135	ARG	2.7
1	A	28	ARG	2.6
1	B	38	GLU	2.6
1	A	34	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	27	VAL	2.6
1	D	82	ALA	2.6
1	E	82	ALA	2.6
1	F	205	ALA	2.5
1	E	99	GLY	2.5
1	C	139	HIS	2.5
1	E	63	TYR	2.5
1	C	5	ASP	2.5
1	B	11	SER	2.5
1	F	36	THR	2.5
1	C	134	GLY	2.4
1	E	43	PHE	2.4
1	E	162	GLY	2.4
1	B	18	ALA	2.4
1	D	18	ALA	2.4
1	E	100	LEU	2.4
1	B	140	HIS	2.4
1	D	33	GLY	2.3
1	E	10	SER	2.3
1	B	146	THR	2.3
1	B	33	GLY	2.3
1	D	147	MET	2.3
1	D	96	GLU	2.3
1	E	98	VAL	2.3
1	E	146	THR	2.3
1	G	31	GLY	2.3
1	D	32	GLY	2.3
1	E	60	VAL	2.3
1	D	36	THR	2.3
1	E	18	ALA	2.3
1	E	201	ALA	2.3
1	F	31	GLY	2.3
1	F	8	THR	2.2
1	E	147	MET	2.2
1	G	30	PRO	2.2
1	G	206	GLU	2.2
1	E	149	TRP	2.2
1	A	6	PHE	2.2
1	D	81	VAL	2.2
1	D	102	ALA	2.2
1	C	207	ARG	2.1
1	E	16	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	31	GLY	2.1
1	E	17	GLY	2.1
1	E	189	LEU	2.1
1	A	63	TYR	2.1
1	B	28	ARG	2.1
1	C	19	ILE	2.1
1	E	19	ILE	2.1
1	B	39	VAL	2.1
1	E	130	LEU	2.1
1	B	142	GLN	2.1
1	C	30	PRO	2.1
1	G	134	GLY	2.1
1	E	32	GLY	2.1
1	E	164	ILE	2.1
1	B	141	GLU	2.0
1	D	22	LEU	2.0
1	D	78	LEU	2.0
1	E	131	ARG	2.0
1	E	206	GLU	2.0
1	A	22	LEU	2.0
1	E	101	GLN	2.0
1	G	5	ASP	2.0
1	D	85	PRO	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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	D	301	5/5	0.73	0.16	111,115,121,124	0
2	SO4	A	402	5/5	0.77	0.18	118,124,127,131	0
3	FMT	C	401	3/3	0.80	0.17	93,93,101,102	0
4	PEG	A	403	7/7	0.82	0.23	41,56,64,65	0
3	FMT	A	401	3/3	0.84	0.20	78,78,83,84	0
2	SO4	G	301	5/5	0.87	0.15	99,101,111,117	0
5	NA	C	403	1/1	0.91	0.15	62,62,62,62	0
5	NA	C	402	1/1	0.94	0.09	70,70,70,70	0

6.5 Other polymers [i](#)

There are no such residues in this entry.