



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 06:51 AM UTC

PDB ID : 2BGC / pdb_00002bgc
Title : PrfA-G145S, a constitutive active mutant of the Transcriptional Regulator In
L.monocytogenes
Authors : Eiting, M.; Hagelueken, G.; Schubert, W.-D.; Heinz, D.W.
Deposited on : 2004-12-20
Resolution : 2.30 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

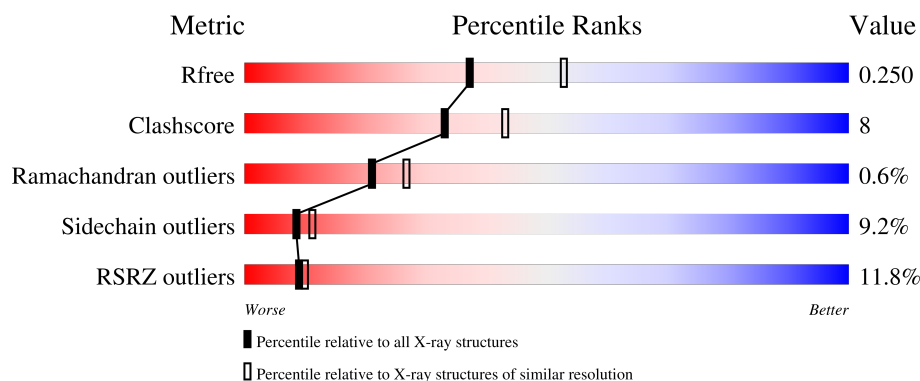
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	238	27% 78% 16% 5% .
1	B	238	21% 81% 17% .
1	D	238	% 69% 20% 5% . 5%
1	E	238	82% 15% .
1	F	238	29% 76% 20% ..

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Mol	Chain	Length	Quality of chain
1	G	238	13% 81% 16% ..
1	H	238	% 62% 26% 5% 6%
1	I	238	80% 16% ..

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15644 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.

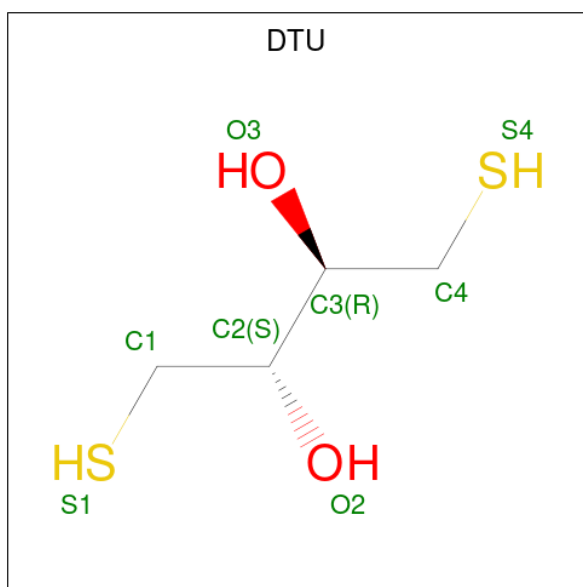
- Molecule 1 is a protein called PRFA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	235	Total	C	N	O	S	0	0	0
			1916	1251	299	358	8			
1	B	237	Total	C	N	O	S	0	0	0
			1932	1260	302	362	8			
1	D	227	Total	C	N	O	S	0	0	0
			1859	1216	289	346	8			
1	E	237	Total	C	N	O	S	0	0	0
			1930	1258	302	362	8			
1	F	236	Total	C	N	O	S	0	0	0
			1924	1255	301	360	8			
1	G	235	Total	C	N	O	S	0	0	0
			1916	1251	299	358	8			
1	H	224	Total	C	N	O	S	0	0	0
			1838	1204	285	341	8			
1	I	236	Total	C	N	O	S	0	0	0
			1924	1255	301	360	8			

There are 8 discrepancies between the modelled and reference sequences:

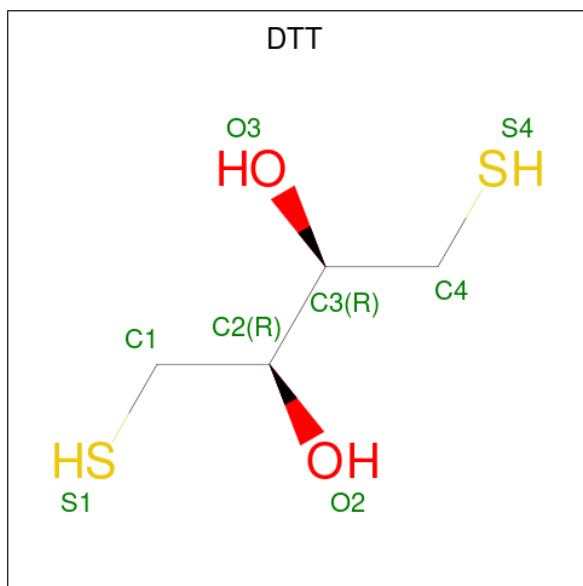
Chain	Residue	Modelled	Actual	Comment	Reference
A	145	SER	GLY	engineered mutation	UNP P22262
B	145	SER	GLY	engineered mutation	UNP P22262
D	145	SER	GLY	engineered mutation	UNP P22262
E	145	SER	GLY	engineered mutation	UNP P22262
F	145	SER	GLY	engineered mutation	UNP P22262
G	145	SER	GLY	engineered mutation	UNP P22262
H	145	SER	GLY	engineered mutation	UNP P22262
I	145	SER	GLY	engineered mutation	UNP P22262

- Molecule 2 is (2R,3S)-1,4-DIMERCAPTOBUTANE-2,3-DIOL (CCD ID: DTU) (formula: $C_4H_{10}O_2S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	S	0	0
			8	4	2	2		

- Molecule 3 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (CCD ID: DTT) (formula: $C_4H_{10}O_2S_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	F	1	Total	C	O	S	0	0
			8	4	2	2		

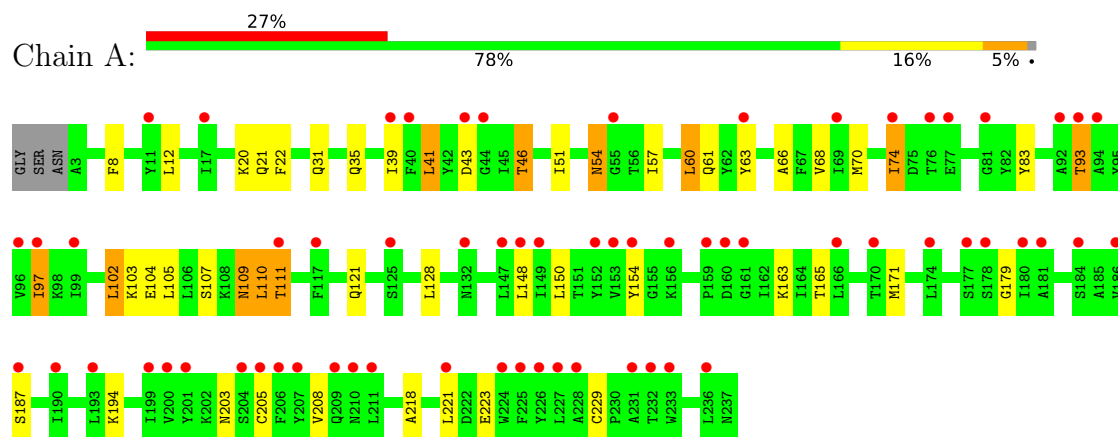
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	35	Total 35	O 35	0	0
4	B	69	Total 69	O 69	0	0
4	D	31	Total 31	O 31	0	0
4	E	64	Total 64	O 64	0	0
4	F	32	Total 32	O 32	0	0
4	G	77	Total 77	O 77	0	0
4	H	30	Total 30	O 30	0	0
4	I	51	Total 51	O 51	0	0

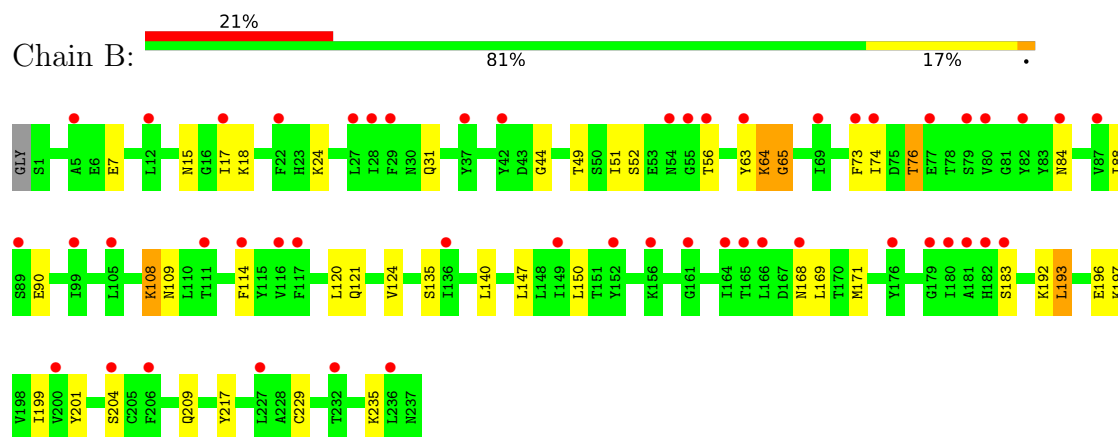
3 Residue-property plots [i](#)

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.

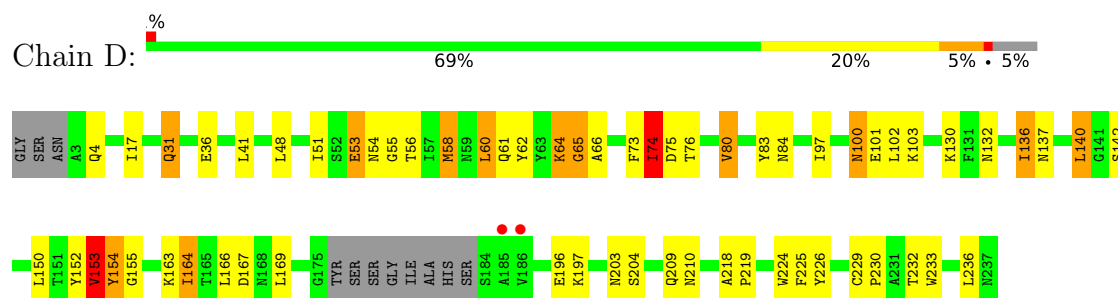
• Molecule 1: PRFA



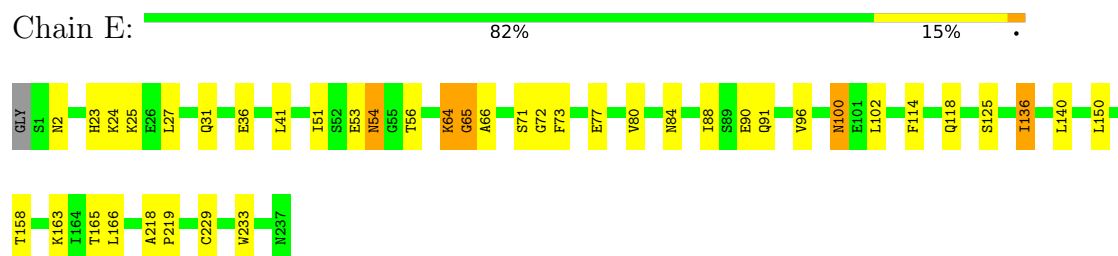
• Molecule 1: PRFA



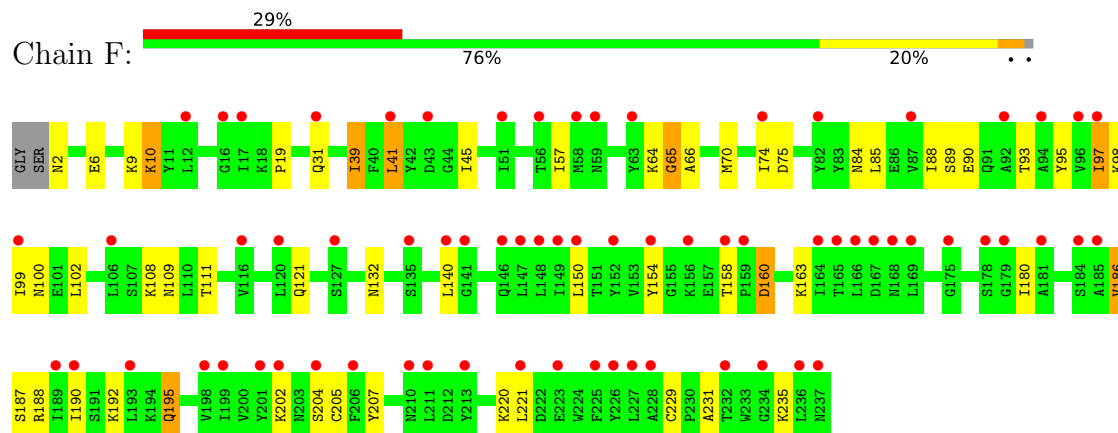
• Molecule 1: PRFA



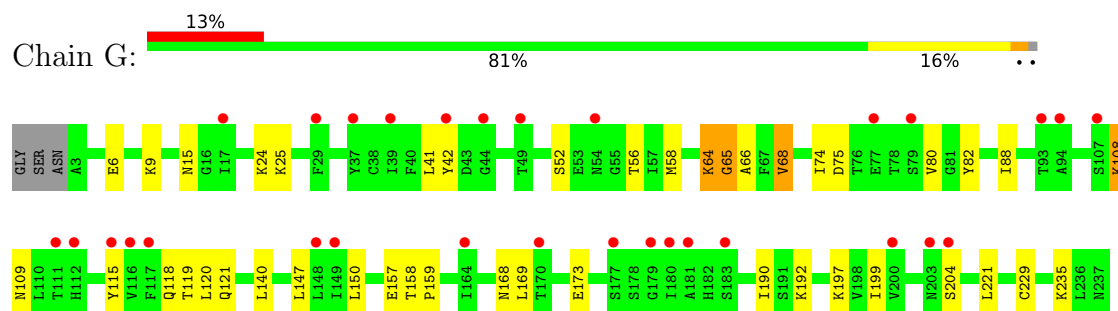
- Molecule 1: PRFA



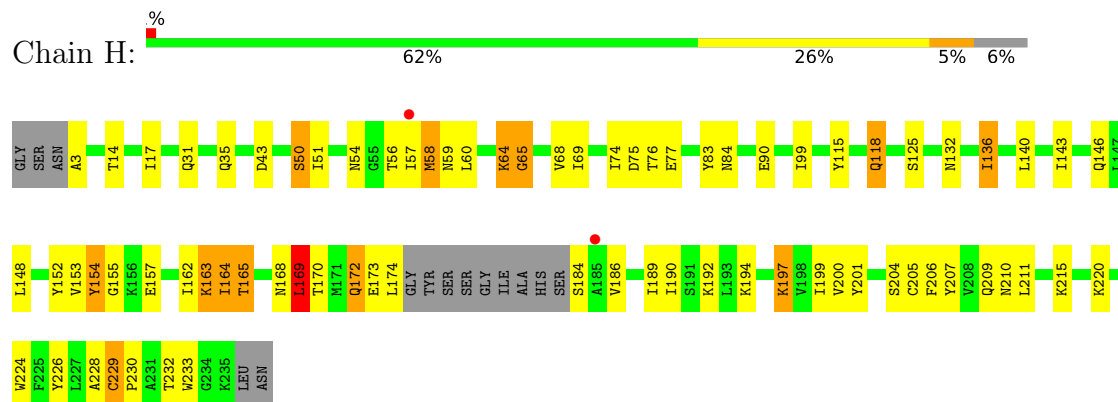
- Molecule 1: PRFA



- Molecule 1: PRFA



- Molecule 1: PRFA



- Molecule 1: PRFA

Chain I:

80%

16%

..



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.25Å 100.24Å 189.56Å 90.00° 90.33° 90.00°	Depositor
Resolution (Å)	182.57 – 2.30 182.57 – 2.30	Depositor EDS
% Data completeness (in resolution range)	95.6 (182.57-2.30) 93.8 (182.57-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.195 , 0.268 0.210 , 0.250	Depositor DCC
R_{free} test set	4648 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	40.6	Xtriage
Anisotropy	0.587	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 170.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.467 for -h,-k,l	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	15644	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 4.28% 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: PR3, DTT, DTU

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	0.99	0/1951	1.05	1/2632 (0.0%)
1	B	1.19	3/1965 (0.2%)	1.11	3/2651 (0.1%)
1	D	1.03	2/1891 (0.1%)	1.06	3/2549 (0.1%)
1	E	1.22	4/1965 (0.2%)	1.17	6/2651 (0.2%)
1	F	0.97	1/1959 (0.1%)	1.00	1/2643 (0.0%)
1	G	1.20	5/1951 (0.3%)	1.11	2/2632 (0.1%)
1	H	1.04	2/1870 (0.1%)	1.03	1/2522 (0.0%)
1	I	1.22	4/1959 (0.2%)	1.15	6/2643 (0.2%)
All	All	1.11	21/15511 (0.1%)	1.09	23/20923 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	2
1	I	0	1
All	All	0	8

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	68	VAL	CA-CB	8.62	1.66	1.54
1	E	65	GLY	N-CA	7.08	1.55	1.45
1	I	233	TRP	N-CA	6.44	1.54	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	65	GLY	CA-C	-6.38	1.44	1.52
1	G	65	GLY	N-CA	6.16	1.54	1.45
1	E	65	GLY	CA-C	-6.03	1.43	1.51
1	F	39	ILE	CA-CB	6.01	1.61	1.54
1	H	65	GLY	CA-C	-6.00	1.46	1.52
1	E	233	TRP	N-CA	5.77	1.53	1.46
1	B	44	GLY	C-O	-5.70	1.18	1.23
1	G	80	VAL	CA-CB	5.63	1.60	1.54
1	D	65	GLY	CA-C	-5.52	1.46	1.52
1	G	65	GLY	CA-C	-5.52	1.46	1.52
1	E	96	VAL	CA-CB	5.35	1.60	1.53
1	I	65	GLY	N-CA	5.34	1.54	1.45
1	G	221	LEU	C-O	-5.32	1.17	1.24
1	B	63	TYR	CA-C	5.31	1.58	1.52
1	B	124	VAL	N-CA	5.25	1.52	1.46
1	D	74	ILE	CA-CB	5.21	1.60	1.54
1	I	149	ILE	C-O	-5.01	1.18	1.24
1	H	69	ILE	CA-CB	5.00	1.60	1.54

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	65	GLY	N-CA-C	-10.39	92.69	112.02
1	E	88	ILE	CB-CA-C	-9.69	102.00	111.30
1	E	65	GLY	N-CA-C	-9.52	90.62	113.18
1	G	65	GLY	N-CA-C	-9.24	96.14	112.22
1	H	65	GLY	N-CA-C	-8.94	96.66	112.22
1	B	65	GLY	N-CA-C	-8.36	96.47	112.02
1	I	88	ILE	CB-CA-C	-7.14	104.44	111.30
1	A	74	ILE	CB-CA-C	-6.75	103.23	111.88
1	D	65	GLY	N-CA-C	-6.62	100.71	112.22
1	B	88	ILE	CB-CA-C	-6.33	105.22	111.30
1	F	65	GLY	N-CA-C	-6.05	101.69	112.22
1	E	158	THR	CA-C-N	-5.81	114.12	119.82
1	E	158	THR	C-N-CA	-5.81	114.12	119.82
1	D	153	VAL	N-CA-C	-5.70	99.33	107.77
1	D	31	GLN	N-CA-C	5.38	119.46	113.01
1	G	88	ILE	CB-CA-C	-5.25	106.26	111.30
1	I	87	VAL	CA-C-N	5.22	127.73	122.66
1	I	87	VAL	C-N-CA	5.22	127.73	122.66
1	I	82	TYR	N-CA-C	5.16	117.12	107.99
1	B	147	LEU	N-CA-C	5.14	116.88	111.28

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	136	ILE	N-CA-C	5.11	115.88	110.72
1	I	65	GLY	CA-C-O	-5.11	115.93	122.01
1	E	233	TRP	N-CA-C	5.04	116.86	111.36

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	64	LYS	Peptide
1	D	64	LYS	Peptide
1	E	64	LYS	Peptide
1	F	64	LYS	Peptide
1	G	64	LYS	Peptide
1	H	229	PR3	Mainchain
1	H	64	LYS	Peptide
1	I	64	LYS	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	1916	0	1914	32	0
1	B	1932	0	1936	24	0
1	D	1859	0	1864	40	0
1	E	1930	0	1928	23	0
1	F	1924	0	1920	39	0
1	G	1916	0	1915	17	0
1	H	1838	0	1843	60	0
1	I	1924	0	1920	35	0
2	A	8	0	10	0	0
3	F	8	0	10	1	0
4	A	35	0	0	1	0
4	B	69	0	0	1	0
4	D	31	0	0	1	0
4	E	64	0	0	2	0
4	F	32	0	0	3	0
4	G	77	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	30	0	0	1	0
4	I	51	0	0	4	0
All	All	15644	0	15260	238	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 8.

All (238) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:31:GLN:HE21	1:B:84:ASN:HD21	1.15	0.94
1:H:74:ILE:H	1:I:121:GLN:HE22	1.21	0.85
1:D:153:VAL:O	1:D:154:TYR:CD2	2.34	0.81
1:F:75:ASP:HB3	1:G:118:GLN:NE2	1.97	0.79
1:H:190:ILE:O	1:H:194:LYS:NZ	2.15	0.79
1:A:110:LEU:HD12	1:A:110:LEU:C	2.09	0.78
1:B:31:GLN:HE22	1:B:51:ILE:H	1.33	0.77
1:F:109:ASN:OD1	1:F:111:THR:HG22	1.85	0.76
1:I:172:GLN:NE2	1:I:176:TYR:CE1	2.53	0.76
1:B:31:GLN:HE21	1:B:84:ASN:ND2	1.84	0.76
1:A:109:ASN:HD21	1:A:111:THR:HG23	1.50	0.75
1:D:153:VAL:O	1:D:154:TYR:CG	2.39	0.75
1:H:75:ASP:HB3	1:I:118:GLN:NE2	2.02	0.75
1:I:31:GLN:HE21	1:I:84:ASN:HD21	1.33	0.74
1:A:31:GLN:HE22	1:A:51:ILE:HG22	1.52	0.73
1:H:75:ASP:HB3	1:I:118:GLN:HE22	1.51	0.73
1:H:210:ASN:HD22	1:H:210:ASN:C	1.97	0.72
1:F:186:VAL:HG12	1:F:186:VAL:O	1.89	0.71
1:F:31:GLN:NE2	1:F:84:ASN:HD21	1.89	0.70
1:F:2:ASN:N	4:F:2001:HOH:O	2.25	0.70
1:H:125:SER:HB3	1:I:80:VAL:HG22	1.72	0.70
1:A:31:GLN:NE2	1:A:51:ILE:HG22	2.07	0.70
1:F:74:ILE:H	1:G:121:GLN:HE22	1.39	0.70
1:F:121:GLN:HE22	1:G:74:ILE:H	1.40	0.70
1:B:15:ASN:HD21	1:B:108:LYS:NZ	1.89	0.69
1:A:46:THR:HG22	1:A:63:TYR:HB2	1.74	0.69
1:G:115:TYR:O	1:G:119:THR:HG23	1.93	0.69
1:H:132:ASN:HD22	1:I:60:LEU:HD21	1.57	0.69
1:F:31:GLN:HE21	1:F:84:ASN:HD21	1.40	0.69
1:I:168:ASN:OD1	1:I:169:LEU:N	2.28	0.67
1:F:75:ASP:HB3	1:G:118:GLN:HE21	1.60	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:223:GLU:OE1	4:A:2034:HOH:O	2.14	0.65
1:B:192:LYS:HE3	1:B:196:GLU:OE1	1.96	0.65
1:D:76:THR:H	1:E:118:GLN:HE22	1.44	0.65
1:F:9:LYS:HE2	1:F:10:LYS:HZ2	1.61	0.65
1:E:72:GLY:HA2	1:E:80:VAL:HG13	1.79	0.65
1:B:15:ASN:HD21	1:B:108:LYS:HZ1	1.42	0.65
1:A:103:LYS:NZ	1:B:114:PHE:CD2	2.65	0.64
1:I:100:ASN:HD22	1:I:100:ASN:H	1.43	0.64
1:B:73:PHE:HB2	1:B:76:THR:HG22	1.80	0.63
1:H:76:THR:H	1:I:118:GLN:HE22	1.47	0.63
1:G:6:GLU:OE2	1:G:42:TYR:OH	2.15	0.62
1:A:121:GLN:HE22	1:B:74:ILE:H	1.46	0.62
1:F:31:GLN:HE21	1:F:84:ASN:ND2	1.97	0.62
1:D:80:VAL:HG22	1:E:125:SER:HB3	1.80	0.62
1:I:23:HIS:ND1	1:I:91:GLN:NE2	2.49	0.61
1:A:109:ASN:C	1:A:109:ASN:HD22	2.08	0.61
1:B:31:GLN:NE2	1:B:84:ASN:HD21	1.93	0.60
1:B:168:ASN:N	4:B:2052:HOH:O	2.24	0.60
1:H:172:GLN:HE21	1:H:172:GLN:C	2.09	0.60
1:I:100:ASN:H	1:I:100:ASN:ND2	1.99	0.60
1:D:100:ASN:HD22	1:D:101:GLU:N	2.00	0.60
1:E:73:PHE:O	1:E:77:GLU:HA	2.00	0.60
1:A:109:ASN:ND2	1:A:111:THR:HG23	2.16	0.60
1:F:6:GLU:HB3	1:F:10:LYS:HZ3	1.66	0.60
1:H:75:ASP:CB	1:I:118:GLN:NE2	2.65	0.60
1:H:50:SER:HB2	1:H:60:LEU:HD11	1.85	0.59
1:D:31:GLN:HE21	1:D:84:ASN:HD21	1.50	0.59
1:H:31:GLN:HE21	1:H:84:ASN:HD21	1.50	0.59
1:F:220:LYS:NZ	1:G:82:TYR:O	2.35	0.59
1:I:74:ILE:HD11	1:I:103:LYS:HB3	1.85	0.59
1:F:41:LEU:O	1:F:66:ALA:HA	2.03	0.58
1:D:153:VAL:C	1:D:154:TYR:CG	2.82	0.58
1:A:163:LYS:HE2	1:A:205:CYS:SG	2.43	0.58
1:H:51:ILE:HG22	1:H:57:ILE:HG12	1.84	0.58
1:H:3:ALA:HB1	1:H:115:TYR:HD1	1.67	0.58
1:E:31:GLN:HE21	1:E:84:ASN:HD21	1.53	0.57
1:D:210:ASN:C	1:D:210:ASN:HD22	2.12	0.57
1:E:31:GLN:HE22	1:E:51:ILE:H	1.50	0.57
1:H:64:LYS:HD3	1:H:153:VAL:HG12	1.86	0.56
1:H:154:TYR:CD1	1:H:154:TYR:N	2.71	0.56
1:F:202:LYS:HB3	1:F:207:TYR:CE1	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:195:GLN:HA	1:F:195:GLN:HE21	1.70	0.56
1:I:132:ASN:O	1:I:136:ILE:HD13	2.05	0.56
1:D:41:LEU:O	1:D:66:ALA:HA	2.05	0.55
1:B:64:LYS:HG2	1:B:65:GLY:N	2.22	0.55
1:G:52:SER:OG	1:G:56:THR:HB	2.07	0.55
1:H:74:ILE:H	1:I:121:GLN:NE2	2.00	0.55
1:H:164:ILE:CD1	1:H:169:LEU:HB3	2.37	0.55
1:H:190:ILE:HD12	1:H:194:LYS:NZ	2.22	0.55
1:I:23:HIS:CE1	1:I:91:GLN:HE22	2.25	0.55
1:D:100:ASN:HD22	1:D:100:ASN:C	2.14	0.54
1:F:10:LYS:HD3	1:F:10:LYS:N	2.22	0.54
1:F:160:ASP:OD2	1:F:202:LYS:NZ	2.41	0.54
1:I:31:GLN:HE22	1:I:51:ILE:H	1.56	0.53
1:G:64:LYS:HG3	1:G:65:GLY:N	2.23	0.53
1:H:51:ILE:CG2	1:H:57:ILE:HG12	2.38	0.53
1:I:36:GLU:HB3	1:I:72:GLY:HA3	1.90	0.53
1:A:110:LEU:C	1:A:110:LEU:CD1	2.79	0.53
1:H:172:GLN:O	1:H:172:GLN:NE2	2.40	0.53
1:H:210:ASN:C	1:H:210:ASN:ND2	2.67	0.52
1:E:163:LYS:HE3	1:E:165:THR:HG22	1.91	0.52
1:G:168:ASN:HD22	1:G:173:GLU:HG3	1.74	0.52
1:I:229:PR3:HB2	1:I:232:THR:HB	1.92	0.51
1:H:143:ILE:HG22	1:H:174:LEU:HD21	1.93	0.51
1:D:53:GLU:C	1:D:55:GLY:H	2.19	0.51
1:E:23:HIS:ND1	1:E:91:GLN:NE2	2.56	0.51
1:H:197:LYS:NZ	1:H:197:LYS:HA	2.25	0.51
1:A:43:ASP:HB3	1:A:93:THR:HG23	1.93	0.51
1:A:74:ILE:H	1:B:121:GLN:HE22	1.59	0.51
1:E:72:GLY:CA	1:E:80:VAL:HG13	2.41	0.51
1:H:163:LYS:NZ	1:H:165:THR:OG1	2.35	0.51
1:A:179:GLY:HA3	1:B:135:SER:O	2.11	0.50
1:A:171:MET:HE1	1:A:187:SER:HA	1.94	0.50
1:B:64:LYS:CG	1:B:65:GLY:N	2.74	0.50
1:F:109:ASN:OD1	1:F:111:THR:CG2	2.58	0.50
1:H:75:ASP:CB	1:I:118:GLN:HE22	2.22	0.50
1:D:150:LEU:O	1:D:154:TYR:HB2	2.12	0.50
1:F:19:PRO:HB3	1:F:95:TYR:CZ	2.47	0.49
1:D:74:ILE:HD11	1:D:102:LEU:HD23	1.95	0.49
1:I:74:ILE:HG23	4:I:2018:HOH:O	2.13	0.49
1:D:150:LEU:HD13	1:D:169:LEU:HD21	1.94	0.49
1:F:45:ILE:HD12	1:F:154:TYR:HE1	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:140:LEU:C	1:H:140:LEU:HD13	2.37	0.49
1:A:97:ILE:CD1	1:A:105:LEU:HD12	2.43	0.49
1:F:187:SER:HA	4:F:2029:HOH:O	2.12	0.49
1:A:154:TYR:O	1:A:165:THR:OG1	2.27	0.49
1:H:60:LEU:HD13	1:H:83:TYR:CE1	2.48	0.49
1:H:31:GLN:NE2	1:H:51:ILE:HG12	2.28	0.48
1:I:103:LYS:NZ	4:I:2021:HOH:O	2.44	0.48
1:D:224:TRP:C	1:D:226:TYR:H	2.21	0.48
1:H:74:ILE:N	1:I:121:GLN:HE22	2.00	0.48
1:F:132:ASN:HD22	1:G:58:MET:HG2	1.79	0.48
1:D:164:ILE:HG22	1:D:164:ILE:O	2.12	0.48
1:H:211:LEU:O	1:H:215:LYS:HG3	2.14	0.48
1:B:201:TYR:CZ	1:B:204:SER:HA	2.49	0.47
1:H:3:ALA:HB3	1:H:118:GLN:HE22	1.79	0.47
1:A:171:MET:CE	1:A:187:SER:HA	2.45	0.47
1:H:197:LYS:HA	1:H:197:LYS:HZ2	1.79	0.47
1:F:65:GLY:HA2	4:F:2007:HOH:O	2.14	0.47
1:F:9:LYS:HE2	1:F:10:LYS:NZ	2.28	0.47
1:D:64:LYS:HG2	1:D:65:GLY:N	2.29	0.47
1:D:140:LEU:HD23	1:D:140:LEU:HA	1.82	0.47
1:B:52:SER:OG	1:B:56:THR:HB	2.15	0.47
1:H:168:ASN:O	1:H:169:LEU:C	2.57	0.47
1:H:211:LEU:CD2	1:H:215:LYS:HD3	2.45	0.47
1:E:24:LYS:O	1:E:25:LYS:HB2	2.15	0.46
1:D:100:ASN:C	1:D:100:ASN:ND2	2.72	0.46
1:E:64:LYS:HG2	1:E:65:GLY:N	2.30	0.46
1:H:184:SER:N	4:H:2030:HOH:O	2.48	0.46
1:H:155:GLY:HA2	1:H:163:LYS:HZ2	1.81	0.46
1:A:46:THR:CG2	1:A:63:TYR:HB2	2.45	0.45
1:B:193:LEU:HB3	1:B:199:ILE:HG12	1.98	0.45
1:A:21:GLN:HE22	1:A:93:THR:HG22	1.81	0.45
1:D:73:PHE:HB3	1:E:118:GLN:HE21	1.81	0.45
1:H:31:GLN:NE2	1:H:51:ILE:CG1	2.79	0.45
1:D:61:GLN:HG2	1:D:62:TYR:O	2.16	0.45
1:F:231:ALA:O	1:F:235:LYS:HG2	2.17	0.45
1:A:8:PHE:O	1:A:12:LEU:HG	2.17	0.45
1:A:54:ASN:C	1:A:54:ASN:ND2	2.75	0.45
1:B:24:LYS:NZ	1:B:90:GLU:CD	2.75	0.45
1:H:211:LEU:HD23	1:H:215:LYS:HD3	1.98	0.45
1:H:153:VAL:HG12	1:H:153:VAL:O	2.17	0.45
1:F:188:ARG:O	1:F:192:LYS:HB2	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:F:1238:DTT:O3	3:F:1238:DTT:S1	2.75	0.44
1:A:41:LEU:O	1:A:66:ALA:HA	2.17	0.44
1:E:36:GLU:HG2	1:E:72:GLY:HA3	2.00	0.44
1:E:65:GLY:HA2	4:E:2013:HOH:O	2.17	0.44
1:H:226:TYR:HB2	1:H:233:TRP:CD1	2.52	0.44
1:I:103:LYS:CE	4:I:2021:HOH:O	2.65	0.44
1:D:136:ILE:HG23	1:D:137:ASN:ND2	2.33	0.44
1:I:41:LEU:O	1:I:66:ALA:HA	2.17	0.44
1:F:180:ILE:HG21	1:F:186:VAL:HG23	2.00	0.44
1:E:54:ASN:ND2	1:E:56:THR:OG1	2.47	0.44
1:H:75:ASP:H	1:I:118:GLN:NE2	2.16	0.44
1:H:75:ASP:H	1:I:118:GLN:HE21	1.65	0.43
1:H:136:ILE:CD1	1:I:58:MET:SD	3.06	0.43
1:A:148:LEU:HD13	1:A:218:ALA:HB3	1.99	0.43
1:D:130:LYS:NZ	4:D:2023:HOH:O	2.51	0.43
1:D:226:TYR:CD1	1:D:233:TRP:CE3	3.06	0.43
1:D:226:TYR:HB2	1:D:233:TRP:CG	2.53	0.43
1:E:36:GLU:HB3	1:E:72:GLY:HA3	2.00	0.43
1:H:31:GLN:HE22	1:H:51:ILE:CG1	2.31	0.43
1:D:17:ILE:HD13	1:D:97:ILE:HG12	1.99	0.43
1:D:153:VAL:O	1:D:154:TYR:CB	2.66	0.43
1:A:21:GLN:HE22	1:A:93:THR:CG2	2.31	0.43
1:D:164:ILE:O	1:D:164:ILE:CG2	2.66	0.43
1:G:24:LYS:O	1:G:25:LYS:HB2	2.18	0.43
1:D:31:GLN:HE22	1:D:51:ILE:H	1.66	0.43
1:B:31:GLN:HE22	1:B:51:ILE:N	2.10	0.43
1:E:41:LEU:O	1:E:66:ALA:HA	2.18	0.43
1:A:109:ASN:C	1:A:109:ASN:ND2	2.75	0.43
1:H:58:MET:HE2	1:I:132:ASN:HD22	1.84	0.43
1:F:163:LYS:HE3	1:F:205:CYS:SG	2.59	0.42
1:H:77:GLU:HG2	1:H:99:ILE:HG23	2.00	0.42
1:H:64:LYS:CG	1:H:65:GLY:N	2.83	0.42
1:D:61:GLN:HG2	1:D:62:TYR:N	2.34	0.42
1:D:230:PRO:O	1:D:233:TRP:HB3	2.19	0.42
1:H:136:ILE:HD11	1:I:58:MET:HB2	2.02	0.42
1:I:31:GLN:HE21	1:I:84:ASN:ND2	2.09	0.42
1:D:58:MET:HG3	1:E:136:ILE:HD11	2.00	0.42
1:E:100:ASN:H	1:E:100:ASN:ND2	2.17	0.42
1:I:74:ILE:CD1	1:I:103:LYS:HB3	2.48	0.42
1:A:70:MET:HE2	1:A:70:MET:HB3	1.78	0.42
1:H:201:TYR:HE2	1:H:206:PHE:CE1	2.38	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:154:TYR:CG	1:D:166:LEU:HD13	2.54	0.42
1:F:6:GLU:CB	1:F:10:LYS:HZ3	2.31	0.42
1:H:155:GLY:CA	1:H:163:LYS:O	2.67	0.42
1:D:103:LYS:HG3	1:E:114:PHE:CZ	2.55	0.42
1:E:31:GLN:HE21	1:E:84:ASN:ND2	2.18	0.42
1:F:109:ASN:OD1	1:F:109:ASN:C	2.62	0.42
1:B:49:THR:OG1	1:B:84:ASN:HB2	2.20	0.41
1:B:109:ASN:C	1:B:109:ASN:HD22	2.28	0.41
1:F:45:ILE:HD12	1:F:154:TYR:CE1	2.55	0.41
1:F:202:LYS:O	1:F:207:TYR:HE1	2.03	0.41
1:H:163:LYS:HB3	1:H:207:TYR:CE1	2.55	0.41
1:I:195:GLN:NE2	4:I:2040:HOH:O	2.51	0.41
1:D:80:VAL:HG21	4:E:2029:HOH:O	2.21	0.41
1:B:140:LEU:HD12	1:B:217:TYR:CE1	2.55	0.41
1:G:190:ILE:HG23	1:G:199:ILE:HD11	2.02	0.41
1:G:158:THR:HB	1:G:159:PRO:HD2	2.03	0.41
1:A:97:ILE:HD11	1:A:102:LEU:HA	2.02	0.41
1:F:45:ILE:CG1	1:F:89:SER:HB3	2.51	0.41
1:F:45:ILE:HG12	1:F:89:SER:HB3	2.02	0.41
1:F:97:ILE:HG13	1:F:98:LYS:N	2.35	0.41
1:G:15:ASN:HD21	1:G:108:LYS:NZ	2.18	0.41
1:H:157:GLU:OE2	1:H:162:ILE:CD1	2.69	0.41
1:H:224:TRP:O	1:H:228:ALA:HB3	2.21	0.41
1:D:60:LEU:HD13	1:D:83:TYR:CE1	2.56	0.41
1:D:73:PHE:HB3	1:E:118:GLN:NE2	2.36	0.41
1:D:218:ALA:N	1:D:219:PRO:CD	2.84	0.41
1:F:186:VAL:O	1:F:190:ILE:HD12	2.21	0.41
1:H:14:THR:O	1:H:14:THR:HG22	2.21	0.41
1:H:194:LYS:HZ1	1:H:199:ILE:HD11	1.85	0.41
1:D:132:ASN:O	1:D:136:ILE:HB	2.21	0.41
1:A:60:LEU:HD13	1:A:83:TYR:CD2	2.56	0.40
1:F:132:ASN:ND2	1:G:58:MET:HG2	2.36	0.40
1:F:6:GLU:CA	1:F:10:LYS:HZ3	2.35	0.40
1:A:20:LYS:HG3	1:A:22:PHE:CE1	2.57	0.40
1:A:103:LYS:NZ	1:B:114:PHE:CE2	2.86	0.40
1:G:41:LEU:O	1:G:66:ALA:HA	2.20	0.40
1:H:31:GLN:HE22	1:H:51:ILE:HG12	1.87	0.40
1:H:64:LYS:HD3	1:H:153:VAL:CG1	2.52	0.40
1:H:226:TYR:O	1:H:230:PRO:HD3	2.21	0.40
1:I:229:PR3:O	1:I:230:PRO:C	2.63	0.40
1:D:155:GLY:HA2	1:D:163:LYS:O	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:218:ALA:N	1:E:219:PRO:CD	2.84	0.40
1:H:201:TYR:CE2	1:H:206:PHE:CE1	3.10	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	232/238 (98%)	220 (95%)	12 (5%)	0	100	100
1	B	234/238 (98%)	227 (97%)	6 (3%)	1 (0%)	30	38
1	D	222/238 (93%)	200 (90%)	16 (7%)	6 (3%)	4	3
1	E	234/238 (98%)	228 (97%)	6 (3%)	0	100	100
1	F	233/238 (98%)	226 (97%)	6 (3%)	1 (0%)	30	38
1	G	232/238 (98%)	226 (97%)	5 (2%)	1 (0%)	30	38
1	H	219/238 (92%)	204 (93%)	13 (6%)	2 (1%)	14	17
1	I	233/238 (98%)	225 (97%)	8 (3%)	0	100	100
All	All	1839/1904 (97%)	1756 (96%)	72 (4%)	11 (1%)	21	27

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	154	TYR
1	D	167	ASP
1	H	169	LEU
1	B	169	LEU
1	G	169	LEU
1	H	186	VAL
1	D	54	ASN
1	D	203	ASN

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Mol	Chain	Res	Type
1	D	204	SER
1	D	225	PHE
1	F	186	VAL

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	210/212 (99%)	187 (89%)	23 (11%)	6	7
1	B	212/212 (100%)	199 (94%)	13 (6%)	17	24
1	D	204/212 (96%)	182 (89%)	22 (11%)	6	7
1	E	212/212 (100%)	201 (95%)	11 (5%)	21	31
1	F	211/212 (100%)	190 (90%)	21 (10%)	7	9
1	G	210/212 (99%)	196 (93%)	14 (7%)	15	21
1	H	202/212 (95%)	170 (84%)	32 (16%)	2	2
1	I	211/212 (100%)	193 (92%)	18 (8%)	10	13
All	All	1672/1696 (99%)	1518 (91%)	154 (9%)	8	11

All (154) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	35	GLN
1	A	39	ILE
1	A	41	LEU
1	A	46	THR
1	A	54	ASN
1	A	57	ILE
1	A	60	LEU
1	A	61	GLN
1	A	68	VAL
1	A	93	THR
1	A	97	ILE
1	A	102	LEU

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Mol	Chain	Res	Type
1	A	104	GLU
1	A	107	SER
1	A	109	ASN
1	A	110	LEU
1	A	111	THR
1	A	128	LEU
1	A	150	LEU
1	A	194	LYS
1	A	203	ASN
1	A	208	VAL
1	A	221	LEU
1	B	7	GLU
1	B	17	ILE
1	B	18	LYS
1	B	76	THR
1	B	108	LYS
1	B	120	LEU
1	B	150	LEU
1	B	171	MET
1	B	183	SER
1	B	193	LEU
1	B	197	LYS
1	B	209	GLN
1	B	235	LYS
1	D	4	GLN
1	D	36	GLU
1	D	48	LEU
1	D	53	GLU
1	D	56	THR
1	D	58	MET
1	D	60	LEU
1	D	74	ILE
1	D	75	ASP
1	D	80	VAL
1	D	100	ASN
1	D	136	ILE
1	D	140	LEU
1	D	142	SER
1	D	152	TYR
1	D	153	VAL
1	D	164	ILE
1	D	196	GLU

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Mol	Chain	Res	Type
1	D	197	LYS
1	D	209	GLN
1	D	232	THR
1	D	236	LEU
1	E	2	ASN
1	E	27	LEU
1	E	53	GLU
1	E	54	ASN
1	E	71	SER
1	E	90	GLU
1	E	100	ASN
1	E	102	LEU
1	E	140	LEU
1	E	150	LEU
1	E	166	LEU
1	F	10	LYS
1	F	39	ILE
1	F	41	LEU
1	F	57	ILE
1	F	70	MET
1	F	85	LEU
1	F	88	ILE
1	F	90	GLU
1	F	93	THR
1	F	97	ILE
1	F	99	ILE
1	F	100	ASN
1	F	102	LEU
1	F	108	LYS
1	F	140	LEU
1	F	150	LEU
1	F	158	THR
1	F	160	ASP
1	F	195	GLN
1	F	204	SER
1	F	221	LEU
1	G	9	LYS
1	G	68	VAL
1	G	75	ASP
1	G	108	LYS
1	G	109	ASN
1	G	120	LEU

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Mol	Chain	Res	Type
1	G	140	LEU
1	G	147	LEU
1	G	150	LEU
1	G	157	GLU
1	G	192	LYS
1	G	197	LYS
1	G	204	SER
1	G	235	LYS
1	H	17	ILE
1	H	35	GLN
1	H	43	ASP
1	H	50	SER
1	H	54	ASN
1	H	56	THR
1	H	58	MET
1	H	59	ASN
1	H	68	VAL
1	H	90	GLU
1	H	118	GLN
1	H	136	ILE
1	H	146	GLN
1	H	148	LEU
1	H	152	TYR
1	H	154	TYR
1	H	163	LYS
1	H	164	ILE
1	H	165	THR
1	H	169	LEU
1	H	170	THR
1	H	172	GLN
1	H	173	GLU
1	H	189	ILE
1	H	192	LYS
1	H	197	LYS
1	H	200	VAL
1	H	204	SER
1	H	205	CYS
1	H	209	GLN
1	H	220	LYS
1	H	232	THR
1	I	7	GLU
1	I	12	LEU

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Mol	Chain	Res	Type
1	I	14	THR
1	I	36	GLU
1	I	64	LYS
1	I	75	ASP
1	I	78	THR
1	I	80	VAL
1	I	90	GLU
1	I	100	ASN
1	I	102	LEU
1	I	103	LYS
1	I	136	ILE
1	I	140	LEU
1	I	150	LEU
1	I	168	ASN
1	I	220	LYS
1	I	235	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (84) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	31	GLN
1	A	54	ASN
1	A	100	ASN
1	A	109	ASN
1	A	121	GLN
1	A	132	ASN
1	A	146	GLN
1	A	195	GLN
1	A	203	ASN
1	B	4	GLN
1	B	15	ASN
1	B	21	GLN
1	B	23	HIS
1	B	31	GLN
1	B	59	ASN
1	B	61	GLN
1	B	100	ASN
1	B	109	ASN
1	B	118	GLN
1	B	121	GLN
1	B	123	GLN

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Mol	Chain	Res	Type
1	B	146	GLN
1	B	209	GLN
1	D	31	GLN
1	D	100	ASN
1	D	123	GLN
1	D	137	ASN
1	D	203	ASN
1	D	209	GLN
1	D	210	ASN
1	E	15	ASN
1	E	31	GLN
1	E	54	ASN
1	E	59	ASN
1	E	91	GLN
1	E	100	ASN
1	E	118	GLN
1	E	132	ASN
1	E	168	ASN
1	E	203	ASN
1	F	4	GLN
1	F	21	GLN
1	F	31	GLN
1	F	35	GLN
1	F	59	ASN
1	F	100	ASN
1	F	118	GLN
1	F	121	GLN
1	F	132	ASN
1	F	146	GLN
1	F	168	ASN
1	F	195	GLN
1	F	209	GLN
1	G	15	ASN
1	G	23	HIS
1	G	59	ASN
1	G	61	GLN
1	G	109	ASN
1	G	118	GLN
1	G	121	GLN
1	G	132	ASN
1	G	168	ASN
1	G	209	GLN

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Mol	Chain	Res	Type
1	H	4	GLN
1	H	31	GLN
1	H	35	GLN
1	H	91	GLN
1	H	100	ASN
1	H	112	HIS
1	H	118	GLN
1	H	132	ASN
1	H	172	GLN
1	H	209	GLN
1	H	210	ASN
1	I	15	ASN
1	I	31	GLN
1	I	59	ASN
1	I	91	GLN
1	I	100	ASN
1	I	118	GLN
1	I	121	GLN
1	I	123	GLN
1	I	132	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

8 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
1	PR3	E	229	1	6,7,9	1.00	0	4,7,9	2.21	1 (25%)
1	PR3	G	229	1	6,7,9	0.81	0	4,7,9	1.61	1 (25%)
1	PR3	F	229	1	6,7,9	0.81	0	4,7,9	1.79	2 (50%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	PR3	D	229	1	6,7,9	0.70	0	4,7,9	2.05	2 (50%)
1	PR3	H	229	1	6,7,9	1.36	1 (16%)	4,7,9	2.73	4 (100%)
1	PR3	I	229	1	6,7,9	1.06	1 (16%)	4,7,9	2.13	2 (50%)
1	PR3	B	229	1	8,9,9	0.90	0	6,9,9	2.25	2 (33%)
1	PR3	A	229	1	6,7,9	0.92	0	4,7,9	2.27	2 (50%)

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
1	PR3	E	229	1	-	0/2/6/8	-
1	PR3	G	229	1	-	0/2/6/8	-
1	PR3	F	229	1	-	0/2/6/8	-
1	PR3	D	229	1	-	2/2/6/8	-
1	PR3	H	229	1	-	1/2/6/8	-
1	PR3	I	229	1	-	0/2/6/8	-
1	PR3	B	229	1	-	2/5/8/8	-
1	PR3	A	229	1	-	0/2/6/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	H	229	PR3	O-C	2.80	1.30	1.20
1	I	229	PR3	CB-SG	-2.13	1.74	1.81

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	229	PR3	CE-SD-SG	4.20	121.91	103.46
1	A	229	PR3	CB-SG-SD	3.46	112.82	103.86
1	D	229	PR3	CB-SG-SD	3.29	112.37	103.86
1	E	229	PR3	CE-SD-SG	3.10	126.94	104.23
1	H	229	PR3	CE-SD-SG	2.87	125.28	104.23
1	H	229	PR3	CB-CA-C	2.87	118.59	110.80
1	H	229	PR3	CA-CB-SG	-2.85	102.78	114.45
1	B	229	PR3	CB-SG-SD	2.83	111.18	103.86
1	I	229	PR3	CE-SD-SG	2.67	123.85	104.23
1	F	229	PR3	CE-SD-SG	2.56	123.01	104.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	229	PR3	CE-SD-SG	2.54	122.88	104.23
1	A	229	PR3	CE-SD-SG	2.52	122.74	104.23
1	I	229	PR3	CB-CA-C	-2.51	103.98	110.80
1	D	229	PR3	CE-SD-SG	2.41	121.91	104.23
1	F	229	PR3	CB-SG-SD	2.32	109.86	103.86
1	H	229	PR3	CB-SG-SD	2.27	109.73	103.86

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	229	PR3	N-CA-CB-SG
1	B	229	PR3	CE-SD-SG-CB
1	B	229	PR3	CZ-CE-SD-SG
1	D	229	PR3	CA-CB-SG-SD
1	H	229	PR3	CA-CB-SG-SD

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	I	229	PR3	2	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	DTU	A	1238	-	7,7,7	0.73	0	4,8,8	1.23	0
3	DTT	F	1238	-	7,7,7	0.79	0	4,8,8	0.77	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	DTU	A	1238	-	-	4/8/8/8	-
3	DTT	F	1238	-	-	0/8/8/8	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1238	DTU	S1-C1-C2-O2
2	A	1238	DTU	S1-C1-C2-C3
2	A	1238	DTU	C2-C3-C4-S4
2	A	1238	DTU	O3-C3-C4-S4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1238	DTT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	234/238 (98%)	1.58	65 (27%) 1 1	32, 55, 84, 101	0
1	B	236/238 (99%)	1.27	50 (21%) 2 3	30, 41, 61, 92	0
1	D	226/238 (94%)	-0.16	2 (0%) 81 82	35, 54, 112, 132	0
1	E	236/238 (99%)	-0.36	0 100 100	30, 41, 64, 94	0
1	F	235/238 (98%)	1.56	70 (29%) 1 1	33, 54, 85, 102	0
1	G	234/238 (98%)	0.95	30 (12%) 7 8	30, 41, 59, 74	0
1	H	223/238 (93%)	-0.14	2 (0%) 81 82	31, 54, 108, 119	0
1	I	235/238 (98%)	-0.39	0 100 100	30, 41, 64, 90	0
All	All	1859/1904 (97%)	0.55	219 (11%) 9 10	30, 47, 86, 132	0

All (219) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	209	GLN	6.2
1	G	181	ALA	5.7
1	B	180	ILE	5.6
1	A	211	LEU	5.2
1	F	228	ALA	5.1
1	G	179	GLY	4.9
1	A	55	GLY	4.8
1	B	5	ALA	4.6
1	F	227	LEU	4.5
1	A	160	ASP	4.5
1	F	179	GLY	4.4
1	F	99	ILE	4.4
1	A	180	ILE	4.3
1	F	167	ASP	4.2
1	F	193	LEU	4.1
1	F	135	SER	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	43	ASP	4.0
1	A	228	ALA	3.9
1	A	17	ILE	3.9
1	F	184	SER	3.9
1	F	185	ALA	3.9
1	B	89	SER	3.8
1	A	227	LEU	3.8
1	F	211	LEU	3.8
1	G	180	ILE	3.7
1	F	178	SER	3.7
1	A	205	CYS	3.7
1	H	185	ALA	3.6
1	B	179	GLY	3.6
1	F	43	ASP	3.5
1	B	117	PHE	3.5
1	B	236	LEU	3.5
1	B	87	VAL	3.4
1	A	187	SER	3.4
1	A	99	ILE	3.4
1	A	207	TYR	3.4
1	F	16	GLY	3.4
1	F	234	GLY	3.4
1	A	149	ILE	3.3
1	B	37	TYR	3.3
1	B	181	ALA	3.3
1	F	140	LEU	3.3
1	F	152	TYR	3.3
1	F	164	ILE	3.3
1	B	165	THR	3.3
1	F	87	VAL	3.3
1	A	74	ILE	3.3
1	B	183	SER	3.3
1	F	148	LEU	3.2
1	A	166	LEU	3.2
1	F	56	THR	3.2
1	A	94	ALA	3.1
1	A	226	TYR	3.1
1	G	203	ASN	3.1
1	G	200	VAL	3.1
1	A	154	TYR	3.1
1	F	189	ILE	3.1
1	A	81	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	181	ALA	3.1
1	F	159	PRO	3.1
1	G	164	ILE	3.1
1	F	175	GLY	3.1
1	F	169	LEU	3.1
1	B	42	TYR	3.0
1	D	186	VAL	3.0
1	A	39	ILE	3.0
1	A	236	LEU	3.0
1	A	44	GLY	3.0
1	F	165	THR	3.0
1	F	236	LEU	2.9
1	B	149	ILE	2.9
1	F	226	TYR	2.9
1	F	225	PHE	2.9
1	F	232	THR	2.9
1	A	201	TYR	2.9
1	B	54	ASN	2.9
1	F	237	ASN	2.9
1	F	41	LEU	2.9
1	A	210	ASN	2.9
1	F	154	TYR	2.9
1	A	174	LEU	2.9
1	A	206	PHE	2.9
1	B	74	ILE	2.9
1	F	149	ILE	2.9
1	B	22	PHE	2.8
1	G	29	PHE	2.8
1	G	117	PHE	2.8
1	A	200	VAL	2.8
1	A	204	SER	2.8
1	B	232	THR	2.8
1	B	29	PHE	2.8
1	F	96	VAL	2.8
1	A	199	ILE	2.8
1	G	204	SER	2.8
1	F	223	GLU	2.8
1	B	80	VAL	2.8
1	F	120	LEU	2.7
1	F	156	LYS	2.7
1	B	105	LEU	2.7
1	F	150	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	F	74	ILE	2.7
1	G	107	SER	2.7
1	F	166	LEU	2.7
1	D	185	ALA	2.7
1	A	148	LEU	2.7
1	A	63	TYR	2.6
1	F	97	ILE	2.6
1	B	56	THR	2.6
1	B	200	VAL	2.6
1	F	141	GLY	2.6
1	B	166	LEU	2.6
1	G	94	ALA	2.6
1	A	225	PHE	2.6
1	A	111	THR	2.6
1	A	153	VAL	2.6
1	A	159	PRO	2.6
1	F	202	LYS	2.6
1	A	92	ALA	2.6
1	G	112	HIS	2.6
1	A	231	ALA	2.5
1	A	97	ILE	2.5
1	F	17	ILE	2.5
1	B	77	GLU	2.5
1	G	93	THR	2.5
1	B	206	PHE	2.5
1	G	42	TYR	2.5
1	B	28	ILE	2.5
1	A	193	LEU	2.5
1	B	12	LEU	2.5
1	A	177	SER	2.4
1	B	116	VAL	2.4
1	A	11	TYR	2.4
1	F	146	GLN	2.4
1	A	76	THR	2.4
1	A	93	THR	2.4
1	B	79	SER	2.4
1	F	82	TYR	2.4
1	B	204	SER	2.4
1	F	127	SER	2.4
1	A	156	LYS	2.4
1	A	190	ILE	2.4
1	F	198	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	152	TYR	2.4
1	B	152	TYR	2.4
1	B	182	HIS	2.4
1	F	168	ASN	2.4
1	B	55	GLY	2.4
1	F	92	ALA	2.4
1	A	170	THR	2.4
1	G	49	THR	2.4
1	A	69	ILE	2.4
1	B	136	ILE	2.4
1	A	184	SER	2.3
1	F	204	SER	2.3
1	G	39	ILE	2.3
1	B	156	LYS	2.3
1	B	161	GLY	2.3
1	B	99	ILE	2.3
1	G	116	VAL	2.3
1	A	221	LEU	2.3
1	B	27	LEU	2.3
1	F	147	LEU	2.3
1	A	224	TRP	2.3
1	F	158	THR	2.3
1	G	77	GLU	2.3
1	A	161	GLY	2.3
1	F	190	ILE	2.3
1	F	116	VAL	2.3
1	B	84	ASN	2.2
1	F	181	ALA	2.2
1	A	233	TRP	2.2
1	G	177	SER	2.2
1	B	82	TYR	2.2
1	F	63	TYR	2.2
1	B	164	ILE	2.2
1	A	232	THR	2.2
1	B	69	ILE	2.2
1	F	59	ASN	2.2
1	A	178	SER	2.2
1	B	114	PHE	2.1
1	F	31	GLN	2.1
1	A	125	SER	2.1
1	B	63	TYR	2.1
1	F	201	TYR	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	199	ILE	2.1
1	G	183	SER	2.1
1	B	168	ASN	2.1
1	F	210	ASN	2.1
1	F	213	TYR	2.1
1	A	40	PHE	2.1
1	G	44	GLY	2.1
1	G	170	THR	2.1
1	F	94	ALA	2.1
1	F	106	LEU	2.1
1	F	221	LEU	2.1
1	B	17	ILE	2.1
1	H	57	ILE	2.1
1	A	96	VAL	2.1
1	A	186	VAL	2.1
1	A	117	PHE	2.1
1	B	73	PHE	2.1
1	G	79	SER	2.0
1	G	111	THR	2.0
1	F	58	MET	2.0
1	A	147	LEU	2.0
1	B	227	LEU	2.0
1	F	12	LEU	2.0
1	G	148	LEU	2.0
1	F	51	ILE	2.0
1	G	17	ILE	2.0
1	B	176	TYR	2.0
1	G	37	TYR	2.0
1	G	115	TYR	2.0
1	F	206	PHE	2.0
1	A	77	GLU	2.0
1	B	111	THR	2.0
1	A	132	ASN	2.0
1	G	54	ASN	2.0
1	G	149	ILE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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
1	PR3	F	229	8/10	0.87	0.17	62,65,81,86	0
1	PR3	G	229	8/10	0.92	0.12	37,41,59,64	0
1	PR3	A	229	8/10	0.94	0.15	60,64,84,87	0
1	PR3	B	229	10/10	0.94	0.12	40,48,65,66	0
1	PR3	D	229	8/10	0.96	0.10	92,94,98,99	0
1	PR3	I	229	8/10	0.96	0.08	52,62,80,84	0
1	PR3	H	229	8/10	0.97	0.09	103,105,107,107	0
1	PR3	E	229	8/10	0.97	0.06	50,61,80,82	0

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
3	DTT	F	1238	8/8	0.95	0.09	80,81,85,88	0
2	DTU	A	1238	8/8	0.96	0.09	51,52,53,54	8

6.5 Other polymers [i](#)

There are no such residues in this entry.