



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 06:45 PM GMT

PDB ID : 3GH8
Title : Crystal structure of Mus musculus iodotyrosine deiodinase (IYD) bound to FMN and di-iodotyrosine (DIT)
Authors : Thomas, S.R.; McTamney, P.M.; Adler, J.M.; LaRonde-LeBlanc, N.; Rokita, S.E.
Deposited on : 2009-03-03
Resolution : 2.61 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

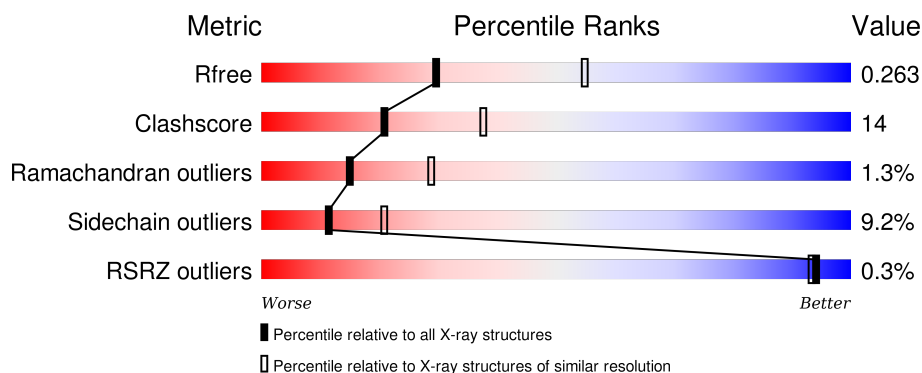
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	2700 (2.64-2.60)
Clashscore	102246	3065 (2.64-2.60)
Ramachandran outliers	100387	3015 (2.64-2.60)
Sidechain outliers	100360	3015 (2.64-2.60)
RSRZ outliers	91569	2706 (2.64-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	259	
1	B	259	
1	C	259	
1	D	259	
1	E	259	

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Mol	Chain	Length	Quality of chain
1	F	259	<div><div></div><div>58%22%15%</div></div>
1	G	259	<div><div>%</div><div></div><div>58%23%15%</div></div>
1	H	259	<div><div></div><div>57%25%15%</div></div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14910 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 Iodotyrosine dehalogenase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	221	Total	C	N	O	S	0	0	0
			1783	1142	317	315	9			
1	B	220	Total	C	N	O	S	0	0	0
			1773	1136	314	314	9			
1	C	221	Total	C	N	O	S	0	0	0
			1783	1142	317	315	9			
1	D	220	Total	C	N	O	S	0	0	0
			1777	1139	316	313	9			
1	E	221	Total	C	N	O	S	0	0	0
			1783	1142	317	315	9			
1	F	220	Total	C	N	O	S	0	0	0
			1773	1136	314	314	9			
1	G	221	Total	C	N	O	S	0	0	0
			1783	1142	317	315	9			
1	H	220	Total	C	N	O	S	0	0	0
			1777	1139	316	313	9			

There are 56 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	33	MET	-	EXPRESSION TAG	UNP Q9DCX8
A	286	HIS	-	EXPRESSION TAG	UNP Q9DCX8
A	287	HIS	-	EXPRESSION TAG	UNP Q9DCX8
A	288	HIS	-	EXPRESSION TAG	UNP Q9DCX8
A	289	HIS	-	EXPRESSION TAG	UNP Q9DCX8
A	290	HIS	-	EXPRESSION TAG	UNP Q9DCX8
A	291	HIS	-	EXPRESSION TAG	UNP Q9DCX8
B	33	MET	-	EXPRESSION TAG	UNP Q9DCX8
B	286	HIS	-	EXPRESSION TAG	UNP Q9DCX8
B	287	HIS	-	EXPRESSION TAG	UNP Q9DCX8
B	288	HIS	-	EXPRESSION TAG	UNP Q9DCX8
B	289	HIS	-	EXPRESSION TAG	UNP Q9DCX8
B	290	HIS	-	EXPRESSION TAG	UNP Q9DCX8

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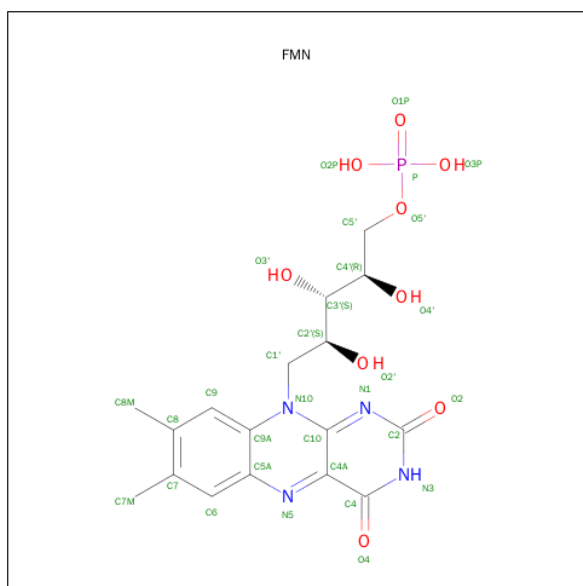
Chain	Residue	Modelled	Actual	Comment	Reference
B	291	HIS	-	EXPRESSION TAG	UNP Q9DCX8
C	33	MET	-	EXPRESSION TAG	UNP Q9DCX8
C	286	HIS	-	EXPRESSION TAG	UNP Q9DCX8
C	287	HIS	-	EXPRESSION TAG	UNP Q9DCX8
C	288	HIS	-	EXPRESSION TAG	UNP Q9DCX8
C	289	HIS	-	EXPRESSION TAG	UNP Q9DCX8
C	290	HIS	-	EXPRESSION TAG	UNP Q9DCX8
C	291	HIS	-	EXPRESSION TAG	UNP Q9DCX8
D	33	MET	-	EXPRESSION TAG	UNP Q9DCX8
D	286	HIS	-	EXPRESSION TAG	UNP Q9DCX8
D	287	HIS	-	EXPRESSION TAG	UNP Q9DCX8
D	288	HIS	-	EXPRESSION TAG	UNP Q9DCX8
D	289	HIS	-	EXPRESSION TAG	UNP Q9DCX8
D	290	HIS	-	EXPRESSION TAG	UNP Q9DCX8
D	291	HIS	-	EXPRESSION TAG	UNP Q9DCX8
E	33	MET	-	EXPRESSION TAG	UNP Q9DCX8
E	286	HIS	-	EXPRESSION TAG	UNP Q9DCX8
E	287	HIS	-	EXPRESSION TAG	UNP Q9DCX8
E	288	HIS	-	EXPRESSION TAG	UNP Q9DCX8
E	289	HIS	-	EXPRESSION TAG	UNP Q9DCX8
E	290	HIS	-	EXPRESSION TAG	UNP Q9DCX8
E	291	HIS	-	EXPRESSION TAG	UNP Q9DCX8
F	33	MET	-	EXPRESSION TAG	UNP Q9DCX8
F	286	HIS	-	EXPRESSION TAG	UNP Q9DCX8
F	287	HIS	-	EXPRESSION TAG	UNP Q9DCX8
F	288	HIS	-	EXPRESSION TAG	UNP Q9DCX8
F	289	HIS	-	EXPRESSION TAG	UNP Q9DCX8
F	290	HIS	-	EXPRESSION TAG	UNP Q9DCX8
F	291	HIS	-	EXPRESSION TAG	UNP Q9DCX8
G	33	MET	-	EXPRESSION TAG	UNP Q9DCX8
G	286	HIS	-	EXPRESSION TAG	UNP Q9DCX8
G	287	HIS	-	EXPRESSION TAG	UNP Q9DCX8
G	288	HIS	-	EXPRESSION TAG	UNP Q9DCX8
G	289	HIS	-	EXPRESSION TAG	UNP Q9DCX8
G	290	HIS	-	EXPRESSION TAG	UNP Q9DCX8
G	291	HIS	-	EXPRESSION TAG	UNP Q9DCX8
H	33	MET	-	EXPRESSION TAG	UNP Q9DCX8
H	286	HIS	-	EXPRESSION TAG	UNP Q9DCX8
H	287	HIS	-	EXPRESSION TAG	UNP Q9DCX8
H	288	HIS	-	EXPRESSION TAG	UNP Q9DCX8
H	289	HIS	-	EXPRESSION TAG	UNP Q9DCX8
H	290	HIS	-	EXPRESSION TAG	UNP Q9DCX8

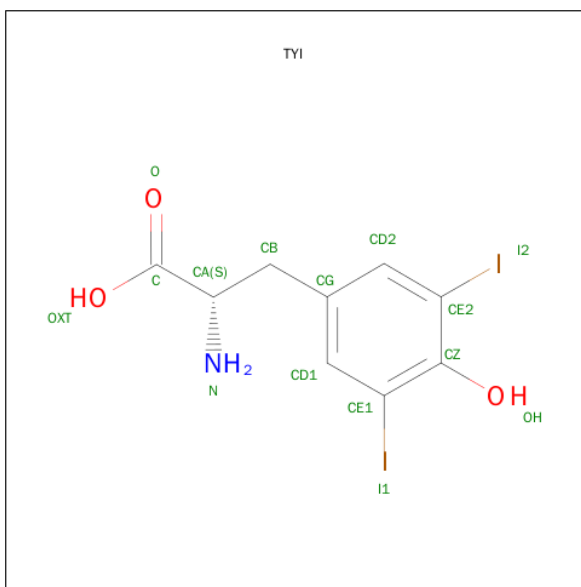
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Chain	Residue	Modelled	Actual	Comment	Reference
H	291	HIS	-	EXPRESSION TAG	UNP Q9DCX8

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: $C_{17}H_{21}N_4O_9P$).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	I	N	O	0	0
			15	9	2	1	3		
3	B	1	Total	C	I	N	O	0	0
			15	9	2	1	3		
3	C	1	Total	C	I	N	O	0	0
			15	9	2	1	3		
3	D	1	Total	C	I	N	O	0	0
			15	9	2	1	3		
3	E	1	Total	C	I	N	O	0	0
			15	9	2	1	3		
3	F	1	Total	C	I	N	O	0	0
			15	9	2	1	3		
3	G	1	Total	C	I	N	O	0	0
			15	9	2	1	3		
3	H	1	Total	C	I	N	O	0	0
			15	9	2	1	3		

- Molecule 4 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	P	0	0
			5	4	1		
4	G	1	Total	O	P	0	0
			5	4	1		

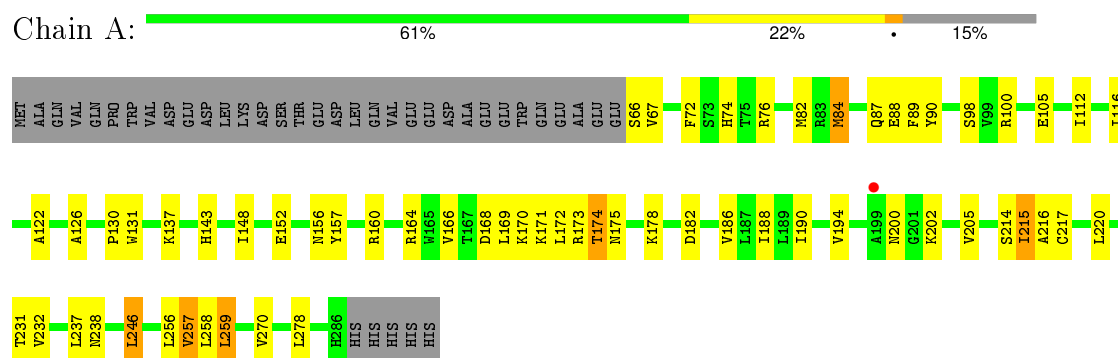
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	36	Total	O	0	0
			36	36		
5	B	38	Total	O	0	0
			38	38		
5	C	39	Total	O	0	0
			39	39		
5	D	23	Total	O	0	0
			23	23		
5	E	48	Total	O	0	0
			48	48		
5	F	40	Total	O	0	0
			40	40		
5	G	38	Total	O	0	0
			38	38		
5	H	38	Total	O	0	0
			38	38		

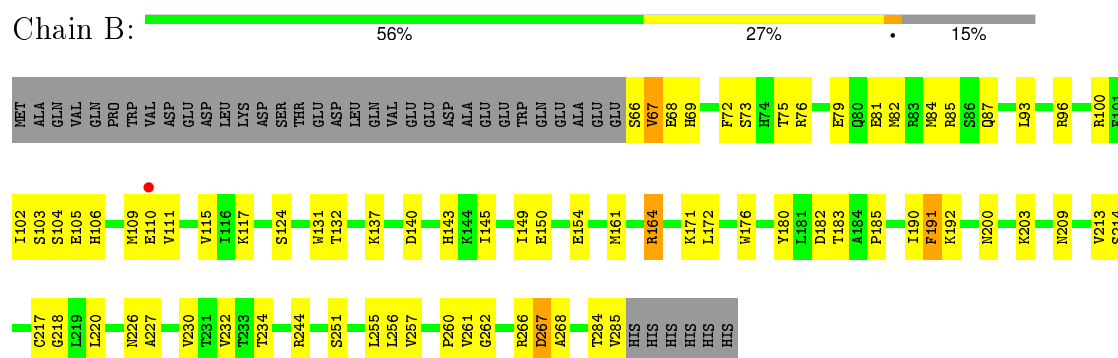
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

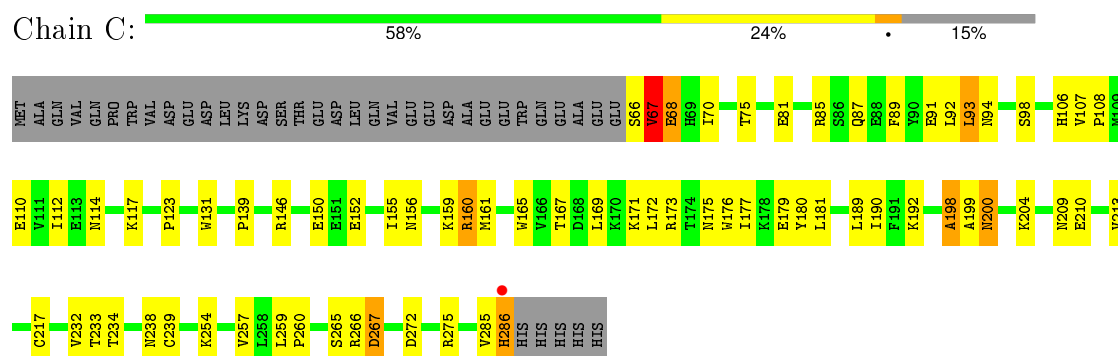
• Molecule 1: Iodotyrosine dehalogenase 1



• Molecule 1: Iodotyrosine dehalogenase 1

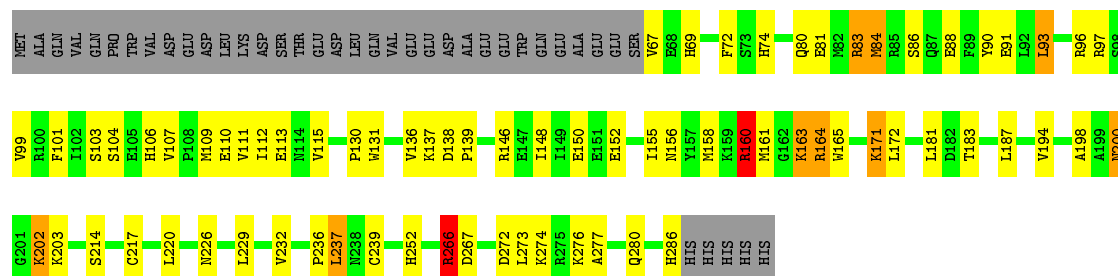


• Molecule 1: Iodotyrosine dehalogenase 1



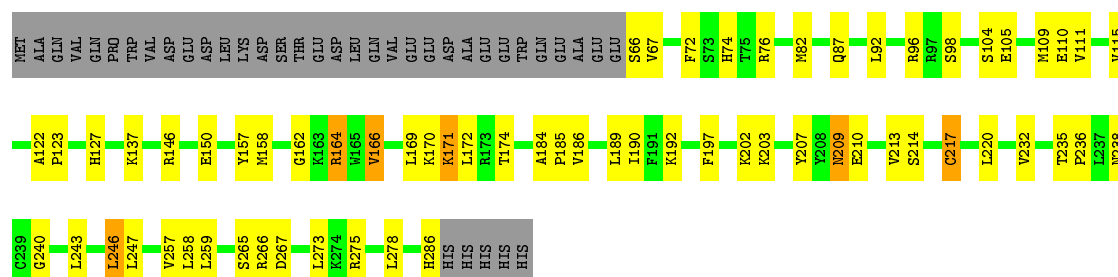
- Molecule 1: Iodotyrosine dehalogenase 1

Chain D: 56% 24% 15%



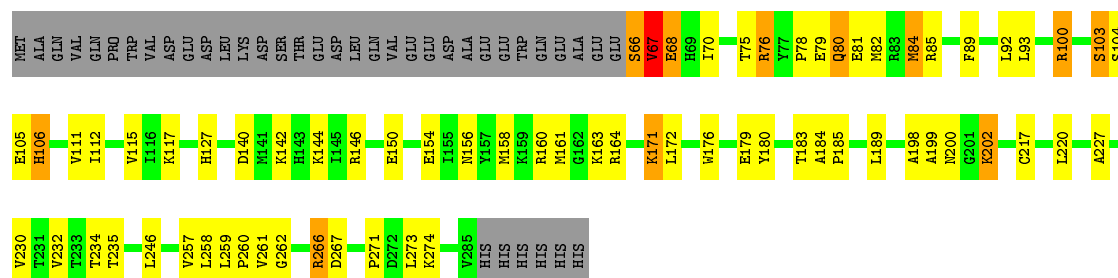
- Molecule 1: Iodotyrosine dehalogenase 1

Chain E:  60% 23% • 15%



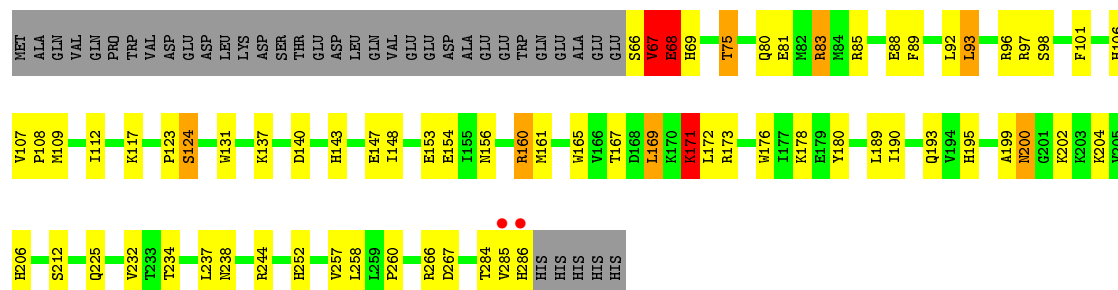
- Molecule 1: Iodotyrosine dehalogenase 1

Chain F:  58% 22% • 15%

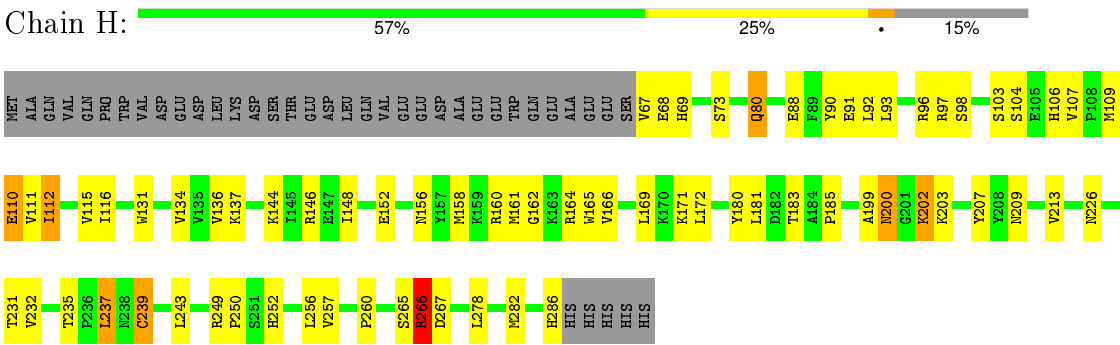


- Molecule 1: Iodotyrosine dehalogenase 1

Chain G:  58% 23% 15%



● Molecule 1: Iodotyrosine dehalogenase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	50.61Å 112.57Å 189.25Å 90.00° 89.92° 90.00°	Depositor
Resolution (Å)	30.00 – 2.61 48.37 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.8 (30.00-2.61) 96.7 (48.37-2.60)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.26 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.181 , 0.264 0.182 , 0.263	Depositor DCC
R_{free} test set	3195 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	34.1	Xtriage
Anisotropy	0.986	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 14.6	EDS
Estimated twinning fraction	0.457 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 62910 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	14910	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.42% 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, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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

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	0.92	0/1823	0.92	2/2468 (0.1%)
1	B	0.89	1/1812 (0.1%)	0.93	1/2453 (0.0%)
1	C	0.86	0/1823	0.91	1/2468 (0.0%)
1	D	0.88	0/1817	0.90	4/2460 (0.2%)
1	E	0.93	2/1823 (0.1%)	0.90	1/2468 (0.0%)
1	F	0.91	1/1812 (0.1%)	0.96	4/2453 (0.2%)
1	G	0.88	0/1823	0.92	0/2468
1	H	0.92	1/1817 (0.1%)	0.90	2/2460 (0.1%)
All	All	0.90	5/14550 (0.0%)	0.92	15/19698 (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	C	0	1
1	F	1	1
1	G	0	1
All	All	1	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	191	PHE	CE2-CZ	6.18	1.49	1.37
1	E	207	TYR	CE2-CZ	5.95	1.46	1.38
1	E	217	CYS	CB-SG	-5.74	1.72	1.81
1	H	239	CYS	CB-SG	-5.20	1.73	1.81
1	F	217	CYS	CB-SG	-5.05	1.73	1.81

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	100	ARG	NE-CZ-NH1	-11.56	114.52	120.30
1	F	100	ARG	NE-CZ-NH2	7.04	123.82	120.30
1	A	246	LEU	CA-CB-CG	6.47	130.18	115.30
1	E	246	LEU	CA-CB-CG	6.33	129.85	115.30
1	H	237	LEU	CA-CB-CG	5.95	128.98	115.30
1	D	160	ARG	NE-CZ-NH1	5.93	123.27	120.30
1	B	102	ILE	CG1-CB-CG2	-5.89	98.44	111.40
1	D	83	ARG	NE-CZ-NH1	5.67	123.13	120.30
1	A	168	ASP	CB-CG-OD1	5.58	123.33	118.30
1	F	259	LEU	CA-CB-CG	5.56	128.09	115.30
1	H	266	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	F	67	VAL	N-CA-C	5.43	125.67	111.00
1	D	266	ARG	NE-CZ-NH1	5.22	122.91	120.30
1	D	237	LEU	CA-CB-CG	5.18	127.22	115.30
1	C	204	LYS	CD-CE-NZ	5.03	123.27	111.70

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	F	67	VAL	CA

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	285	VAL	Peptide
1	F	66	SER	Peptide
1	G	285	VAL	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	1783	0	1839	42	0
1	B	1773	0	1832	58	0
1	C	1783	0	1839	69	0
1	D	1777	0	1834	70	0
1	E	1783	0	1839	34	0
1	F	1773	0	1832	58	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	1783	0	1839	55	0
1	H	1777	0	1834	68	0
2	A	31	0	19	3	0
2	B	31	0	19	4	0
2	C	31	0	19	2	0
2	D	31	0	19	0	0
2	E	31	0	19	1	0
2	F	31	0	19	1	0
2	G	31	0	19	1	0
2	H	31	0	19	1	0
3	A	15	0	8	3	0
3	B	15	0	8	4	0
3	C	15	0	8	2	0
3	D	15	0	7	2	0
3	E	15	0	8	0	0
3	F	15	0	8	3	0
3	G	15	0	8	1	0
3	H	15	0	7	3	0
4	C	5	0	0	0	0
4	G	5	0	0	0	0
5	A	36	0	0	8	0
5	B	38	0	0	12	0
5	C	39	0	0	10	0
5	D	23	0	0	7	0
5	E	48	0	0	8	0
5	F	40	0	0	13	0
5	G	38	0	0	12	0
5	H	38	0	0	19	0
All	All	14910	0	14902	424	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 14.

All (424) 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:164:ARG:HD3	5:E:305:HOH:O	1.38	1.21
1:B:191:PHE:HB2	5:B:294:HOH:O	1.43	1.14
1:D:266:ARG:HH11	1:D:266:ARG:CB	1.61	1.13
1:B:132:THR:HB	5:B:294:HOH:O	1.51	1.08
1:E:110:GLU:HA	5:E:403:HOH:O	1.53	1.07

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:266:ARG:HH11	1:D:266:ARG:HB3	1.16	1.06
1:G:156:ASN:HD22	1:G:160:ARG:HD3	1.08	1.06
1:G:156:ASN:ND2	1:G:160:ARG:HD3	1.69	1.06
1:F:84:MET:HG3	5:F:297:HOH:O	1.57	1.03
1:B:67:VAL:HG12	1:B:68:GLU:N	1.77	1.00
1:A:164:ARG:HG3	5:A:461:HOH:O	1.63	0.98
1:B:106:HIS:HB2	5:B:311:HOH:O	1.64	0.96
1:G:67:VAL:HG13	1:H:171:LYS:HA	1.44	0.96
1:D:164:ARG:HG3	1:D:164:ARG:HH11	1.30	0.95
1:F:67:VAL:O	1:F:68:GLU:CB	2.16	0.94
1:C:200:ASN:HD22	1:C:200:ASN:H	1.14	0.93
1:G:67:VAL:O	1:G:68:GLU:HB3	1.65	0.93
1:G:200:ASN:HD22	1:G:200:ASN:H	1.12	0.92
1:F:76:ARG:HH11	1:F:76:ARG:HG2	1.37	0.89
1:B:67:VAL:HG12	1:B:68:GLU:H	1.35	0.88
1:C:173:ARG:HG3	1:D:69:HIS:CE1	2.09	0.87
1:F:67:VAL:O	1:F:68:GLU:HB3	1.73	0.86
1:B:172:LEU:HD13	3:B:302:TYI:I1	2.47	0.85
1:D:156:ASN:HA	1:D:160:ARG:HB2	1.58	0.85
1:G:200:ASN:ND2	1:G:200:ASN:H	1.73	0.85
1:D:266:ARG:HB3	1:D:266:ARG:NH1	1.92	0.84
1:E:171:LYS:HD2	5:E:432:HOH:O	1.77	0.83
1:D:156:ASN:ND2	1:D:160:ARG:NH1	2.25	0.82
1:G:106:HIS:HD2	5:H:414:HOH:O	1.63	0.82
1:C:286:HIS:HB3	5:C:296:HOH:O	1.78	0.81
1:B:284:THR:HG22	5:B:493:HOH:O	1.80	0.81
1:A:171:LYS:HA	1:B:67:VAL:HG22	1.63	0.80
1:F:202:LYS:HA	1:F:202:LYS:HE2	1.63	0.80
1:A:157:TYR:OH	1:A:174:THR:HG23	1.82	0.80
1:E:164:ARG:HG2	5:E:294:HOH:O	1.83	0.78
1:C:156:ASN:HD22	1:C:160:ARG:HD2	1.48	0.77
1:C:198:ALA:CB	1:C:200:ASN:HD21	1.95	0.77
1:C:67:VAL:O	1:C:68:GLU:CB	2.32	0.77
5:A:409:HOH:O	1:B:82:MET:CE	2.33	0.75
1:E:157:TYR:OH	1:E:174:THR:HG23	1.86	0.75
1:D:164:ARG:NH1	1:D:164:ARG:HG3	1.97	0.74
1:D:266:ARG:CB	1:D:266:ARG:NH1	2.45	0.74
1:C:156:ASN:ND2	1:C:160:ARG:HD2	2.03	0.74
1:E:98:SER:HB3	1:E:232:VAL:HG23	1.70	0.74
1:F:172:LEU:HD13	3:F:302:TYI:I1	2.57	0.74
1:D:266:ARG:HH11	1:D:266:ARG:HB2	1.54	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:156:ASN:HD22	1:G:160:ARG:CD	1.95	0.73
1:A:72:PHE:CE2	1:A:74:HIS:HB2	2.23	0.73
1:H:181:LEU:HB3	5:H:297:HOH:O	1.87	0.72
1:C:198:ALA:CB	1:C:200:ASN:ND2	2.53	0.72
2:F:301:FMN:O1P	5:F:423:HOH:O	2.06	0.72
1:H:146:ARG:CA	5:H:297:HOH:O	2.38	0.71
1:C:114:ASN:HB2	1:D:86:SER:HB2	1.72	0.71
1:C:198:ALA:HB3	1:C:200:ASN:ND2	2.06	0.71
1:D:172:LEU:HD13	3:D:302:TYI:I1	2.60	0.71
1:C:67:VAL:O	1:C:68:GLU:HB3	1.89	0.71
1:H:146:ARG:N	5:H:297:HOH:O	2.22	0.71
1:H:111:VAL:O	1:H:115:VAL:HG13	1.90	0.70
1:H:200:ASN:HD22	1:H:202:LYS:H	1.38	0.70
1:F:81:GLU:O	1:F:85:ARG:HG3	1.91	0.70
1:C:233:THR:HA	1:C:259:LEU:HD23	1.71	0.70
1:C:200:ASN:HD22	1:C:200:ASN:N	1.88	0.70
1:D:286:HIS:CE1	5:D:358:HOH:O	2.44	0.69
1:C:190:ILE:HD12	1:C:257:VAL:HG23	1.73	0.69
1:C:200:ASN:H	1:C:200:ASN:ND2	1.90	0.69
1:F:200:ASN:ND2	5:F:415:HOH:O	2.26	0.69
1:H:286:HIS:O	5:H:481:HOH:O	2.10	0.69
1:E:111:VAL:O	1:E:115:VAL:HG13	1.93	0.69
1:B:143:HIS:HD2	1:B:182:ASP:OD2	1.76	0.68
1:E:162:GLY:O	1:E:166:VAL:HG12	1.93	0.68
1:B:140:ASP:HB3	5:B:364:HOH:O	1.92	0.68
1:D:200:ASN:C	1:D:200:ASN:HD22	1.97	0.68
1:B:81:GLU:O	1:B:85:ARG:HG3	1.94	0.67
1:C:173:ARG:HD2	5:C:305:HOH:O	1.93	0.67
1:A:76:ARG:NH2	1:B:105:GLU:OE2	2.28	0.67
1:D:277:ALA:N	1:D:280:GLN:OE1	2.22	0.66
1:G:173:ARG:HD2	1:H:69:HIS:CE1	2.31	0.66
1:A:257:VAL:HG23	1:A:259:LEU:HD23	1.77	0.66
1:H:156:ASN:ND2	1:H:160:ARG:HH11	1.93	0.66
1:F:103:SER:OG	1:F:105:GLU:HG3	1.96	0.66
1:G:83:ARG:HG2	1:H:110:GLU:HG2	1.77	0.66
1:B:244:ARG:HG2	1:B:244:ARG:HH11	1.61	0.66
1:A:112:ILE:O	1:A:116:ILE:HG13	1.96	0.66
5:C:340:HOH:O	1:D:69:HIS:HD2	1.78	0.66
1:F:76:ARG:HH11	1:F:76:ARG:CG	2.07	0.65
1:F:142:LYS:HE3	1:F:184:ALA:O	1.96	0.65
1:F:266:ARG:HG3	5:F:300:HOH:O	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:161:MET:HE3	3:H:302:TYI:HB2	1.77	0.65
1:F:104:SER:HB2	5:F:449:HOH:O	1.96	0.65
1:H:106:HIS:CE1	5:H:296:HOH:O	2.49	0.65
1:E:192:LYS:NZ	1:E:210:GLU:OE1	2.31	0.64
1:A:257:VAL:HG23	1:A:259:LEU:CD2	2.26	0.64
1:D:67:VAL:N	5:D:322:HOH:O	2.30	0.64
1:B:150:GLU:HG2	1:B:176:TRP:O	1.96	0.64
1:F:198:ALA:HB3	5:F:415:HOH:O	1.97	0.64
1:C:81:GLU:O	1:C:85:ARG:HG3	1.97	0.64
1:G:117:LYS:HB3	1:H:90:TYR:CD1	2.33	0.64
1:D:109:MET:O	1:D:113:GLU:HG3	1.97	0.63
1:E:66:SER:N	5:E:452:HOH:O	2.30	0.63
1:A:202:LYS:HG2	5:A:384:HOH:O	1.98	0.63
1:C:156:ASN:ND2	1:C:160:ARG:HH11	1.96	0.63
1:A:172:LEU:HD13	3:A:302:TYI:I1	2.69	0.62
1:C:198:ALA:HB1	1:C:200:ASN:HD21	1.62	0.62
1:A:137:LYS:HE2	5:A:294:HOH:O	1.99	0.62
1:G:81:GLU:O	1:G:85:ARG:HG3	1.98	0.62
5:E:432:HOH:O	1:F:67:VAL:HG21	1.98	0.62
1:G:178:LYS:HD2	1:G:180:TYR:OH	1.98	0.62
1:B:87:GLN:HA	5:B:297:HOH:O	1.99	0.62
1:F:266:ARG:CG	1:F:266:ARG:HH11	2.13	0.62
1:H:156:ASN:HD22	1:H:160:ARG:HD2	1.63	0.62
1:F:274:LYS:HE2	5:F:451:HOH:O	1.99	0.62
1:C:173:ARG:CD	5:C:305:HOH:O	2.47	0.61
1:C:233:THR:HA	1:C:259:LEU:CD2	2.29	0.61
1:D:136:VAL:HG13	1:D:187:LEU:HB2	1.81	0.61
1:F:67:VAL:O	1:F:68:GLU:HB2	2.00	0.61
1:C:232:VAL:O	1:C:234:THR:HG23	2.01	0.61
1:H:200:ASN:ND2	1:H:202:LYS:H	1.98	0.61
1:D:156:ASN:ND2	1:D:160:ARG:HH11	1.97	0.60
1:C:67:VAL:HG13	5:C:433:HOH:O	1.99	0.60
1:H:172:LEU:HD13	3:H:302:TYI:I1	2.71	0.60
1:D:155:ILE:HG22	1:D:160:ARG:HD3	1.83	0.60
1:B:67:VAL:CG1	1:B:68:GLU:N	2.51	0.60
1:B:232:VAL:O	1:B:234:THR:HG23	2.01	0.60
1:D:214:SER:O	1:D:217:CYS:HB3	2.02	0.60
5:G:470:HOH:O	1:H:109:MET:HE2	2.02	0.60
1:F:104:SER:CB	5:F:370:HOH:O	2.49	0.60
1:H:278:LEU:HD11	1:H:282:MET:SD	2.42	0.60
1:F:266:ARG:HH11	1:F:266:ARG:HG3	1.67	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:127:HIS:O	1:E:127:HIS:CG	2.55	0.59
1:C:172:LEU:HD13	3:C:302:TYI:I1	2.72	0.59
1:C:139:PRO:HG2	1:H:73:SER:HB3	1.85	0.59
1:H:80:GLN:HA	1:H:80:GLN:NE2	2.17	0.59
1:G:232:VAL:O	1:G:234:THR:HG23	2.03	0.59
1:C:110:GLU:HG3	5:C:294:HOH:O	2.02	0.59
1:H:137:LYS:NZ	5:H:400:HOH:O	2.34	0.59
1:G:83:ARG:HD2	5:G:327:HOH:O	2.04	0.58
1:A:148:ILE:O	1:A:152:GLU:HG2	2.02	0.58
1:E:267:ASP:OD1	1:E:267:ASP:N	2.34	0.58
1:A:82:MET:HG2	1:B:227:ALA:O	2.02	0.58
1:G:83:ARG:CG	1:H:110:GLU:HG2	2.34	0.58
1:G:171:LYS:HB2	5:G:482:HOH:O	2.04	0.58
1:D:136:VAL:CG1	1:D:187:LEU:HB2	2.34	0.58
1:A:205:VAL:H	1:B:164:ARG:NH2	2.02	0.57
2:B:301:FMN:O1P	5:B:300:HOH:O	2.17	0.57
5:A:409:HOH:O	1:B:82:MET:HE2	1.99	0.57
1:H:266:ARG:HB3	1:H:266:ARG:NH1	2.20	0.57
1:E:258:LEU:HD23	1:E:259:LEU:N	2.20	0.57
1:B:180:TYR:CD2	1:B:260:PRO:HG3	2.40	0.57
1:D:104:SER:HA	1:D:183:THR:O	2.04	0.57
1:F:66:SER:HB2	1:F:67:VAL:HG23	1.87	0.57
1:A:100:ARG:NH2	3:A:302:TYI:I1	3.08	0.56
5:G:498:HOH:O	1:H:69:HIS:HD2	1.88	0.56
1:G:200:ASN:ND2	1:G:200:ASN:N	2.49	0.56
1:H:146:ARG:HG3	1:H:181:LEU:HB2	1.87	0.56
1:D:198:ALA:HB3	1:D:200:ASN:ND2	2.21	0.56
1:B:180:TYR:CE2	1:B:260:PRO:HG3	2.40	0.56
1:D:146:ARG:HG3	1:D:181:LEU:HB2	1.88	0.56
1:C:156:ASN:HD21	1:C:238:ASN:HD22	1.53	0.55
1:G:109:MET:SD	1:G:137:LYS:HD3	2.47	0.55
1:C:198:ALA:HB1	1:C:200:ASN:ND2	2.19	0.55
1:H:80:GLN:HB2	5:H:359:HOH:O	2.06	0.55
1:A:175:ASN:HB2	5:A:408:HOH:O	2.05	0.55
1:H:98:SER:HB3	1:H:232:VAL:HG23	1.88	0.55
1:F:180:TYR:CD2	1:F:260:PRO:HG3	2.41	0.55
1:F:140:ASP:O	1:F:144:LYS:HG3	2.07	0.55
1:E:190:ILE:HD12	1:E:257:VAL:HG23	1.87	0.55
1:D:106:HIS:HD2	5:D:313:HOH:O	1.89	0.55
1:C:159:LYS:HG3	1:C:160:ARG:N	2.22	0.55
1:F:161:MET:HE1	3:F:302:TYI:HB2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:106:HIS:HB2	5:F:21:HOH:O	2.06	0.54
1:C:107:VAL:HG23	1:C:112:ILE:HD13	1.88	0.54
1:C:198:ALA:HB3	1:C:200:ASN:HD21	1.68	0.54
1:G:204:LYS:NZ	5:G:361:HOH:O	2.40	0.54
1:G:284:THR:HG21	5:G:470:HOH:O	2.07	0.54
1:C:107:VAL:HG21	1:C:112:ILE:HD11	1.90	0.54
1:G:101:PHE:HB3	5:G:490:HOH:O	2.08	0.54
1:D:72:PHE:CE2	1:D:74:HIS:HB2	2.43	0.54
1:G:68:GLU:OE1	1:G:69:HIS:N	2.41	0.53
1:E:76:ARG:HH22	1:F:105:GLU:CD	2.11	0.53
1:A:98:SER:OG	2:A:301:FMN:O2P	2.25	0.53
1:G:143:HIS:HB3	5:G:456:HOH:O	2.08	0.53
1:E:171:LYS:CD	5:E:432:HOH:O	2.44	0.53
5:G:470:HOH:O	1:H:109:MET:CE	2.55	0.53
1:D:107:VAL:HG21	1:D:112:ILE:HD11	1.90	0.53
1:D:156:ASN:HD21	1:D:160:ARG:NH1	2.05	0.53
1:D:194:VAL:HG22	1:D:252:HIS:O	2.08	0.53
1:A:190:ILE:HD13	1:A:257:VAL:HG22	1.89	0.53
1:G:66:SER:O	1:H:171:LYS:HB3	2.09	0.53
1:D:286:HIS:HE1	5:D:358:HOH:O	1.87	0.53
1:D:198:ALA:HB3	1:D:200:ASN:HD21	1.73	0.53
1:F:185:PRO:HD2	1:F:261:VAL:O	2.09	0.52
1:H:209:ASN:O	1:H:213:VAL:HG23	2.09	0.52
1:B:145:ILE:O	1:B:149:ILE:HG13	2.09	0.52
5:A:409:HOH:O	1:B:82:MET:HE3	2.04	0.52
1:A:257:VAL:CG2	1:A:259:LEU:HD21	2.39	0.52
1:D:202:LYS:HD2	1:D:203:LYS:H	1.74	0.52
1:E:189:LEU:HG	1:E:258:LEU:HG	1.91	0.52
1:B:109:MET:CE	5:B:438:HOH:O	2.57	0.52
1:C:171:LYS:HG2	1:D:67:VAL:HG12	1.90	0.52
1:F:100:ARG:NH2	3:F:302:TYI:I1	3.13	0.52
1:B:105:GLU:O	1:B:185:PRO:HG3	2.10	0.52
2:A:301:FMN:H4'	1:B:124:SER:O	2.09	0.52
1:B:244:ARG:NH1	1:B:244:ARG:HG2	2.24	0.52
1:C:67:VAL:HG13	1:D:171:LYS:HA	1.91	0.51
1:C:150:GLU:HG2	1:C:176:TRP:O	2.10	0.51
1:H:202:LYS:HD2	1:H:203:LYS:H	1.74	0.51
1:C:98:SER:HB3	1:C:232:VAL:HG23	1.92	0.51
1:H:96:ARG:O	1:H:97:ARG:HD2	2.09	0.51
1:D:110:GLU:HB3	5:D:295:HOH:O	2.11	0.51
1:A:122:ALA:HB2	1:A:216:ALA:HA	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:301:FMN:O4	3:B:302:TYI:N	2.43	0.51
1:H:156:ASN:HA	1:H:160:ARG:HB2	1.91	0.51
1:D:276:LYS:HB3	1:D:280:GLN:HB2	1.92	0.51
1:H:171:LYS:HD3	5:H:314:HOH:O	2.11	0.51
1:C:175:ASN:HD21	1:C:177:ILE:HD12	1.76	0.51
1:G:258:LEU:C	1:G:258:LEU:HD23	2.32	0.51
1:H:185:PRO:HB2	5:H:400:HOH:O	2.10	0.50
1:C:161:MET:HG2	1:C:165:TRP:CD2	2.46	0.50
1:C:152:GLU:HB2	1:C:239:CYS:SG	2.52	0.50
1:D:200:ASN:ND2	1:D:202:LYS:H	2.10	0.50
1:G:190:ILE:HD12	1:G:257:VAL:HG23	1.92	0.50
1:D:96:ARG:O	1:D:97:ARG:HD2	2.11	0.50
1:F:156:ASN:HA	1:F:160:ARG:HB2	1.93	0.50
1:G:225:GLN:HA	5:G:506:HOH:O	2.11	0.50
1:B:96:ARG:NH1	5:B:303:HOH:O	2.39	0.50
1:H:266:ARG:HB3	1:H:266:ARG:HH11	1.75	0.50
1:H:162:GLY:O	1:H:166:VAL:HG23	2.12	0.50
1:F:89:PHE:HA	5:F:410:HOH:O	2.12	0.49
1:F:154:GLU:O	1:F:158:MET:HG3	2.12	0.49
1:F:154:GLU:HG3	1:F:176:TRP:CE2	2.48	0.49
1:E:214:SER:O	1:E:217:CYS:HB3	2.12	0.49
1:C:117:LYS:HB3	1:D:90:TYR:CD1	2.47	0.49
1:A:173:ARG:NE	1:B:67:VAL:HG11	2.28	0.49
1:D:165:TRP:O	1:D:165:TRP:HD1	1.95	0.49
5:G:406:HOH:O	1:H:235:THR:HB	2.13	0.49
1:A:156:ASN:HA	1:A:160:ARG:HB3	1.94	0.49
1:G:153:GLU:HA	1:G:156:ASN:HB2	1.95	0.49
1:H:146:ARG:CB	5:H:297:HOH:O	2.58	0.48
1:F:111:VAL:O	1:F:115:VAL:HG13	2.13	0.48
1:B:161:MET:HE2	3:B:302:TYI:HB2	1.94	0.48
1:H:156:ASN:ND2	1:H:160:ARG:HD2	2.28	0.48
1:B:214:SER:O	1:B:217:CYS:HB3	2.13	0.48
1:H:180:TYR:CD2	1:H:260:PRO:HG3	2.47	0.48
1:B:209:ASN:O	1:B:213:VAL:HG23	2.13	0.48
1:D:130:PRO:HG3	5:D:17:HOH:O	2.12	0.48
1:C:180:TYR:CD2	1:C:260:PRO:HG3	2.48	0.48
1:E:273:LEU:HD13	1:F:127:HIS:CG	2.49	0.48
1:B:190:ILE:O	1:B:255:LEU:HD12	2.14	0.48
1:D:81:GLU:HA	1:D:84:MET:SD	2.53	0.47
1:H:112:ILE:O	1:H:116:ILE:HG12	2.14	0.47
1:D:200:ASN:ND2	1:D:200:ASN:C	2.67	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:278:LEU:HD13	1:B:117:LYS:HG2	1.96	0.47
1:E:98:SER:OG	2:E:301:FMN:O2P	2.33	0.47
1:C:89:PHE:HB2	1:D:226:ASN:ND2	2.29	0.47
1:G:172:LEU:HD13	3:G:302:TYI:I1	2.84	0.47
1:C:67:VAL:O	1:C:68:GLU:HB2	2.12	0.47
1:A:178:LYS:NZ	3:A:302:TYI:OXT	2.38	0.47
1:H:144:LYS:O	1:H:148:ILE:HG13	2.15	0.47
1:F:180:TYR:HA	1:F:183:THR:OG1	2.15	0.47
1:D:163:LYS:HD3	1:D:163:LYS:N	2.30	0.47
1:C:171:LYS:O	1:D:69:HIS:HE1	1.98	0.47
1:C:106:HIS:CE1	5:C:405:HOH:O	2.68	0.47
2:C:301:FMN:O4	3:C:302:TYI:N	2.48	0.47
1:A:215:ILE:HG23	1:B:218:GLY:HA2	1.95	0.47
1:A:143:HIS:HD2	1:A:182:ASP:OD2	1.97	0.46
1:D:99:VAL:HG12	1:D:101:PHE:H	1.80	0.46
1:D:146:ARG:O	1:D:150:GLU:HG3	2.15	0.46
1:F:127:HIS:CG	1:F:127:HIS:O	2.67	0.46
1:B:285:VAL:C	5:B:493:HOH:O	2.53	0.46
1:B:192:LYS:CB	1:B:213:VAL:HG21	2.46	0.46
1:A:90:TYR:CE1	1:B:117:LYS:HB3	2.51	0.46
1:E:72:PHE:CE2	1:E:74:HIS:HB2	2.50	0.46
1:C:66:SER:HB3	5:C:297:HOH:O	2.16	0.46
1:H:96:ARG:HD2	5:H:321:HOH:O	2.15	0.46
1:E:96:ARG:O	1:E:275:ARG:NH2	2.47	0.46
1:G:106:HIS:CD2	5:H:414:HOH:O	2.51	0.46
1:H:266:ARG:NH1	1:H:266:ARG:CB	2.79	0.46
1:D:164:ARG:HH11	1:D:164:ARG:CG	2.14	0.46
1:F:232:VAL:O	1:F:234:THR:HG23	2.16	0.46
1:H:165:TRP:HB2	5:H:356:HOH:O	2.16	0.46
1:A:171:LYS:HA	1:B:67:VAL:CG2	2.42	0.45
1:H:146:ARG:HB2	5:H:297:HOH:O	2.14	0.45
1:B:96:ARG:HH11	1:B:96:ARG:HG2	1.80	0.45
1:G:123:PRO:HB2	2:H:301:FMN:HM81	1.98	0.45
1:H:180:TYR:CE2	1:H:260:PRO:HG3	2.51	0.45
1:A:171:LYS:HG2	5:A:296:HOH:O	2.16	0.45
1:G:68:GLU:OE1	1:G:68:GLU:C	2.54	0.45
1:H:169:LEU:HD22	3:H:302:TYI:CE1	2.46	0.45
5:E:419:HOH:O	1:F:82:MET:CE	2.64	0.45
1:F:246:LEU:O	1:F:246:LEU:HG	2.16	0.45
1:B:96:ARG:NH1	1:B:96:ARG:HG2	2.31	0.45
1:D:111:VAL:O	1:D:115:VAL:HG13	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:G:301:FMN:HM83	2:G:301:FMN:HM71	1.78	0.45
1:A:84:MET:O	1:A:88:GLU:HG3	2.16	0.45
1:E:171:LYS:O	1:F:67:VAL:HG12	2.17	0.45
1:D:156:ASN:O	1:D:161:MET:HG3	2.16	0.45
1:E:209:ASN:O	1:E:213:VAL:HG23	2.16	0.45
1:B:104:SER:HB3	5:B:295:HOH:O	2.17	0.45
1:G:161:MET:HG2	1:G:165:TRP:CE3	2.51	0.45
1:A:256:LEU:O	1:A:257:VAL:HG12	2.17	0.45
1:F:150:GLU:HG2	1:F:176:TRP:O	2.17	0.45
1:G:96:ARG:HG2	1:G:97:ARG:N	2.32	0.45
1:G:195:HIS:CE1	1:G:252:HIS:HB3	2.52	0.45
1:F:112:ILE:O	1:F:115:VAL:HG22	2.16	0.44
1:H:165:TRP:HD1	1:H:165:TRP:O	2.00	0.44
1:E:82:MET:HG2	1:F:227:ALA:O	2.18	0.44
1:D:93:LEU:HA	1:D:93:LEU:HD12	1.78	0.44
1:C:189:LEU:N	1:C:189:LEU:HD12	2.32	0.44
1:D:236:PRO:HB2	1:D:239:CYS:HB2	2.00	0.44
1:C:87:GLN:HG3	1:C:91:GLU:OE2	2.17	0.44
1:C:146:ARG:HA	1:C:181:LEU:HD13	2.00	0.44
1:H:164:ARG:HD2	5:H:295:HOH:O	2.17	0.44
1:B:100:ARG:NH2	3:B:302:TYI:I1	3.21	0.44
5:C:405:HOH:O	1:G:267:ASP:HB2	2.18	0.44
1:B:267:ASP:HA	5:B:436:HOH:O	2.17	0.44
1:F:171:LYS:H	1:F:171:LYS:HG2	1.55	0.44
1:A:231:THR:OG1	1:A:232:VAL:N	2.51	0.44
2:B:301:FMN:H2'	2:B:301:FMN:C9	2.48	0.43
1:E:162:GLY:O	1:E:166:VAL:CG1	2.64	0.43
1:G:140:ASP:HA	5:G:456:HOH:O	2.18	0.43
1:F:258:LEU:HD23	1:F:258:LEU:C	2.38	0.43
1:C:267:ASP:OD1	1:C:267:ASP:N	2.51	0.43
1:G:156:ASN:OD1	1:G:237:LEU:HB3	2.18	0.43
1:G:171:LYS:HG2	1:H:67:VAL:HG12	2.00	0.43
1:F:146:ARG:NH2	1:F:179:GLU:HA	2.33	0.43
1:F:266:ARG:HD3	5:F:298:HOH:O	2.17	0.43
1:C:161:MET:HG2	1:C:165:TRP:CE3	2.53	0.43
1:D:80:GLN:NE2	1:D:83:ARG:HH21	2.17	0.43
1:E:197:PHE:HA	1:E:202:LYS:O	2.19	0.43
1:G:180:TYR:CD2	1:G:260:PRO:HG3	2.53	0.43
1:C:200:ASN:ND2	1:C:200:ASN:N	2.58	0.43
1:F:76:ARG:CG	1:F:76:ARG:NH1	2.77	0.43
1:D:161:MET:HE3	3:D:302:TYI:HB2	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:ASN:CB	1:D:86:SER:HB2	2.45	0.43
1:C:98:SER:OG	2:C:301:FMN:O2P	2.27	0.43
1:B:180:TYR:HA	1:B:183:THR:OG1	2.19	0.43
1:C:94:ASN:ND2	1:C:275:ARG:HH11	2.17	0.43
1:G:112:ILE:HA	1:G:112:ILE:HD13	1.78	0.43
1:H:266:ARG:CG	1:H:266:ARG:HH11	2.31	0.43
1:H:104:SER:HA	1:H:183:THR:O	2.19	0.43
1:D:274:LYS:HA	1:D:274:LYS:HD3	1.67	0.43
1:F:230:VAL:HG22	1:F:262:GLY:O	2.18	0.43
1:E:122:ALA:HB1	1:E:123:PRO:HD2	2.01	0.43
1:C:272:ASP:O	1:D:67:VAL:HG21	2.18	0.43
1:G:98:SER:HB3	1:G:232:VAL:HG23	2.00	0.43
1:D:148:ILE:O	1:D:152:GLU:HG2	2.19	0.43
1:C:123:PRO:HD3	1:D:96:ARG:CZ	2.49	0.43
1:G:80:GLN:HA	1:G:80:GLN:OE1	2.19	0.43
1:D:156:ASN:HD22	1:D:160:ARG:HH11	1.65	0.42
1:H:156:ASN:HD22	1:H:160:ARG:CD	2.30	0.42
1:C:107:VAL:CG2	1:C:112:ILE:CD1	2.97	0.42
1:D:286:HIS:C	5:D:10:HOH:O	2.58	0.42
1:A:270:VAL:HG13	1:B:72:PHE:HB2	2.00	0.42
1:C:209:ASN:O	1:C:213:VAL:HG23	2.19	0.42
1:A:98:SER:HG	2:A:301:FMN:P	2.42	0.42
1:C:146:ARG:NE	1:C:150:GLU:OE2	2.50	0.42
1:A:156:ASN:ND2	1:A:237:LEU:HB3	2.35	0.42
1:G:156:ASN:HD21	1:G:238:ASN:HD22	1.67	0.42
1:H:266:ARG:CB	1:H:266:ARG:HH11	2.32	0.42
1:H:231:THR:OG1	1:H:232:VAL:N	2.53	0.42
1:B:143:HIS:CD2	1:B:182:ASP:OD2	2.65	0.42
1:E:235:THR:HG22	1:E:257:VAL:HG12	2.02	0.42
1:D:273:LEU:O	1:D:274:LYS:HD3	2.20	0.42
1:G:244:ARG:HH11	1:G:244:ARG:HG2	1.85	0.42
1:A:89:PHE:HB2	1:B:226:ASN:ND2	2.35	0.42
1:H:239:CYS:HB3	1:H:243:LEU:CD1	2.49	0.42
1:B:66:SER:O	1:B:67:VAL:HB	2.20	0.42
1:C:266:ARG:HD3	1:C:266:ARG:HA	1.88	0.42
1:D:229:LEU:HA	1:D:229:LEU:HD23	1.83	0.42
1:C:171:LYS:HB2	5:C:348:HOH:O	2.20	0.42
1:A:257:VAL:HG21	1:A:259:LEU:HD21	2.01	0.42
1:B:256:LEU:HD12	1:B:256:LEU:HA	1.89	0.42
1:B:67:VAL:CG1	1:B:69:HIS:HD2	2.32	0.42
1:C:68:GLU:OE1	1:C:68:GLU:HA	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:200:ASN:HD22	1:D:202:LYS:H	1.67	0.42
1:H:107:VAL:HG21	1:H:112:ILE:HD11	2.01	0.42
1:H:256:LEU:HG	1:H:257:VAL:HG23	2.02	0.42
1:A:258:LEU:C	1:A:259:LEU:HD23	2.41	0.41
1:G:154:GLU:HG3	1:G:176:TRP:CE2	2.54	0.41
1:E:278:LEU:HD13	1:F:117:LYS:HG2	2.02	0.41
1:E:146:ARG:HE	1:E:150:GLU:CD	2.23	0.41
1:G:193:GLN:HE21	1:G:206:HIS:HE1	1.67	0.41
1:G:124:SER:HA	1:G:212:SER:HB3	2.02	0.41
1:C:192:LYS:NZ	1:C:210:GLU:OE1	2.52	0.41
1:B:185:PRO:HD2	1:B:261:VAL:O	2.20	0.41
1:A:156:ASN:OD1	1:A:160:ARG:NE	2.48	0.41
1:H:250:PRO:HB2	1:H:252:HIS:CE1	2.56	0.41
1:D:138:ASP:HA	1:D:139:PRO:HD3	1.81	0.41
1:A:214:SER:O	1:A:217:CYS:HB3	2.19	0.41
1:B:66:SER:C	1:B:67:VAL:HG23	2.41	0.41
1:G:189:LEU:N	1:G:189:LEU:HD12	2.36	0.41
1:G:89:PHE:HB2	1:H:226:ASN:ND2	2.36	0.41
1:H:207:TYR:HA	5:H:7:HOH:O	2.20	0.41
1:F:266:ARG:CB	1:F:266:ARG:HH11	2.34	0.41
1:D:146:ARG:HA	1:D:181:LEU:HD13	2.02	0.41
1:F:189:LEU:N	1:F:189:LEU:HD12	2.36	0.41
1:F:104:SER:HB2	5:F:370:HOH:O	2.19	0.41
1:C:107:VAL:HG23	1:C:112:ILE:CD1	2.51	0.41
1:G:165:TRP:CD1	1:G:169:LEU:HD22	2.56	0.41
1:G:107:VAL:HA	1:G:108:PRO:HD3	1.89	0.41
1:E:184:ALA:HA	1:E:185:PRO:HD2	1.90	0.41
1:H:265:SER:HB3	1:H:267:ASP:OD1	2.21	0.41
1:C:217:CYS:SG	1:C:257:VAL:HG21	2.61	0.41
1:F:266:ARG:CB	1:F:266:ARG:NH1	2.84	0.41
1:F:104:SER:HB3	5:F:370:HOH:O	2.18	0.41
1:B:230:VAL:HG22	1:B:262:GLY:O	2.20	0.41
1:C:93:LEU:HA	1:C:93:LEU:HD12	1.74	0.41
1:B:111:VAL:O	1:B:115:VAL:HG13	2.21	0.41
1:A:173:ARG:HE	1:B:67:VAL:HG11	1.85	0.40
1:H:134:VAL:HG21	1:H:249:ARG:HD3	2.02	0.40
1:E:243:LEU:O	1:E:247:LEU:HD12	2.21	0.40
1:H:106:HIS:HE1	5:H:296:HOH:O	1.98	0.40
1:E:127:HIS:CG	1:F:273:LEU:HD13	2.57	0.40
2:B:301:FMN:H2'	2:B:301:FMN:H9	2.03	0.40
1:H:152:GLU:HB2	1:H:239:CYS:SG	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:70:ILE:HG13	1:C:70:ILE:O	2.21	0.40
1:A:130:PRO:HD2	1:A:131:TRP:CE3	2.57	0.40
1:H:106:HIS:HA	5:H:400:HOH:O	2.21	0.40
1:F:271:PRO:HB2	1:F:273:LEU:HG	2.04	0.40
1:C:107:VAL:HA	1:C:108:PRO:HD3	1.82	0.40
1:D:163:LYS:CD	1:D:163:LYS:N	2.85	0.40
1:F:78:PRO:O	1:F:80:GLN:N	2.55	0.40
1:G:93:LEU:HA	1:G:93:LEU:HD12	1.69	0.40
1:G:266:ARG:HA	1:G:266:ARG:HD3	1.72	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	219/259 (85%)	201 (92%)	16 (7%)	2 (1%)	21	41
1	B	218/259 (84%)	199 (91%)	16 (7%)	3 (1%)	14	26
1	C	219/259 (85%)	202 (92%)	13 (6%)	4 (2%)	11	20
1	D	218/259 (84%)	204 (94%)	13 (6%)	1 (0%)	34	58
1	E	219/259 (85%)	206 (94%)	10 (5%)	3 (1%)	14	26
1	F	218/259 (84%)	201 (92%)	13 (6%)	4 (2%)	11	20
1	G	219/259 (85%)	200 (91%)	14 (6%)	5 (2%)	8	13
1	H	218/259 (84%)	203 (93%)	14 (6%)	1 (0%)	34	58
All	All	1748/2072 (84%)	1616 (92%)	109 (6%)	23 (1%)	15	29

All (23) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	VAL

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Mol	Chain	Res	Type
1	A	126	ALA
1	B	67	VAL
1	B	79	GLU
1	C	68	GLU
1	C	198	ALA
1	E	67	VAL
1	F	67	VAL
1	F	68	GLU
1	F	79	GLU
1	G	68	GLU
1	C	199	ALA
1	F	199	ALA
1	G	171	LYS
1	G	199	ALA
1	D	272	ASP
1	G	75	THR
1	C	67	VAL
1	B	268	ALA
1	E	236	PRO
1	H	199	ALA
1	G	67	VAL
1	E	240	GLY

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	198/233 (85%)	180 (91%)	18 (9%)	12	22
1	B	197/233 (84%)	178 (90%)	19 (10%)	10	19
1	C	198/233 (85%)	183 (92%)	15 (8%)	16	31
1	D	197/233 (84%)	178 (90%)	19 (10%)	10	19
1	E	198/233 (85%)	176 (89%)	22 (11%)	8	13
1	F	197/233 (84%)	178 (90%)	19 (10%)	10	19
1	G	198/233 (85%)	180 (91%)	18 (9%)	12	22

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	H	197/233 (84%)	181 (92%)	16 (8%)	15	27
All	All	1580/1864 (85%)	1434 (91%)	146 (9%)	11	21

All (146) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	SER
1	A	84	MET
1	A	87	GLN
1	A	105	GLU
1	A	166	VAL
1	A	169	LEU
1	A	170	LYS
1	A	174	THR
1	A	186	VAL
1	A	188	ILE
1	A	194	VAL
1	A	200	ASN
1	A	215	ILE
1	A	220	LEU
1	A	238	ASN
1	A	246	LEU
1	A	257	VAL
1	A	259	LEU
1	B	73	SER
1	B	75	THR
1	B	76	ARG
1	B	84	MET
1	B	93	LEU
1	B	103	SER
1	B	110	GLU
1	B	131	TRP
1	B	137	LYS
1	B	154	GLU
1	B	164	ARG
1	B	171	LYS
1	B	200	ASN
1	B	203	LYS
1	B	220	LEU
1	B	251	SER
1	B	257	VAL
1	B	266	ARG

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Mol	Chain	Res	Type
1	B	267	ASP
1	C	67	VAL
1	C	75	THR
1	C	92	LEU
1	C	93	LEU
1	C	131	TRP
1	C	155	ILE
1	C	160	ARG
1	C	167	THR
1	C	169	LEU
1	C	179	GLU
1	C	200	ASN
1	C	254	LYS
1	C	265	SER
1	C	267	ASP
1	C	286	HIS
1	D	84	MET
1	D	88	GLU
1	D	91	GLU
1	D	93	LEU
1	D	103	SER
1	D	131	TRP
1	D	137	LYS
1	D	158	MET
1	D	160	ARG
1	D	163	LYS
1	D	164	ARG
1	D	171	LYS
1	D	200	ASN
1	D	202	LYS
1	D	220	LEU
1	D	232	VAL
1	D	237	LEU
1	D	266	ARG
1	D	267	ASP
1	E	87	GLN
1	E	92	LEU
1	E	104	SER
1	E	105	GLU
1	E	109	MET
1	E	137	LYS
1	E	158	MET

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Mol	Chain	Res	Type
1	E	164	ARG
1	E	166	VAL
1	E	169	LEU
1	E	170	LYS
1	E	171	LYS
1	E	172	LEU
1	E	186	VAL
1	E	203	LYS
1	E	209	ASN
1	E	220	LEU
1	E	238	ASN
1	E	246	LEU
1	E	265	SER
1	E	266	ARG
1	E	286	HIS
1	F	67	VAL
1	F	70	ILE
1	F	75	THR
1	F	76	ARG
1	F	80	GLN
1	F	84	MET
1	F	92	LEU
1	F	93	LEU
1	F	103	SER
1	F	106	HIS
1	F	163	LYS
1	F	164	ARG
1	F	171	LYS
1	F	202	LYS
1	F	220	LEU
1	F	235	THR
1	F	257	VAL
1	F	266	ARG
1	F	267	ASP
1	G	67	VAL
1	G	68	GLU
1	G	75	THR
1	G	83	ARG
1	G	88	GLU
1	G	92	LEU
1	G	93	LEU
1	G	124	SER

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Mol	Chain	Res	Type
1	G	131	TRP
1	G	147	GLU
1	G	148	ILE
1	G	160	ARG
1	G	167	THR
1	G	169	LEU
1	G	171	LYS
1	G	200	ASN
1	G	202	LYS
1	G	286	HIS
1	H	68	GLU
1	H	80	GLN
1	H	88	GLU
1	H	91	GLU
1	H	92	LEU
1	H	93	LEU
1	H	103	SER
1	H	110	GLU
1	H	112	ILE
1	H	131	TRP
1	H	136	VAL
1	H	158	MET
1	H	200	ASN
1	H	202	LYS
1	H	237	LEU
1	H	266	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (39) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	74	HIS
1	A	143	HIS
1	B	69	HIS
1	B	143	HIS
1	B	200	ASN
1	B	226	ASN
1	C	87	GLN
1	C	94	ASN
1	C	106	HIS
1	C	143	HIS
1	C	156	ASN
1	C	175	ASN

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Mol	Chain	Res	Type
1	C	193	GLN
1	C	200	ASN
1	C	238	ASN
1	D	69	HIS
1	D	80	GLN
1	D	143	HIS
1	D	156	ASN
1	D	200	ASN
1	D	238	ASN
1	E	74	HIS
1	E	143	HIS
1	F	106	HIS
1	F	114	ASN
1	F	143	HIS
1	F	200	ASN
1	G	74	HIS
1	G	94	ASN
1	G	156	ASN
1	G	193	GLN
1	G	200	ASN
1	G	238	ASN
1	H	69	HIS
1	H	80	GLN
1	H	143	HIS
1	H	156	ASN
1	H	200	ASN
1	H	238	ASN

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 carbohydrates in this entry.

5.6 Ligand geometry

18 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	FMN	A	301	-	32,33,33	1.45	3 (9%)	34,50,50	2.35	8 (23%)
3	TYI	A	302	-	12,15,15	1.25	1 (8%)	15,21,21	1.77	3 (20%)
2	FMN	B	301	-	32,33,33	1.48	6 (18%)	34,50,50	2.40	9 (26%)
3	TYI	B	302	-	12,15,15	1.79	3 (25%)	15,21,21	1.88	4 (26%)
4	PO4	C	1	-	4,4,4	0.47	0	6,6,6	0.25	0
2	FMN	C	301	-	32,33,33	1.23	4 (12%)	34,50,50	1.85	7 (20%)
3	TYI	C	302	-	12,15,15	1.52	2 (16%)	15,21,21	1.99	5 (33%)
2	FMN	D	301	-	32,33,33	1.44	4 (12%)	34,50,50	2.39	10 (29%)
3	TYI	D	302	-	12,15,15	1.15	2 (16%)	15,21,21	2.23	6 (40%)
2	FMN	E	301	-	32,33,33	1.31	2 (6%)	34,50,50	2.26	9 (26%)
3	TYI	E	302	-	12,15,15	1.40	2 (16%)	15,21,21	1.57	5 (33%)
2	FMN	F	301	-	32,33,33	1.31	4 (12%)	34,50,50	1.96	6 (17%)
3	TYI	F	302	-	12,15,15	1.61	2 (16%)	15,21,21	1.68	4 (26%)
4	PO4	G	2	-	4,4,4	0.52	0	6,6,6	0.24	0
2	FMN	G	301	-	32,33,33	1.51	5 (15%)	34,50,50	2.01	11 (32%)
3	TYI	G	302	-	12,15,15	1.37	2 (16%)	15,21,21	2.01	3 (20%)
2	FMN	H	301	-	32,33,33	1.33	4 (12%)	34,50,50	2.08	7 (20%)
3	TYI	H	302	-	12,15,15	0.90	0	15,21,21	1.53	4 (26%)

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	FMN	A	301	-	-	0/18/18/18	0/3/3/3
3	TYI	A	302	-	-	0/4/8/8	0/1/1/1
2	FMN	B	301	-	-	0/18/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	TYI	B	302	-	-	0/4/8/8	0/1/1/1
4	PO4	C	1	-	-	0/0/0/0	0/0/0/0
2	FMN	C	301	-	-	0/18/18/18	0/3/3/3
3	TYI	C	302	-	-	0/4/8/8	0/1/1/1
2	FMN	D	301	-	-	0/18/18/18	0/3/3/3
3	TYI	D	302	-	-	0/4/8/8	0/1/1/1
2	FMN	E	301	-	-	0/18/18/18	0/3/3/3
3	TYI	E	302	-	-	0/4/8/8	0/1/1/1
2	FMN	F	301	-	-	0/18/18/18	0/3/3/3
3	TYI	F	302	-	-	0/4/8/8	0/1/1/1
4	PO4	G	2	-	-	0/0/0/0	0/0/0/0
2	FMN	G	301	-	-	0/18/18/18	0/3/3/3
3	TYI	G	302	-	-	0/4/8/8	0/1/1/1
2	FMN	H	301	-	-	0/18/18/18	0/3/3/3
3	TYI	H	302	-	-	0/4/8/8	0/1/1/1

All (46) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	G	301	FMN	C4'-C3'	-2.60	1.48	1.53
2	B	301	FMN	C10-N10	-2.31	1.36	1.39
2	G	301	FMN	C2'-C3'	-2.26	1.49	1.53
2	F	301	FMN	O3'-C3'	-2.20	1.37	1.43
2	F	301	FMN	C6-C5A	-2.14	1.38	1.41
3	B	302	TYI	CE1-I1	-2.11	2.04	2.10
2	C	301	FMN	C1'-N10	2.02	1.50	1.48
2	B	301	FMN	P-O5'	2.05	1.65	1.59
2	D	301	FMN	P-O1P	2.10	1.57	1.50
3	G	302	TYI	CZ-CE1	2.14	1.45	1.40
2	B	301	FMN	C5'-C4'	2.32	1.55	1.51
2	C	301	FMN	C10-N1	2.33	1.39	1.35
2	H	301	FMN	C5A-N5	2.36	1.39	1.35
2	C	301	FMN	C5A-N5	2.37	1.39	1.35
3	D	302	TYI	CZ-CE1	2.41	1.45	1.40
2	B	301	FMN	C4A-N5	2.48	1.37	1.33
3	D	302	TYI	CZ-CE2	2.52	1.46	1.40
3	E	302	TYI	CZ-CE2	2.53	1.46	1.40
2	A	301	FMN	C4A-N5	2.54	1.37	1.33
2	G	301	FMN	C5A-N5	2.68	1.39	1.35
2	G	301	FMN	C4-N3	2.78	1.38	1.33
2	C	301	FMN	C4A-N5	2.90	1.37	1.33
2	F	301	FMN	C4A-N5	2.95	1.37	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	301	FMN	C4-N3	2.99	1.38	1.33
2	D	301	FMN	C4A-N5	3.06	1.38	1.33
2	H	301	FMN	C1'-N10	3.06	1.51	1.48
2	D	301	FMN	C4-N3	3.15	1.38	1.33
3	C	302	TYI	CZ-CE1	3.17	1.47	1.40
3	E	302	TYI	CZ-CE1	3.18	1.47	1.40
3	B	302	TYI	CZ-CE2	3.24	1.47	1.40
2	E	301	FMN	C1'-N10	3.33	1.51	1.48
2	H	301	FMN	C4A-N5	3.34	1.38	1.33
3	A	302	TYI	CZ-CE1	3.42	1.48	1.40
2	B	301	FMN	C4-N3	3.45	1.39	1.33
3	F	302	TYI	CZ-CE2	3.48	1.48	1.40
3	F	302	TYI	CZ-CE1	3.56	1.48	1.40
3	C	302	TYI	CZ-CE2	3.57	1.48	1.40
2	B	301	FMN	C1'-N10	3.64	1.52	1.48
2	E	301	FMN	C4-N3	3.66	1.39	1.33
2	A	301	FMN	C4-N3	3.68	1.39	1.33
3	G	302	TYI	CZ-CE2	3.70	1.49	1.40
2	H	301	FMN	C4-N3	3.79	1.39	1.33
3	B	302	TYI	CZ-CE1	4.03	1.49	1.40
2	G	301	FMN	C4A-N5	4.27	1.39	1.33
2	A	301	FMN	C1'-N10	4.38	1.53	1.48
2	D	301	FMN	C1'-N10	4.52	1.53	1.48

All (101) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	FMN	N3-C2-N1	-5.87	117.81	127.69
2	D	301	FMN	C4A-C4-N3	-5.05	116.92	123.52
2	F	301	FMN	N3-C2-N1	-5.01	119.25	127.69
2	B	301	FMN	N3-C2-N1	-4.88	119.47	127.69
2	E	301	FMN	C4A-C4-N3	-4.67	117.42	123.52
2	G	301	FMN	N3-C2-N1	-4.40	120.28	127.69
2	C	301	FMN	N3-C2-N1	-4.39	120.30	127.69
2	D	301	FMN	N3-C2-N1	-4.39	120.30	127.69
3	G	302	TYI	CZ-CE1-I1	-4.37	111.06	119.46
3	B	302	TYI	CZ-CE1-I1	-4.35	111.09	119.46
2	E	301	FMN	N3-C2-N1	-4.23	120.56	127.69
3	C	302	TYI	CZ-CE1-I1	-4.19	111.40	119.46
2	H	301	FMN	C4A-C4-N3	-3.87	118.47	123.52
2	H	301	FMN	N3-C2-N1	-3.74	121.39	127.69
2	A	301	FMN	C4A-C4-N3	-3.66	118.73	123.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	302	TYI	CZ-CE2-I2	-3.55	112.63	119.46
2	B	301	FMN	C4A-C4-N3	-3.47	118.99	123.52
3	D	302	TYI	CZ-CE1-I1	-3.29	113.13	119.46
3	D	302	TYI	CB-CG-CD2	-3.26	114.14	120.32
3	B	302	TYI	CB-CG-CD2	-3.06	114.51	120.32
2	G	301	FMN	C4-C4A-C10	-3.05	117.99	119.94
2	G	301	FMN	C1'-C2'-C3'	-3.00	101.25	109.82
2	G	301	FMN	C7M-C7-C8	-2.99	114.30	120.73
2	F	301	FMN	C4A-C4-N3	-2.98	119.62	123.52
2	C	301	FMN	C4A-C4-N3	-2.81	119.84	123.52
2	A	301	FMN	C7M-C7-C6	-2.78	112.47	120.33
3	F	302	TYI	CZ-CE1-I1	-2.76	114.16	119.46
3	E	302	TYI	CZ-CE2-I2	-2.75	114.17	119.46
2	E	301	FMN	O2'-C2'-C1'	-2.72	103.20	109.93
3	C	302	TYI	CB-CG-CD2	-2.64	115.30	120.32
2	D	301	FMN	O3'-C3'-C2'	-2.59	102.01	108.73
3	H	302	TYI	CZ-CE2-I2	-2.56	114.53	119.46
2	G	301	FMN	C8M-C8-C7	-2.32	115.74	120.73
2	D	301	FMN	O4'-C4'-C5'	-2.30	105.08	110.09
2	H	301	FMN	O2P-P-O1P	-2.21	103.41	110.63
2	D	301	FMN	O2P-P-O5'	-2.15	100.46	106.72
2	G	301	FMN	O3'-C3'-C4'	-2.09	103.31	108.73
3	E	302	TYI	CB-CG-CD2	-2.09	116.35	120.32
3	F	302	TYI	CB-CG-CD2	-2.08	116.37	120.32
2	F	301	FMN	C7M-C7-C6	-2.05	114.55	120.33
2	E	301	FMN	O3'-C3'-C2'	2.00	113.92	108.73
3	E	302	TYI	CB-CG-CD1	2.02	124.15	120.32
3	G	302	TYI	CD2-CE2-I2	2.02	122.40	118.56
3	A	302	TYI	OH-CZ-CE1	2.05	126.06	120.44
2	C	301	FMN	O3P-P-O5'	2.05	112.70	106.72
2	D	301	FMN	C4A-N5-C5A	2.05	119.14	116.72
2	C	301	FMN	O2P-P-O5'	2.07	112.77	106.72
2	A	301	FMN	C4A-C10-N10	2.07	122.02	120.52
2	F	301	FMN	O2P-P-O5'	2.10	112.86	106.72
3	D	302	TYI	CD2-CE2-I2	2.11	122.57	118.56
3	B	302	TYI	CB-CG-CD1	2.12	124.34	120.32
3	H	302	TYI	CD1-CE1-I1	2.14	122.63	118.56
2	A	301	FMN	O5'-P-O1P	2.16	112.51	107.08
3	C	302	TYI	CD2-CG-CD1	2.17	122.03	118.97
2	C	301	FMN	C4-C4A-C10	2.28	121.40	119.94
3	E	302	TYI	CG-CB-CA	2.34	119.89	114.24
3	H	302	TYI	CG-CB-CA	2.43	120.11	114.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	FMN	C1'-C2'-C3'	2.44	116.80	109.82
3	D	302	TYI	CB-CG-CD1	2.47	125.02	120.32
2	G	301	FMN	C6-C5A-N5	2.53	122.07	118.92
2	B	301	FMN	C6-C5A-C9A	2.59	121.97	119.11
2	B	301	FMN	O4'-C4'-C5'	2.60	115.75	110.09
2	G	301	FMN	C1'-N10-C9A	2.60	121.85	118.83
3	C	302	TYI	CD2-CE2-I2	2.76	123.81	118.56
3	E	302	TYI	OH-CZ-CE1	2.77	128.03	120.44
3	H	302	TYI	CD2-CE2-I2	2.80	123.87	118.56
3	F	302	TYI	CD2-CE2-I2	2.82	123.92	118.56
2	H	301	FMN	O3P-P-O2P	2.92	118.15	107.44
2	G	301	FMN	C4A-N5-C5A	2.98	120.23	116.72
3	B	302	TYI	CD1-CE1-I1	2.99	124.23	118.56
2	D	301	FMN	C1'-N10-C9A	3.12	122.45	118.83
2	B	301	FMN	O3P-P-O5'	3.20	116.07	106.72
2	E	301	FMN	C4-C4A-C10	3.33	122.08	119.94
2	E	301	FMN	O5'-P-O1P	3.36	115.53	107.08
2	G	301	FMN	C4-C4A-N5	3.36	122.79	118.70
2	B	301	FMN	C5A-C9A-N10	3.39	120.11	117.58
2	C	301	FMN	C4A-N5-C5A	3.49	120.84	116.72
2	F	301	FMN	C1'-N10-C9A	3.54	122.93	118.83
2	H	301	FMN	O5'-P-O1P	3.65	116.25	107.08
2	D	301	FMN	O5'-P-O1P	3.71	116.41	107.08
3	F	302	TYI	CD1-CE1-I1	3.74	125.67	118.56
2	A	301	FMN	C5A-C9A-N10	3.88	120.48	117.58
3	D	302	TYI	CG-CB-CA	3.91	123.67	114.24
2	D	301	FMN	C5A-C9A-N10	4.05	120.61	117.58
3	C	302	TYI	CD1-CE1-I1	4.07	126.28	118.56
3	A	302	TYI	CD2-CE2-I2	4.10	126.35	118.56
2	E	301	FMN	C5A-C9A-N10	4.36	120.85	117.58
3	D	302	TYI	CD1-CE1-I1	4.76	127.59	118.56
2	A	301	FMN	C1'-N10-C9A	4.92	124.53	118.83
2	H	301	FMN	C5A-C9A-N10	5.02	121.34	117.58
3	G	302	TYI	CD1-CE1-I1	5.07	128.19	118.56
2	B	301	FMN	C4A-C10-N10	5.15	124.26	120.52
2	B	301	FMN	C4-N3-C2	5.17	119.47	115.16
2	G	301	FMN	C4-N3-C2	5.35	119.62	115.16
2	C	301	FMN	C4-N3-C2	5.85	120.04	115.16
2	B	301	FMN	C1'-N10-C9A	6.03	125.82	118.83
2	H	301	FMN	C4-N3-C2	6.05	120.20	115.16
2	E	301	FMN	C4-N3-C2	6.81	120.84	115.16
2	F	301	FMN	C4-N3-C2	6.84	120.86	115.16

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	301	FMN	C4-N3-C2	8.03	121.86	115.16
2	D	301	FMN	C4-N3-C2	8.21	122.01	115.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

14 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	FMN	3	0
3	A	302	TYI	3	0
2	B	301	FMN	4	0
3	B	302	TYI	4	0
2	C	301	FMN	2	0
3	C	302	TYI	2	0
3	D	302	TYI	2	0
2	E	301	FMN	1	0
2	F	301	FMN	1	0
3	F	302	TYI	3	0
2	G	301	FMN	1	0
3	G	302	TYI	1	0
2	H	301	FMN	1	0
3	H	302	TYI	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	221/259 (85%)	-0.41	1 (0%) 91 90	24, 33, 45, 56	2 (0%)
1	B	220/259 (84%)	-0.46	1 (0%) 91 90	22, 31, 47, 55	1 (0%)
1	C	221/259 (85%)	-0.38	1 (0%) 91 90	24, 35, 46, 68	0
1	D	220/259 (84%)	-0.46	0 100 100	25, 35, 45, 59	0
1	E	221/259 (85%)	-0.61	0 100 100	18, 35, 51, 63	2 (0%)
1	F	220/259 (84%)	-0.64	0 100 100	18, 33, 52, 61	1 (0%)
1	G	221/259 (85%)	-0.54	2 (0%) 85 83	20, 37, 53, 67	0
1	H	220/259 (84%)	-0.63	0 100 100	22, 36, 51, 56	0
All	All	1764/2072 (85%)	-0.51	5 (0%) 94 93	18, 34, 50, 68	6 (0%)

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	286	HIS	3.8
1	A	199	ALA	2.8
1	C	286	HIS	2.4
1	B	110	GLU	2.3
1	G	285	VAL	2.2

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	FMN	E	301	31/31	0.97	0.14	0.51	18,25,28,29	0
3	TYI	G	302	15/15	0.99	0.14	0.22	42,44,48,49	1
3	TYI	F	302	15/15	0.99	0.13	0.00	38,42,43,50	1
3	TYI	A	302	15/15	0.98	0.14	-0.24	37,39,41,42	2
3	TYI	D	302	15/15	0.98	0.14	-0.30	39,41,44,50	1
2	FMN	A	301	31/31	0.97	0.13	-0.33	16,27,29,30	0
3	TYI	E	302	15/15	0.99	0.12	-0.39	35,38,41,43	2
2	FMN	G	301	31/31	0.98	0.12	-0.43	14,24,27,27	0
2	FMN	H	301	31/31	0.97	0.12	-0.50	23,27,30,32	0
3	TYI	H	302	15/15	0.98	0.11	-0.75	33,35,40,47	1
2	FMN	B	301	31/31	0.98	0.12	-0.97	15,24,26,30	0
2	FMN	C	301	31/31	0.98	0.11	-0.99	17,24,26,26	0
2	FMN	D	301	31/31	0.97	0.12	-1.00	24,28,29,31	0
2	FMN	F	301	31/31	0.99	0.10	-1.05	11,21,23,26	0
3	TYI	C	302	15/15	0.98	0.10	-1.59	39,40,45,49	1
3	TYI	B	302	15/15	0.99	0.10	-1.71	35,38,40,46	1
4	PO4	G	2	5/5	0.92	0.14	-	78,80,82,82	0
4	PO4	C	1	5/5	0.87	0.20	-	76,79,80,80	0

6.5 Other polymers [i](#)

There are no such residues in this entry.