



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:54 PM GMT

PDB ID : 4MZU
Title : Crystal structure of FdtD, a bifunctional ketoisomerase/N-acetyltransferase from *Shewanella denitrificans*
Authors : Chantigian, D.P.; Thoden, J.B.; Holden, H.M.
Deposited on : 2013-09-30
Resolution : 2.20 Å(reported)

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

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

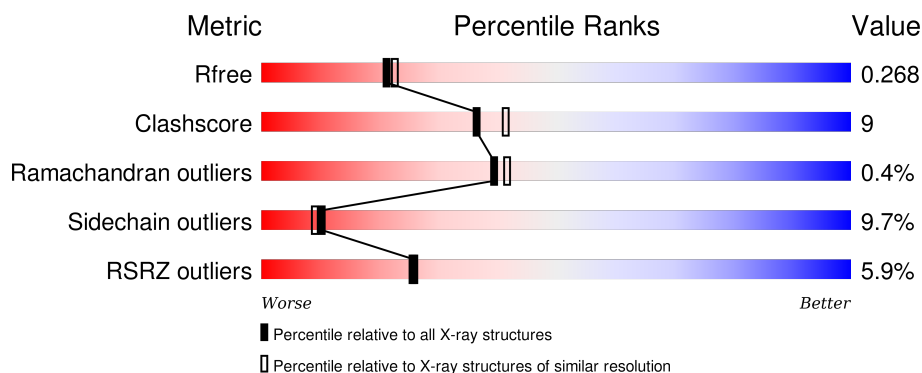
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	3774 (2.20-2.20)
Clashscore	102246	4477 (2.20-2.20)
Ramachandran outliers	100387	4404 (2.20-2.20)
Sidechain outliers	100360	4405 (2.20-2.20)
RSRZ outliers	91569	3781 (2.20-2.20)

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	312	
1	B	312	
1	C	312	
1	D	312	
1	E	312	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	312	
1	G	312	
1	H	312	
1	I	312	
1	J	312	
1	K	312	
1	L	312	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	TDR	D	403	-	-	-	X
4	TDR	J	403	-	-	-	X
4	TDR	L	403	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 28412 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 WxcM-like protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	0	0
			2220	1412	379	418	11			
1	B	290	Total	C	N	O	S	0	0	0
			2262	1438	387	426	11			
1	C	285	Total	C	N	O	S	0	1	0
			2222	1416	379	416	11			
1	D	283	Total	C	N	O	S	0	0	0
			2204	1403	375	415	11			
1	E	286	Total	C	N	O	S	0	0	0
			2231	1422	379	419	11			
1	F	294	Total	C	N	O	S	0	0	0
			2288	1455	393	429	11			
1	G	283	Total	C	N	O	S	0	1	0
			2206	1404	376	415	11			
1	H	278	Total	C	N	O	S	0	0	0
			2159	1379	364	405	11			
1	I	285	Total	C	N	O	S	0	0	0
			2217	1412	377	417	11			
1	J	275	Total	C	N	O	S	0	1	0
			2140	1368	361	401	10			
1	K	285	Total	C	N	O	S	0	1	0
			2226	1418	378	419	11			
1	L	286	Total	C	N	O	S	0	1	0
			2228	1418	380	419	11			

There are 96 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
A	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
A	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
A	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
A	309	HIS	-	EXPRESSION TAG	UNP Q12KT8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
A	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
A	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
B	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
B	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
B	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
B	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
B	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
B	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
B	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
B	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
C	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
C	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
C	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
C	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
C	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
C	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
C	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
C	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
D	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
D	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
D	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
D	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
D	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
D	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
D	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
D	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
E	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
E	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
E	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
E	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
E	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
E	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
E	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
E	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
F	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
F	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
F	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
F	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
F	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
F	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
F	311	HIS	-	EXPRESSION TAG	UNP Q12KT8

Continued on next page...

Continued from previous page...

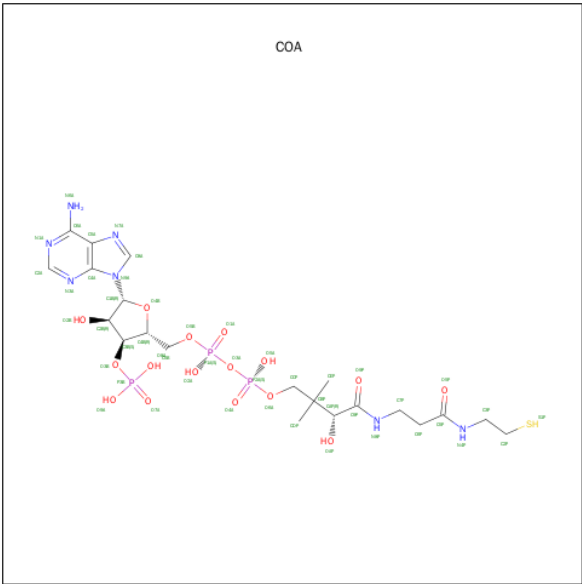
Chain	Residue	Modelled	Actual	Comment	Reference
F	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
G	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
G	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
G	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
G	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
G	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
G	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
G	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
G	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
H	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
H	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
H	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
H	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
H	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
H	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
H	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
H	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
I	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
I	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
I	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
I	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
I	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
I	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
I	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
I	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
J	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
J	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
J	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
J	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
J	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
J	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
J	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
J	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
K	305	LEU	-	EXPRESSION TAG	UNP Q12KT8
K	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
K	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
K	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
K	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
K	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
K	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
K	312	HIS	-	EXPRESSION TAG	UNP Q12KT8
L	305	LEU	-	EXPRESSION TAG	UNP Q12KT8

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
L	306	GLU	-	EXPRESSION TAG	UNP Q12KT8
L	307	HIS	-	EXPRESSION TAG	UNP Q12KT8
L	308	HIS	-	EXPRESSION TAG	UNP Q12KT8
L	309	HIS	-	EXPRESSION TAG	UNP Q12KT8
L	310	HIS	-	EXPRESSION TAG	UNP Q12KT8
L	311	HIS	-	EXPRESSION TAG	UNP Q12KT8
L	312	HIS	-	EXPRESSION TAG	UNP Q12KT8

- Molecule 2 is COENZYME A (three-letter code: COA) (formula: C₂₁H₃₆N₇O₁₆P₃S).



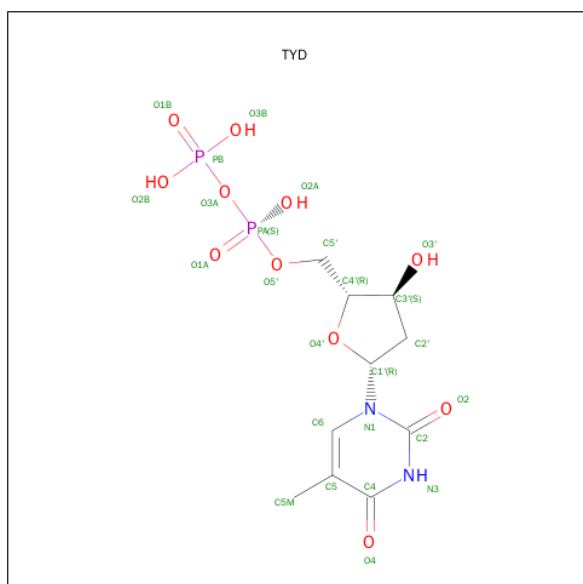
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	B	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	C	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	D	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	E	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	F	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	G	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	G	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	I	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	J	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	K	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		
2	L	1	Total	C	N	O	P	S	0	0
			48	21	7	16	3	1		

- Molecule 3 is THYMIDINE-5'-DIPHOSPHATE (three-letter code: TYD) (formula: $C_{10}H_{16}N_2O_{11}P_2$).



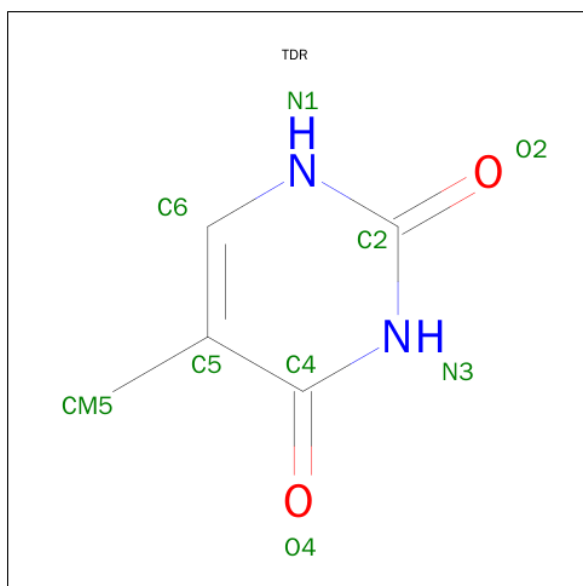
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P		0	0
			25	10	2	11	2			
3	B	1	Total	C	N	O	P		0	0
			25	10	2	11	2			
3	C	1	Total	C	N	O	P		0	0
			25	10	2	11	2			
3	D	1	Total	C	N	O	P		0	0
			25	10	2	11	2			
3	E	1	Total	C	N	O	P		0	0
			25	10	2	11	2			
3	F	1	Total	C	N	O	P		0	0
			25	10	2	11	2			
3	G	1	Total	C	N	O	P		0	0
			25	10	2	11	2			

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	H	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	I	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	J	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	K	1	Total	C	N	O	P	0	0
			25	10	2	11	2		
3	L	1	Total	C	N	O	P	0	0
			25	10	2	11	2		

- Molecule 4 is THYMINE (three-letter code: TDR) (formula: C₅H₆N₂O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			9	5	2	2		
4	B	1	Total	C	N	O	0	0
			9	5	2	2		
4	C	1	Total	C	N	O	0	0
			9	5	2	2		
4	D	1	Total	C	N	O	0	0
			9	5	2	2		
4	E	1	Total	C	N	O	0	0
			9	5	2	2		
4	F	1	Total	C	N	O	0	0
			9	5	2	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	J	1	Total	C	N	O	0	0
			9	5	2	2		
4	K	1	Total	C	N	O	0	0
			9	5	2	2		
4	L	1	Total	C	N	O	0	0
			9	5	2	2		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	G	1	Total	Mg	0	0
			1	1		
5	B	1	Total	Mg	0	0
			1	1		
5	D	1	Total	Mg	0	0
			1	1		
5	C	1	Total	Mg	0	0
			1	1		
5	J	1	Total	Mg	0	0
			1	1		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	93	Total	O	0	0
			93	93		
6	B	100	Total	O	0	0
			100	100		
6	C	87	Total	O	0	0
			87	87		
6	D	53	Total	O	0	0
			53	53		
6	E	66	Total	O	0	0
			66	66		
6	F	61	Total	O	0	0
			61	61		
6	G	80	Total	O	0	0
			80	80		
6	H	42	Total	O	0	0
			42	42		
6	I	67	Total	O	0	0
			67	67		

Continued on next page...

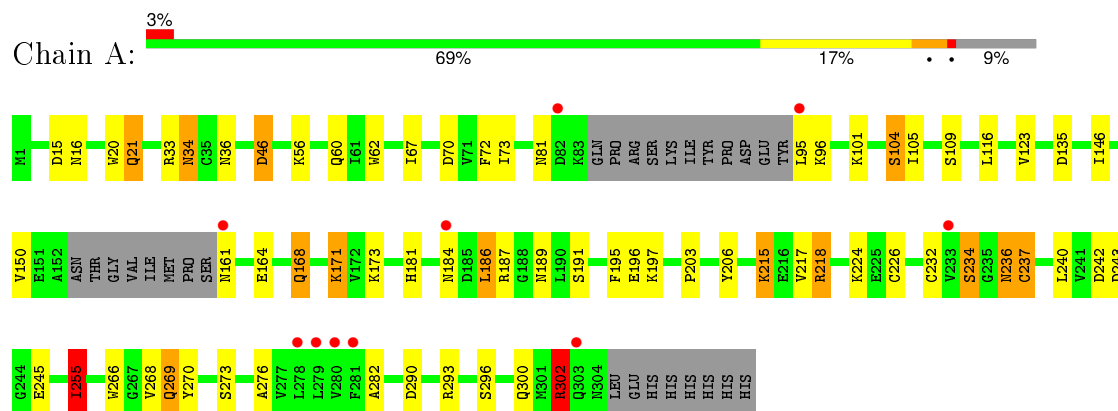
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	J	54	Total 54	O 54	0	0
6	K	82	Total 82	O 82	0	0
6	L	62	Total 62	O 62	0	0

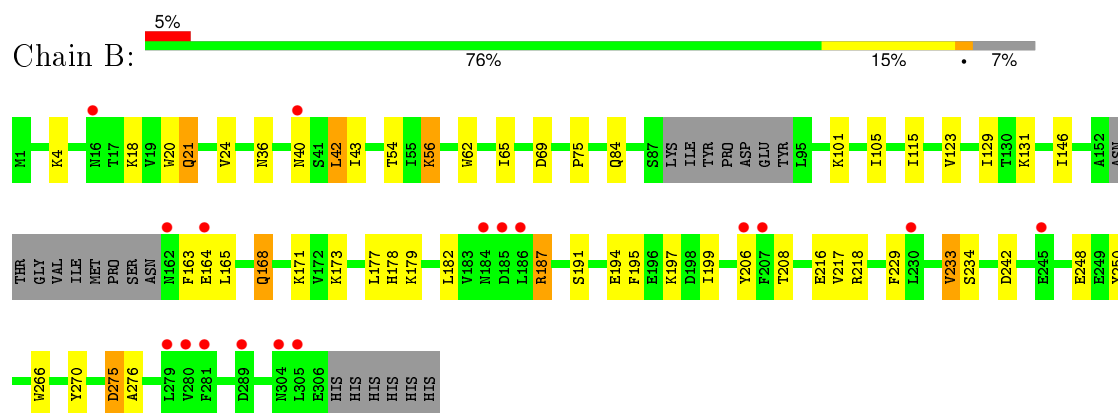
3 Residue-property plots [i](#)

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

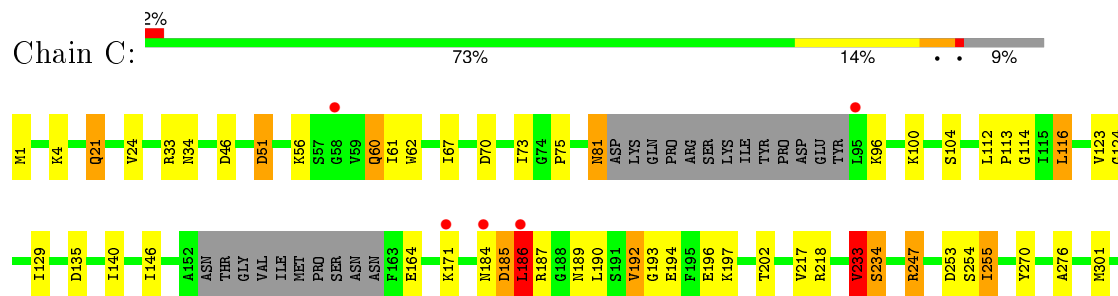
• Molecule 1: WxcM-like protein

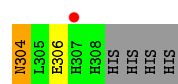


• Molecule 1: WxcM-like protein

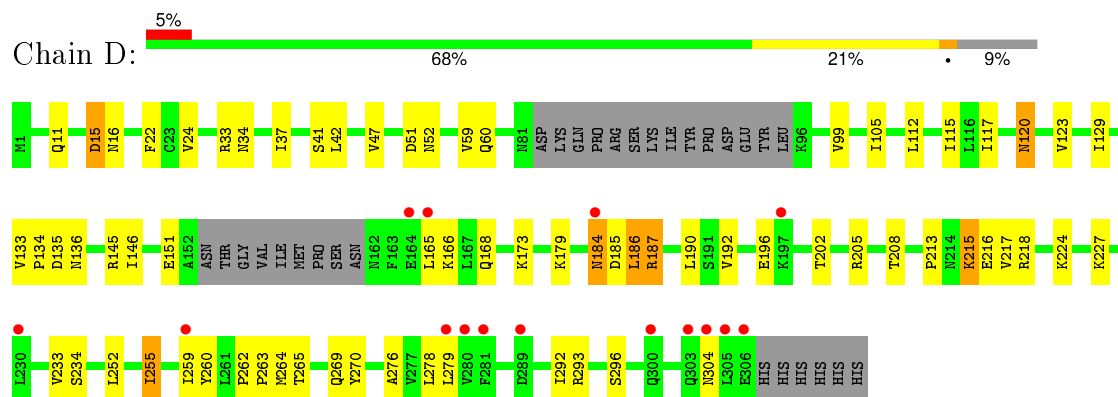


• Molecule 1: WxcM-like protein

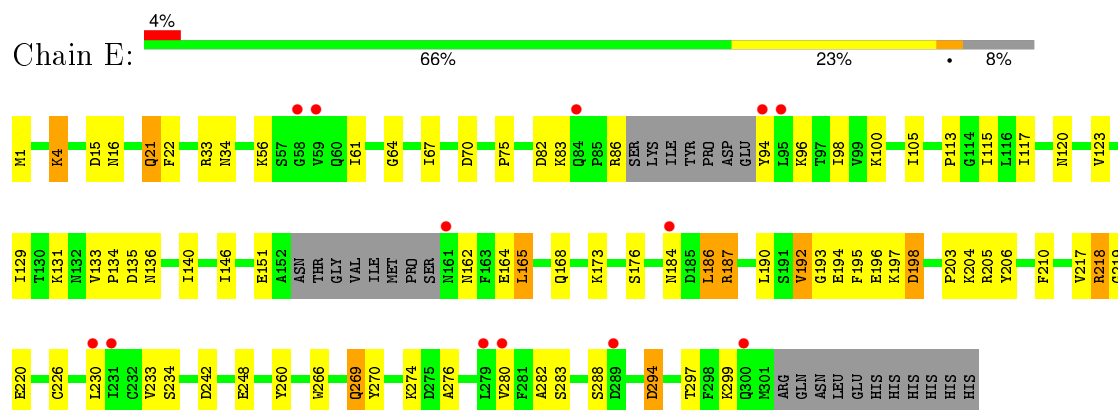




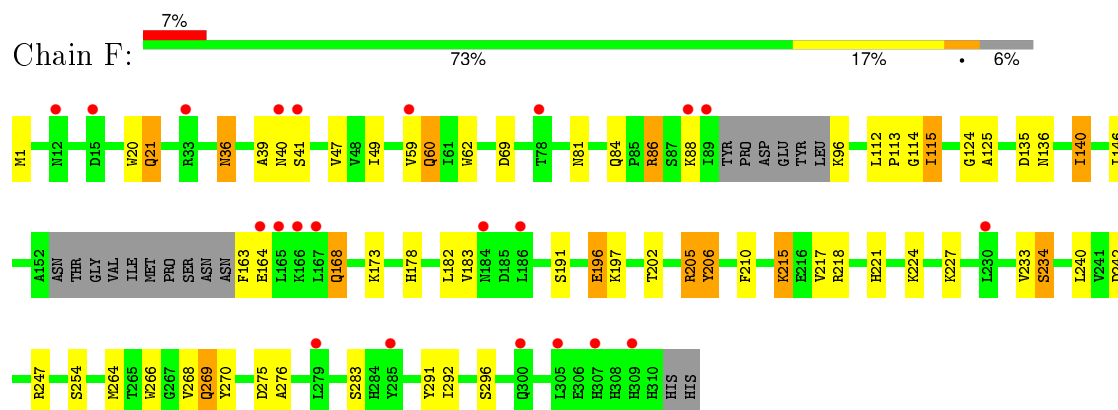
- Molecule 1: WxcM-like protein



- Molecule 1: WxcM-like protein

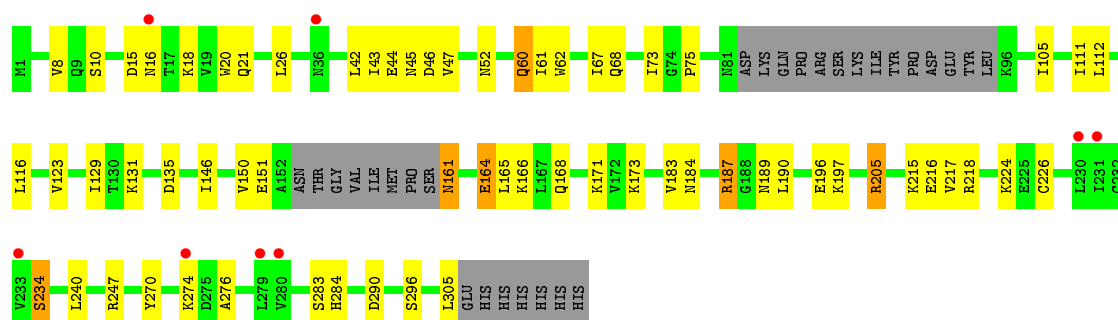


- Molecule 1: WxcM-like protein

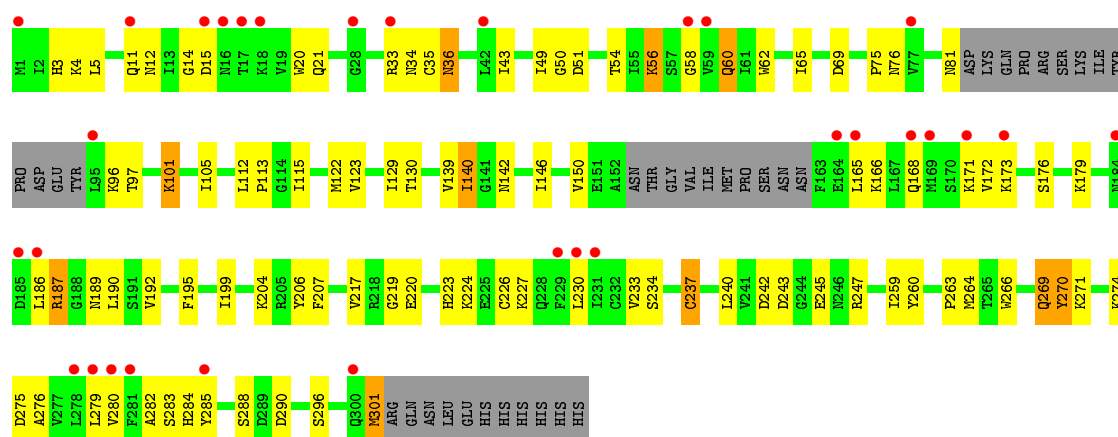


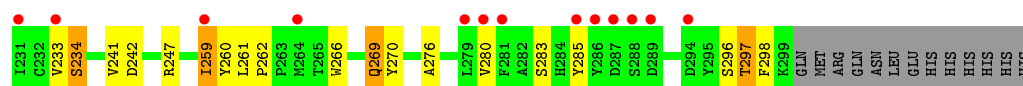
- Molecule 1: WxcM-like protein



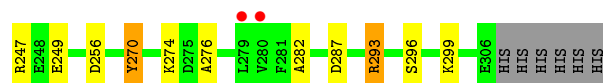
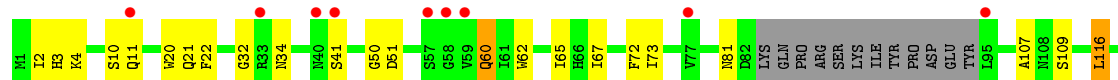


• Molecule 1: WxcM-like protein

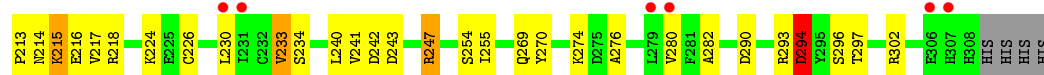
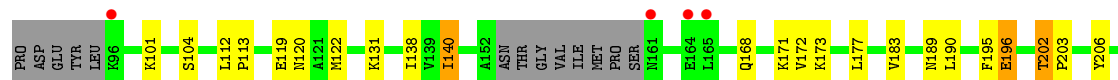




• Molecule 1: WxcM-like protein



• Molecule 1: WxcM-like protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	85.31Å 109.44Å 127.85Å 79.23° 79.98° 84.89°	Depositor
Resolution (Å)	30.00 – 2.20 28.75 – 2.20	Depositor EDS
% Data completeness (in resolution range)	90.9 (30.00-2.20) 85.9 (28.75-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.17 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.204 , 0.270 0.204 , 0.268	Depositor DCC
R_{free} test set	10284 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	30.6	Xtriage
Anisotropy	0.040	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 48.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 205770 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	28412	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 7.12% 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: COA, TYD, MG, TDR

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	0.70	1/2261 (0.0%)	1.11	9/3059 (0.3%)
1	B	0.66	0/2304	1.06	4/3117 (0.1%)
1	C	0.68	0/2266	1.13	11/3066 (0.4%)
1	D	0.60	0/2245	1.06	6/3038 (0.2%)
1	E	0.61	0/2274	1.06	7/3078 (0.2%)
1	F	0.64	0/2331	1.09	6/3153 (0.2%)
1	G	0.63	0/2250	1.04	4/3045 (0.1%)
1	H	0.52	1/2200 (0.0%)	0.95	5/2978 (0.2%)
1	I	0.60	0/2258	1.04	4/3056 (0.1%)
1	J	0.56	0/2184	0.98	5/2956 (0.2%)
1	K	0.65	0/2270	1.08	10/3071 (0.3%)
1	L	0.61	0/2272	1.05	3/3074 (0.1%)
All	All	0.62	2/27115 (0.0%)	1.05	74/36691 (0.2%)

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

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	237	CYS	CB-SG	-6.57	1.71	1.82
1	H	237	CYS	CB-SG	-5.43	1.73	1.81

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	247	ARG	NE-CZ-NH2	-14.92	112.84	120.30
1	C	247	ARG	NE-CZ-NH1	10.56	125.58	120.30
1	A	56	LYS	CD-CE-NZ	7.64	129.28	111.70
1	A	237	CYS	N-CA-CB	-7.60	96.93	110.60
1	K	135	ASP	CB-CG-OD1	7.56	125.10	118.30
1	E	218	ARG	NE-CZ-NH2	-7.47	116.56	120.30
1	I	218	ARG	NE-CZ-NH2	-7.25	116.68	120.30
1	G	135	ASP	CB-CG-OD1	7.10	124.69	118.30
1	E	56	LYS	CD-CE-NZ	7.07	127.95	111.70
1	F	115	ILE	CG1-CB-CG2	-7.03	95.92	111.40
1	F	275	ASP	CB-CG-OD2	6.97	124.57	118.30
1	A	302	ARG	NE-CZ-NH1	6.87	123.74	120.30
1	C	218	ARG	NE-CZ-NH1	-6.80	116.90	120.30
1	B	69	ASP	CB-CG-OD1	6.79	124.41	118.30
1	A	135	ASP	CB-CG-OD1	6.70	124.33	118.30
1	G	187	ARG	NE-CZ-NH2	-6.54	117.03	120.30
1	K	293	ARG	NE-CZ-NH2	6.40	123.50	120.30
1	K	293	ARG	NE-CZ-NH1	-6.38	117.11	120.30
1	L	294	ASP	CB-CG-OD2	-6.35	112.59	118.30
1	F	69	ASP	CB-CG-OD1	6.28	123.95	118.30
1	C	247	ARG	CG-CD-NE	-6.20	98.78	111.80
1	K	116	LEU	CB-CG-CD1	6.12	121.41	111.00
1	B	101	LYS	CD-CE-NZ	-5.98	97.94	111.70
1	J	63	ASP	CB-CG-OD1	5.97	123.68	118.30
1	C	135	ASP	CB-CG-OD1	5.97	123.67	118.30
1	E	33	ARG	NE-CZ-NH1	5.92	123.26	120.30
1	C	46	ASP	N-CA-CB	5.92	121.25	110.60
1	D	112	LEU	CA-CB-CG	-5.90	101.73	115.30
1	K	109	SER	CB-CA-C	-5.87	98.94	110.10
1	B	69	ASP	CB-CG-OD2	-5.82	113.06	118.30
1	C	185	ASP	CB-CG-OD1	5.81	123.53	118.30
1	K	256	ASP	CB-CG-OD1	5.81	123.53	118.30
1	I	135	ASP	CB-CG-OD1	5.75	123.48	118.30
1	J	115	ILE	CG1-CB-CG2	-5.75	98.76	111.40
1	H	237	CYS	CB-CA-C	-5.73	98.95	110.40
1	D	145	ARG	NE-CZ-NH2	-5.72	117.44	120.30
1	K	167	LEU	CA-CB-CG	5.65	128.29	115.30
1	H	269	GLN	CA-CB-CG	5.64	125.82	113.40
1	F	86	ARG	NE-CZ-NH1	5.63	123.11	120.30
1	H	187	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	B	131	LYS	CB-CA-C	-5.61	99.19	110.40
1	G	218	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	I	269	GLN	CA-CB-CG	5.58	125.69	113.40

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	142	ASN	C-N-CD	-5.55	108.40	120.60
1	J	192	VAL	CB-CA-C	-5.50	100.95	111.40
1	D	145	ARG	NE-CZ-NH1	5.48	123.04	120.30
1	E	218	ARG	NE-CZ-NH1	5.46	123.03	120.30
1	C	51	ASP	CB-CG-OD1	5.46	123.21	118.30
1	A	46	ASP	CB-CA-C	5.40	121.20	110.40
1	K	218	ARG	NE-CZ-NH1	-5.36	117.62	120.30
1	E	133	VAL	C-N-CD	5.34	139.62	128.40
1	F	86	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	E	192	VAL	CB-CA-C	-5.33	101.28	111.40
1	C	186	LEU	CA-CB-CG	5.32	127.54	115.30
1	L	247	ARG	NE-CZ-NH1	-5.32	117.64	120.30
1	H	301	MET	CG-SD-CE	5.30	108.68	100.20
1	L	294	ASP	N-CA-CB	-5.28	101.09	110.60
1	D	255	ILE	CG1-CB-CG2	-5.28	99.79	111.40
1	C	192	VAL	CB-CA-C	-5.27	101.39	111.40
1	C	21	GLN	CA-CB-CG	5.26	124.97	113.40
1	K	287	ASP	CB-CG-OD2	-5.22	113.60	118.30
1	E	187	ARG	NE-CZ-NH2	-5.19	117.71	120.30
1	G	46	ASP	CB-CG-OD1	-5.18	113.64	118.30
1	D	192	VAL	CB-CA-C	-5.13	101.65	111.40
1	A	109	SER	CB-CA-C	-5.13	100.36	110.10
1	D	47	VAL	N-CA-C	-5.12	97.18	111.00
1	I	177	LEU	CA-CB-CG	-5.10	103.58	115.30
1	A	56	LYS	CB-CA-C	5.09	120.58	110.40
1	A	302	ARG	NE-CZ-NH2	-5.09	117.76	120.30
1	F	206	TYR	CB-CG-CD2	-5.05	117.97	121.00
1	K	81	ASN	N-CA-C	5.04	124.60	111.00
1	J	135	ASP	CB-CG-OD1	5.03	122.83	118.30
1	A	255	ILE	CB-CA-C	-5.01	101.59	111.60
1	J	186	LEU	CA-CB-CG	5.00	126.81	115.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	233	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	2220	0	2214	57	0
1	B	2262	0	2258	38	0
1	C	2222	0	2219	48	0
1	D	2204	0	2197	37	0
1	E	2231	0	2224	45	0
1	F	2288	0	2278	51	0
1	G	2206	0	2202	48	0
1	H	2159	0	2158	61	0
1	I	2217	0	2210	57	0
1	J	2140	0	2143	45	0
1	K	2226	0	2225	37	0
1	L	2228	0	2220	49	0
2	A	48	0	32	0	0
2	B	48	0	32	1	0
2	C	48	0	32	0	0
2	D	48	0	32	1	0
2	E	48	0	32	0	0
2	F	48	0	32	0	0
2	G	96	0	64	1	0
2	I	48	0	32	2	0
2	J	48	0	32	4	0
2	K	48	0	32	3	0
2	L	48	0	32	3	0
3	A	25	0	13	0	0
3	B	25	0	13	0	0
3	C	25	0	13	0	0
3	D	25	0	13	2	0
3	E	25	0	13	4	0
3	F	25	0	13	1	0
3	G	25	0	13	1	0
3	H	25	0	13	1	0
3	I	25	0	13	0	0
3	J	25	0	13	0	0
3	K	25	0	13	0	0
3	L	25	0	13	1	0
4	A	9	0	6	1	0
4	B	9	0	6	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	9	0	6	0	0
4	D	9	0	6	0	0
4	E	9	0	6	0	0
4	F	9	0	6	0	0
4	J	9	0	6	0	0
4	K	9	0	6	0	0
4	L	9	0	6	1	0
5	B	1	0	0	0	0
5	C	1	0	0	0	0
5	D	1	0	0	0	0
5	G	1	0	0	0	0
5	J	1	0	0	0	0
6	A	93	0	0	1	0
6	B	100	0	0	2	0
6	C	87	0	0	1	0
6	D	53	0	0	0	0
6	E	66	0	0	1	0
6	F	61	0	0	3	0
6	G	80	0	0	1	1
6	H	42	0	0	1	0
6	I	67	0	0	1	0
6	J	54	0	0	1	1
6	K	82	0	0	2	0
6	L	62	0	0	2	0
All	All	28412	0	27142	517	1

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 9.

All (517) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:236:ASN:HD21	1:A:273:SER:HB3	1.05	1.12
1:A:236:ASN:ND2	1:A:273:SER:HB3	1.64	1.11
1:A:60:GLN:HG3	1:A:62:TRP:CZ2	1.91	1.05
1:A:184:ASN:HB3	1:A:189:ASN:HD22	1.23	1.04
1:K:215[A]:LYS:H	1:K:215[A]:LYS:HE3	1.22	1.03
1:I:264:MET:HE1	1:I:292:ILE:HD12	1.39	1.00
1:B:123:VAL:HG13	1:B:129:ILE:HD11	1.48	0.95
1:C:100:LYS:HD2	1:C:116:LEU:HD21	1.46	0.94
1:A:236:ASN:HD21	1:A:273:SER:CB	1.80	0.94

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:21:GLN:HE21	1:E:21:GLN:H	1.14	0.92
1:A:168:GLN:HE22	1:G:168:GLN:HE22	1.10	0.92
3:G:402:TYD:O1B	1:K:187:ARG:NH1	2.02	0.92
1:D:187:ARG:HH11	1:D:187:ARG:HG2	1.34	0.91
1:F:215:LYS:HE3	1:F:215:LYS:H	1.33	0.91
1:H:207:PHE:HB3	1:J:192:VAL:HG13	1.53	0.90
2:J:401:COA:H143	1:L:140:ILE:HD11	1.52	0.90
1:A:236:ASN:ND2	1:A:273:SER:CB	2.35	0.89
1:I:60:GLN:HG3	1:I:62:TRP:CZ2	2.08	0.89
1:F:215:LYS:HE3	1:F:215:LYS:N	1.88	0.87
1:I:150:VAL:HG12	1:I:151:GLU:HG2	1.57	0.86
1:A:168:GLN:HE22	1:G:168:GLN:NE2	1.73	0.86
1:A:184:ASN:HB3	1:A:189:ASN:ND2	1.92	0.85
1:H:242:ASP:HB3	1:H:266:TRP:HB3	1.60	0.84
1:A:21:GLN:NE2	1:A:21:GLN:H	1.75	0.84
1:E:21:GLN:NE2	1:E:21:GLN:H	1.75	0.83
1:C:123:VAL:HG13	1:C:129:ILE:CD1	2.07	0.83
1:B:242:ASP:HB3	1:B:266:TRP:HB3	1.60	0.83
1:I:186:LEU:CD2	1:I:186:LEU:H	1.92	0.81
1:D:185:ASP:HB2	1:D:186:LEU:HD23	1.62	0.81
1:F:224:LYS:HA	1:F:264:MET:CE	2.10	0.81
1:E:269:GLN:HG3	6:E:526:HOH:O	1.81	0.81
1:G:216:GLU:OE1	1:K:187:ARG:HD2	1.82	0.80
1:A:21:GLN:HE21	1:A:21:GLN:H	1.28	0.80
1:I:186:LEU:HD23	1:I:186:LEU:H	1.45	0.80
1:C:56:LYS:NZ	6:C:547:HOH:O	2.15	0.79
1:B:187:ARG:HH11	1:B:187:ARG:HG2	1.48	0.78
1:I:264:MET:CE	1:I:292:ILE:HD12	2.14	0.78
1:C:100:LYS:HD2	1:C:116:LEU:CD2	2.14	0.78
1:H:123:VAL:HG13	1:H:129:ILE:HD11	1.65	0.78
1:A:168:GLN:NE2	1:G:168:GLN:HE22	1.81	0.78
1:I:173:LYS:HG3	1:I:243:ASP:OD1	1.83	0.78
1:D:227:LYS:HG2	1:D:260:TYR:OH	1.84	0.77
1:C:60:GLN:HG3	1:C:62:TRP:CZ2	2.18	0.77
1:F:224:LYS:HA	1:F:264:MET:HE2	1.65	0.77
1:A:21:GLN:NE2	4:A:403:TDR:O4	2.17	0.76
1:J:60:GLN:HE21	1:L:75:PRO:HB2	1.50	0.76
1:H:140:ILE:HD11	2:I:401:COA:CEP	2.16	0.76
1:A:302:ARG:HH11	1:A:302:ARG:HG3	1.51	0.75
1:F:60:GLN:HG3	1:F:62:TRP:CZ2	2.22	0.75
1:J:269:GLN:HG3	6:J:521:HOH:O	1.87	0.74

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:33:ARG:N	1:H:51:ASP:OD1	2.17	0.74
1:I:185:ASP:HB2	1:I:186:LEU:HD23	1.69	0.73
1:C:123:VAL:HG13	1:C:129:ILE:HD11	1.68	0.73
1:C:123:VAL:CG1	1:C:129:ILE:CD1	2.66	0.73
1:B:123:VAL:HG13	1:B:129:ILE:CD1	2.18	0.73
1:C:190:LEU:HD21	1:C:192:VAL:HG22	1.70	0.73
1:B:187:ARG:HG2	1:D:216:GLU:OE1	1.89	0.73
1:A:184:ASN:CB	1:A:189:ASN:HD22	2.01	0.72
1:H:69:ASP:HB2	1:H:101:LYS:HD3	1.70	0.72
1:K:72:PHE:CZ	2:L:401:COA:H22	2.24	0.72
1:G:60:GLN:NE2	1:I:76:ASN:HD21	1.87	0.71
1:A:302:ARG:CG	1:A:302:ARG:HH11	2.02	0.71
1:I:269:GLN:HG2	6:I:553:HOH:O	1.90	0.71
1:C:100:LYS:CD	1:C:116:LEU:HD21	2.21	0.70
1:A:184:ASN:CB	1:A:189:ASN:ND2	2.52	0.70
1:H:65:ILE:HG13	1:H:97:THR:HB	1.73	0.70
1:A:171:LYS:HG3	1:G:165:LEU:HD21	1.71	0.70
1:B:21:GLN:HG3	1:C:24:VAL:CG2	2.21	0.70
1:F:20:TRP:HB3	1:F:21:GLN:OE1	1.92	0.70
1:H:176:SER:OG	1:H:260:TYR:HB3	1.92	0.70
1:E:204:LYS:HG3	1:E:283:SER:O	1.92	0.69
1:I:3:HIS:HE1	1:I:5:LEU:HD12	1.56	0.69
1:F:146:ILE:HD12	1:F:217:VAL:HG21	1.73	0.69
2:J:401:COA:CEP	1:L:140:ILE:HD11	2.22	0.69
1:H:140:ILE:HD11	2:I:401:COA:H143	1.75	0.69
1:H:283:SER:OG	1:H:284:HIS:HD2	1.75	0.69
1:C:185:ASP:HB2	1:C:186:LEU:HD23	1.73	0.69
1:F:264:MET:HE3	1:F:292:ILE:HD11	1.75	0.68
1:A:67:ILE:HD13	1:A:73:ILE:HD11	1.76	0.68
1:I:264:MET:CE	1:I:292:ILE:CD1	2.72	0.68
1:I:184:ASN:HD22	1:I:189:ASN:HD21	1.42	0.68
1:A:70:ASP:OD2	1:A:101:LYS:NZ	2.27	0.68
2:K:401:COA:S1P	6:K:515:HOH:O	2.52	0.67
1:K:216:GLU:OE1	6:K:566:HOH:O	2.10	0.67
1:E:186:LEU:HD23	1:E:186:LEU:H	1.60	0.67
1:J:242:ASP:OD2	1:J:247:ARG:HB3	1.95	0.66
1:C:184:ASN:ND2	1:C:189:ASN:OD1	2.28	0.66
3:F:402:TYD:H6	3:F:402:TYD:H5'1	1.76	0.66
1:J:76:ASN:OD1	1:K:60:GLN:NE2	2.28	0.66
1:L:242:ASP:OD2	1:L:247:ARG:NH1	2.28	0.66
1:B:234:SER:O	1:B:276:ALA:HA	1.94	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:167:LEU:HG	1:I:168:GLN:N	2.08	0.65
1:B:21:GLN:HG3	1:C:24:VAL:HG22	1.77	0.65
1:K:60:GLN:HG3	1:K:62:TRP:CZ2	2.32	0.65
1:K:62:TRP:N	1:K:65:ILE:HD12	2.11	0.65
1:H:233:VAL:HG11	1:J:233:VAL:HG11	1.76	0.65
1:C:61:ILE:HD12	1:C:67:ILE:HD11	1.78	0.64
1:H:20:TRP:HB3	1:H:21:GLN:OE1	1.97	0.64
1:G:42:LEU:HD23	1:G:43:ILE:N	2.13	0.64
1:C:186:LEU:H	1:C:186:LEU:HD23	1.63	0.64
1:G:26:LEU:HD22	1:G:44:GLU:HA	1.80	0.64
1:H:20:TRP:HE1	1:H:36:ASN:HD21	1.45	0.63
1:E:21:GLN:N	1:E:21:GLN:HE21	1.91	0.63
1:E:123:VAL:HG13	1:E:129:ILE:HD11	1.81	0.63
1:H:15:ASP:O	1:H:33:ARG:HB2	2.00	0.62
1:A:224:LYS:HB2	1:A:290:ASP:OD1	1.98	0.62
1:I:224:LYS:HA	1:I:264:MET:HE2	1.81	0.62
1:C:194:GLU:HG2	1:F:205:ARG:HB2	1.79	0.62
1:C:96:LYS:O	1:C:114:GLY:HA2	2.00	0.62
1:G:60:GLN:HG3	1:G:62:TRP:CZ2	2.35	0.62
1:F:96:LYS:O	1:F:114:GLY:HA2	2.00	0.62
1:G:60:GLN:NE2	1:I:76:ASN:ND2	2.47	0.61
1:A:60:GLN:HE21	1:C:75:PRO:HB2	1.64	0.61
1:J:204:LYS:HD3	1:J:285:TYR:CE1	2.35	0.61
1:J:152:ALA:HB2	1:J:247:ARG:HG3	1.82	0.61
1:B:233:VAL:HG11	1:D:233:VAL:HG21	1.81	0.61
1:H:58:GLY:HA3	1:H:76:ASN:HD22	1.64	0.61
1:H:58:GLY:HA3	1:H:76:ASN:ND2	2.16	0.61
1:L:39:ALA:O	1:L:57:SER:HB3	2.01	0.61
1:B:216:GLU:OE1	1:D:187:ARG:NH1	2.33	0.60
1:F:224:LYS:HA	1:F:264:MET:HE1	1.82	0.60
1:G:67:ILE:HD13	1:G:73:ILE:HD11	1.84	0.60
1:K:240:LEU:HD11	1:K:247:ARG:HG2	1.84	0.60
1:F:264:MET:CE	1:F:292:ILE:HD11	2.31	0.60
1:E:164:GLU:H	1:E:168:GLN:HE22	1.49	0.60
1:J:199:ILE:O	1:J:201:PHE:N	2.31	0.60
1:D:146:ILE:HD12	1:D:217:VAL:HG21	1.84	0.60
3:L:402:TYD:O3B	6:L:512:HOH:O	2.16	0.60
1:I:264:MET:HE1	1:I:292:ILE:CD1	2.21	0.59
1:K:123:VAL:HG13	1:K:129:ILE:HD11	1.82	0.59
1:J:241:VAL:O	1:J:247:ARG:HA	2.03	0.59
1:L:33:ARG:O	1:L:34:ASN:CB	2.51	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:20:TRP:HB3	1:L:21:GLN:OE1	2.03	0.59
1:H:242:ASP:OD2	1:H:247:ARG:NH1	2.36	0.59
1:G:10:SER:HB2	1:G:26:LEU:O	2.02	0.58
1:A:146:ILE:HD12	1:A:217:VAL:HG21	1.84	0.58
1:D:135:ASP:O	1:D:136:ASN:HB2	2.03	0.58
1:A:60:GLN:HG3	1:A:62:TRP:HZ2	1.57	0.58
1:H:165:LEU:HD22	6:H:526:HOH:O	2.04	0.58
1:C:112:LEU:HB3	1:C:113:PRO:CD	2.34	0.58
1:D:184:ASN:HD22	1:D:184:ASN:C	2.07	0.58
1:I:122:MET:HB3	1:I:138:ILE:CD1	2.34	0.58
2:G:403:COA:H21	1:H:81:ASN:H	1.68	0.58
1:H:240:LEU:HD11	1:H:247:ARG:HG2	1.86	0.58
1:H:33:ARG:HG3	1:H:34:ASN:HD22	1.68	0.58
1:J:234:SER:O	1:J:276:ALA:HA	2.03	0.58
1:G:26:LEU:HD23	1:G:45:ASN:ND2	2.18	0.58
1:L:33:ARG:O	1:L:34:ASN:HB2	2.03	0.58
1:H:224:LYS:HB2	1:H:290:ASP:OD1	2.03	0.58
1:E:234:SER:O	1:E:276:ALA:HA	2.04	0.58
1:D:205:ARG:NH2	3:D:402:TYD:O4	2.36	0.57
1:L:122:MET:HB3	1:L:138:ILE:HD13	1.85	0.57
1:G:123:VAL:HG13	1:G:129:ILE:HD11	1.86	0.57
1:G:283:SER:OG	1:G:284:HIS:HD2	1.88	0.57
1:A:195:PHE:CE1	1:A:203:PRO:HG3	2.40	0.57
1:B:21:GLN:CG	1:C:24:VAL:HG21	2.34	0.57
1:I:3:HIS:CE1	1:I:5:LEU:HD12	2.39	0.57
1:G:123:VAL:CG1	1:G:129:ILE:HD11	2.33	0.57
1:G:161:ASN:HA	1:G:164:GLU:OE1	2.05	0.57
1:H:204:LYS:HB3	1:H:285:TYR:CE2	2.39	0.57
1:K:226:CYS:SG	1:K:282:ALA:HB1	2.45	0.57
1:F:60:GLN:HG2	6:F:557:HOH:O	2.04	0.57
1:A:187:ARG:HH22	3:E:402:TYD:PB	2.28	0.57
1:K:107:ALA:HB1	1:L:78:THR:HG21	1.87	0.56
1:D:252:LEU:HD21	1:D:259:ILE:HG13	1.87	0.56
1:B:168:GLN:HB2	6:B:542:HOH:O	2.05	0.56
1:B:123:VAL:CG1	1:B:129:ILE:CD1	2.84	0.56
1:F:234:SER:O	1:F:276:ALA:HA	2.06	0.56
1:I:46:ASP:OD1	1:I:63:ASP:HB3	2.06	0.56
1:J:297:THR:O	1:J:298:PHE:C	2.44	0.56
1:H:172:VAL:HG13	1:H:243:ASP:HB3	1.88	0.55
1:A:293:ARG:HG3	1:A:293:ARG:HH11	1.72	0.55
1:E:15:ASP:O	1:E:16:ASN:HB2	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:186:LEU:HD23	1:D:186:LEU:H	1.71	0.55
1:E:230:LEU:HD21	1:E:269:GLN:HE22	1.71	0.55
1:E:218:ARG:HD2	3:E:402:TYD:O1B	2.07	0.55
1:D:22:PHE:CZ	1:E:22:PHE:HA	2.41	0.55
1:F:60:GLN:HG3	1:F:62:TRP:HZ2	1.69	0.55
1:F:41:SER:HB2	1:F:59:VAL:O	2.06	0.55
1:J:178:HIS:N	1:J:178:HIS:CD2	2.74	0.55
1:A:242:ASP:HB3	1:A:266:TRP:HB3	1.87	0.55
1:J:174:GLY:HA3	1:J:262:PRO:HG2	1.87	0.55
1:F:242:ASP:OD2	1:F:247:ARG:NH1	2.40	0.54
1:J:215[A]:LYS:H	1:J:215[A]:LYS:HD2	1.72	0.54
1:C:233:VAL:HA	1:C:255:ILE:HG23	1.90	0.54
1:G:161:ASN:N	1:G:161:ASN:OD1	2.41	0.54
1:B:163:PHE:O	1:B:179:LYS:HD2	2.08	0.54
1:K:167:LEU:HD12	1:K:168:GLN:N	2.22	0.54
1:J:204:LYS:HG3	1:J:283:SER:O	2.08	0.54
1:K:62:TRP:H	1:K:65:ILE:HD12	1.71	0.54
1:A:168:GLN:NE2	1:G:168:GLN:NE2	2.48	0.54
1:C:190:LEU:CD2	1:C:192:VAL:HG22	2.38	0.53
1:I:34:ASN:ND2	1:I:52:ASN:OD1	2.40	0.53
1:E:96:LYS:HE3	1:E:98:ILE:HD11	1.90	0.53
1:I:41:SER:HB2	1:I:59:VAL:O	2.09	0.53
1:J:140:ILE:HD11	2:K:401:COA:H143	1.89	0.53
1:G:240:LEU:HD11	1:G:247:ARG:HG2	1.90	0.53
1:D:184:ASN:HD22	1:D:185:ASP:N	2.06	0.53
1:I:122:MET:HB3	1:I:138:ILE:HD13	1.90	0.53
1:E:242:ASP:HB3	1:E:266:TRP:HB3	1.91	0.53
1:A:60:GLN:NE2	1:C:75:PRO:HB2	2.24	0.53
1:E:195:PHE:CD1	1:E:203:PRO:HD3	2.44	0.53
1:H:146:ILE:HD12	1:H:217:VAL:HG21	1.91	0.52
1:K:20:TRP:HB3	1:K:21:GLN:OE1	2.09	0.52
1:I:186:LEU:HD23	1:I:186:LEU:N	2.21	0.52
1:B:187:ARG:NH2	3:D:402:TYD:O2B	2.42	0.52
1:C:190:LEU:HD23	1:C:190:LEU:C	2.30	0.52
1:A:255:ILE:HD11	1:E:210:PHE:CZ	2.45	0.52
1:H:54:THR:HG22	1:H:56:LYS:HD3	1.91	0.52
1:H:166:LYS:HD3	1:H:179:LYS:O	2.10	0.52
1:J:198:ASP:O	1:J:200:PRO:HD3	2.10	0.52
1:A:217:VAL:O	1:E:187:ARG:NH2	2.43	0.52
1:F:112:LEU:HB3	1:F:113:PRO:CD	2.40	0.51
1:D:123:VAL:HG13	1:D:129:ILE:HD12	1.93	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:165:LEU:H	1:E:168:GLN:NE2	2.08	0.51
1:L:234:SER:O	1:L:276:ALA:HA	2.10	0.51
1:F:47:VAL:CG1	1:F:49:ILE:HD12	2.40	0.51
1:B:177:LEU:HD11	1:B:250:TYR:CE1	2.45	0.51
1:A:20:TRP:HB3	1:A:21:GLN:NE2	2.26	0.51
1:G:111:ILE:HD12	1:G:129:ILE:HD13	1.92	0.51
1:I:210:PHE:CE2	1:L:255:ILE:HG21	2.45	0.51
1:K:219:GLY:O	1:K:220:GLU:HB2	2.09	0.51
1:J:22:PHE:CZ	1:K:22:PHE:HA	2.45	0.51
1:H:139:VAL:O	1:H:140:ILE:HD12	2.10	0.51
1:C:33:ARG:HG2	1:C:51:ASP:OD1	2.09	0.51
2:D:401:COA:H143	1:F:140:ILE:HD11	1.92	0.51
1:I:302:ARG:O	1:I:306:GLU:HG2	2.11	0.51
1:H:112:LEU:HB3	1:H:113:PRO:HD2	1.91	0.51
1:C:234:SER:O	1:C:276:ALA:HA	2.11	0.51
1:J:176:SER:OG	1:J:260:TYR:HB3	2.11	0.51
1:A:72:PHE:CZ	2:B:401:COA:H22	2.45	0.51
1:B:146:ILE:HD12	1:B:217:VAL:HG21	1.92	0.51
1:L:196:GLU:OE2	1:L:202:THR:HG23	2.11	0.50
1:J:172:VAL:HG21	1:J:241:VAL:HG23	1.92	0.50
1:L:21:GLN:N	1:L:21:GLN:OE1	2.26	0.50
1:A:72:PHE:HB3	1:A:104:SER:HB2	1.93	0.50
1:H:60:GLN:HB2	1:H:62:TRP:CE2	2.47	0.50
1:C:146:ILE:HD12	1:C:217:VAL:HG21	1.92	0.50
1:C:60:GLN:HG3	1:C:62:TRP:HZ2	1.74	0.50
1:H:263:PRO:O	1:H:264:MET:HB2	2.11	0.50
2:J:401:COA:S1P	1:L:56:LYS:NZ	2.84	0.50
1:E:186:LEU:H	1:E:186:LEU:CD2	2.25	0.50
1:J:259:ILE:HG22	1:J:261:LEU:HD12	1.93	0.50
1:K:138:ILE:HD11	1:K:150:VAL:CG2	2.42	0.50
1:L:20:TRP:CE3	4:L:403:TDR:C2	2.95	0.49
1:D:41:SER:HB2	1:D:59:VAL:O	2.12	0.49
1:H:187:ARG:O	1:J:218:ARG:NH2	2.45	0.49
1:H:230:LEU:HG	1:H:280:VAL:HG22	1.93	0.49
1:H:123:VAL:CG1	1:H:129:ILE:HD11	2.38	0.49
1:H:227:LYS:HB2	1:H:283:SER:HB3	1.95	0.49
1:L:48:VAL:HB	1:L:66:HIS:ND1	2.27	0.49
1:H:234:SER:O	1:H:276:ALA:HA	2.13	0.49
1:K:150:VAL:HG12	1:K:151:GLU:HG3	1.93	0.49
1:G:15:ASP:HB3	1:G:16:ASN:ND2	2.27	0.49
1:F:221:HIS:CE1	1:F:291:TYR:HE2	2.30	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:1:MET:C	1:C:1:MET:SD	2.90	0.49
1:D:99:VAL:HG22	1:D:117:ILE:HD12	1.94	0.49
1:J:168:GLN:HE21	1:J:169:MET:N	2.11	0.49
1:I:124:GLY:HA3	1:I:140:ILE:HG22	1.93	0.49
1:I:224:LYS:HA	1:I:264:MET:CE	2.42	0.49
1:E:64:GLY:O	1:E:96:LYS:HG3	2.13	0.49
1:G:60:GLN:HE21	1:I:76:ASN:HD21	1.61	0.49
1:G:283:SER:OG	1:G:284:HIS:CD2	2.65	0.49
1:B:187:ARG:O	1:D:218:ARG:NH2	2.46	0.49
1:K:234:SER:O	1:K:276:ALA:HA	2.13	0.49
1:J:9:GLN:O	1:J:27:ALA:HA	2.12	0.49
1:E:206:TYR:HA	1:E:280:VAL:O	2.12	0.49
1:I:223:HIS:O	1:I:264:MET:HE2	2.13	0.49
1:H:223:HIS:O	1:H:264:MET:N	2.42	0.49
1:H:195:PHE:CE1	1:H:199:ILE:HD12	2.48	0.49
1:A:15:ASP:O	1:A:16:ASN:HB2	2.13	0.48
1:E:146:ILE:HD12	1:E:217:VAL:HG21	1.95	0.48
1:L:1:MET:SD	1:L:1:MET:C	2.92	0.48
1:L:215[A]:LYS:HE2	2:L:401:COA:O8A	2.13	0.48
1:C:184:ASN:CG	1:C:189:ASN:OD1	2.52	0.48
1:G:224:LYS:HB2	1:G:290:ASP:OD1	2.13	0.48
1:L:243:ASP:O	1:L:302:ARG:HG2	2.13	0.48
1:F:1:MET:C	1:F:1:MET:SD	2.92	0.48
1:K:67:ILE:HG12	1:K:73:ILE:HD11	1.96	0.48
1:E:294:ASP:HB2	1:E:297:THR:HB	1.95	0.48
1:I:72:PHE:C	1:I:72:PHE:CD2	2.86	0.48
1:J:242:ASP:OD2	1:J:247:ARG:NE	2.45	0.48
1:E:134:PRO:CD	1:E:146:ILE:HD11	2.43	0.48
1:A:236:ASN:ND2	1:A:273:SER:OG	2.45	0.48
1:L:240:LEU:HD11	1:L:247:ARG:HG2	1.95	0.48
1:B:177:LEU:N	1:B:177:LEU:HD23	2.29	0.48
1:L:67:ILE:HD13	1:L:73:ILE:CD1	2.44	0.48
1:L:67:ILE:HD13	1:L:73:ILE:HD11	1.94	0.48
1:B:168:GLN:HB3	1:B:168:GLN:HE21	1.47	0.48
1:H:35:CYS:SG	1:H:50:GLY:O	2.71	0.48
1:K:2:ILE:O	1:K:2:ILE:HG22	2.14	0.48
1:I:208:THR:O	1:L:190:LEU:HA	2.14	0.48
1:B:18:LYS:HE3	1:B:36:ASN:OD1	2.14	0.48
1:I:138:ILE:HD11	1:I:150:VAL:HG22	1.95	0.48
1:B:195:PHE:CE1	1:B:199:ILE:HD12	2.48	0.48
1:C:306:GLU:OE1	1:C:306:GLU:HA	2.14	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:3:HIS:HE1	1:J:5:LEU:HD12	1.78	0.48
1:D:263:PRO:O	1:D:264:MET:HB2	2.14	0.47
1:I:262:PRO:O	1:I:265:THR:OG1	2.32	0.47
1:A:240:LEU:HB3	1:A:268:VAL:HB	1.96	0.47
1:H:43:ILE:HD13	1:H:49:ILE:CD1	2.44	0.47
1:L:224:LYS:HB2	1:L:290:ASP:OD1	2.13	0.47
1:D:262:PRO:HG2	1:D:265:THR:CG2	2.44	0.47
1:H:226:CYS:SG	1:H:282:ALA:HB1	2.54	0.47
1:G:61:ILE:HD12	1:G:67:ILE:HD11	1.96	0.47
1:G:105:ILE:HA	1:G:123:VAL:HB	1.97	0.47
1:A:269:GLN:HG2	6:A:528:HOH:O	2.14	0.47
1:G:112:LEU:HD11	1:I:125:ALA:HB3	1.97	0.47
1:A:302:ARG:NH1	1:A:302:ARG:HG3	2.17	0.47
1:K:60:GLN:HG3	1:K:62:TRP:HZ2	1.77	0.47
1:H:43:ILE:HD13	1:H:49:ILE:HD11	1.97	0.47
1:G:42:LEU:HD23	1:G:42:LEU:C	2.35	0.47
1:D:51:ASP:O	1:D:52:ASN:HB2	2.15	0.47
1:D:187:ARG:NH1	1:D:187:ARG:HG2	2.13	0.47
1:J:142:ASN:OD1	2:J:401:COA:H2A	2.15	0.47
1:C:187[A]:ARG:NH2	1:F:217:VAL:O	2.48	0.47
1:E:219:GLY:O	1:E:220:GLU:HB2	2.15	0.47
1:F:240:LEU:HB3	1:F:268:VAL:HB	1.97	0.47
1:G:234:SER:O	1:G:276:ALA:HA	2.14	0.47
1:D:234:SER:O	1:D:276:ALA:HA	2.15	0.47
1:C:100:LYS:CE	1:C:116:LEU:HD21	2.45	0.46
1:C:193:GLY:HA3	1:F:206:TYR:CE2	2.49	0.46
1:L:168:GLN:HG3	1:L:177:LEU:HD12	1.96	0.46
1:I:264:MET:HE3	1:I:292:ILE:HD11	1.96	0.46
1:A:215:LYS:HB3	1:A:215:LYS:HE3	1.67	0.46
1:E:194:GLU:N	1:E:198:ASP:OD2	2.39	0.46
1:C:123:VAL:HG11	1:C:129:ILE:CD1	2.44	0.46
1:F:196:GLU:OE2	1:F:202:THR:OG1	2.34	0.46
1:E:135:ASP:O	1:E:136:ASN:HB2	2.15	0.46
1:A:105:ILE:HA	1:A:123:VAL:HB	1.96	0.46
1:B:75:PRO:HB3	1:C:62:TRP:HZ2	1.79	0.46
1:A:195:PHE:CD1	1:A:203:PRO:HD3	2.50	0.46
1:H:105:ILE:HA	1:H:123:VAL:HB	1.98	0.46
1:E:205:ARG:NH2	3:E:402:TYD:O4	2.47	0.46
1:F:39:ALA:HB1	1:F:40:ASN:ND2	2.31	0.46
1:L:195:PHE:CD1	1:L:203:PRO:HD3	2.50	0.46
1:E:4:LYS:HB3	1:E:4:LYS:HE2	1.63	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:60:GLN:CG	1:F:62:TRP:CZ2	2.98	0.46
1:K:65:ILE:HG22	1:K:67:ILE:CD1	2.46	0.46
1:K:249:GLU:OE1	1:K:270:TYR:OH	2.32	0.46
1:B:206:TYR:C	1:B:206:TYR:CD1	2.89	0.46
1:K:150:VAL:HG12	1:K:151:GLU:CG	2.46	0.46
1:D:105:ILE:HA	1:D:123:VAL:HB	1.97	0.45
1:J:22:PHE:CE2	1:K:22:PHE:HA	2.51	0.45
1:D:255:ILE:HD13	1:D:255:ILE:HG21	1.48	0.45
1:I:112:LEU:HD22	1:I:130:THR:HA	1.99	0.45
1:F:240:LEU:HD11	1:F:247:ARG:HG2	1.97	0.45
1:F:227:LYS:HB2	1:F:283:SER:HB3	1.99	0.45
1:G:60:GLN:HE21	1:I:76:ASN:ND2	2.14	0.45
1:F:47:VAL:HG12	1:F:49:ILE:HD12	1.99	0.45
1:E:206:TYR:C	1:E:206:TYR:CD1	2.90	0.45
1:A:234:SER:O	1:A:276:ALA:HA	2.17	0.45
1:L:213:PRO:HG2	1:L:216:GLU:HG2	1.98	0.45
1:C:123:VAL:CG1	1:C:129:ILE:HD12	2.47	0.45
1:J:140:ILE:HD11	2:K:401:COA:CEP	2.47	0.45
1:C:233:VAL:HG11	1:F:233:VAL:HG21	1.99	0.45
1:K:165:LEU:HD13	1:K:167:LEU:O	2.17	0.45
1:F:36:ASN:OD1	1:F:36:ASN:N	2.50	0.45
1:K:138:ILE:HD11	1:K:150:VAL:HG22	1.99	0.45
1:B:21:GLN:CG	1:C:24:VAL:CG2	2.90	0.45
1:A:67:ILE:HD13	1:A:73:ILE:CD1	2.45	0.45
1:A:181:HIS:O	1:A:191:SER:HA	2.17	0.45
1:I:193:GLY:HA3	1:L:206:TYR:CE2	2.52	0.45
1:L:24:VAL:HB	1:L:42:LEU:HD12	1.99	0.45
1:L:60:GLN:HB2	1:L:62:TRP:CZ2	2.51	0.45
1:H:33:ARG:NH1	1:H:33:ARG:HB3	2.31	0.45
1:H:101:LYS:HE3	1:H:101:LYS:HB2	1.60	0.45
1:H:21:GLN:N	1:H:21:GLN:OE1	2.34	0.45
1:D:123:VAL:HG13	1:D:129:ILE:CD1	2.47	0.45
1:H:275:ASP:N	1:H:275:ASP:OD2	2.44	0.45
1:G:205:ARG:NH2	1:G:284:HIS:O	2.39	0.44
1:J:201:PHE:CD1	1:J:283:SER:HB3	2.52	0.44
1:F:227:LYS:HD2	1:F:283:SER:CB	2.47	0.44
1:F:269:GLN:HG2	6:F:516:HOH:O	2.17	0.44
1:L:6:ALA:HB2	1:L:20:TRP:O	2.18	0.44
1:A:95:LEU:HB3	1:A:96:LYS:H	1.67	0.44
1:G:60:GLN:HE22	1:I:76:ASN:HD21	1.64	0.44
1:G:43:ILE:HG23	1:G:47:VAL:HG11	2.00	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:215[B]:LYS:H	1:L:215[B]:LYS:HG2	1.58	0.44
1:L:247:ARG:HG3	1:L:247:ARG:HH11	1.81	0.44
1:E:105:ILE:HA	1:E:123:VAL:HB	1.99	0.44
1:D:224:LYS:HG3	1:D:292:ILE:HD11	1.99	0.44
1:E:226:CYS:SG	1:E:282:ALA:HB1	2.58	0.44
1:B:20:TRP:HB3	1:B:21:GLN:OE1	2.17	0.44
1:I:240:LEU:HD12	1:I:248:GLU:O	2.18	0.44
1:H:75:PRO:HB2	1:I:60:GLN:NE2	2.33	0.44
1:F:182:LEU:HD13	1:F:191:SER:HB3	1.99	0.44
1:F:124:GLY:O	1:F:125:ALA:C	2.55	0.44
1:J:39:ALA:O	1:J:57:SER:HB3	2.18	0.44
1:D:187:ARG:CG	1:D:187:ARG:HH11	2.15	0.43
1:H:112:LEU:HD22	1:H:130:THR:HA	2.00	0.43
1:L:3:HIS:O	1:L:4:LYS:C	2.57	0.43
1:I:119:GLU:O	1:I:120:ASN:HB2	2.18	0.43
1:C:124:GLY:HA3	1:C:140:ILE:HG22	1.98	0.43
1:A:187:ARG:NH2	3:E:402:TYD:O1B	2.50	0.43
1:E:100:LYS:HB2	1:E:117:ILE:O	2.18	0.43
1:I:11:GLN:HA	1:I:11:GLN:OE1	2.18	0.43
1:I:226:CYS:SG	1:I:282:ALA:HB1	2.58	0.43
1:J:62:TRP:CH2	1:L:56:LYS:HD3	2.53	0.43
1:J:3:HIS:O	1:J:4:LYS:C	2.56	0.43
1:L:230:LEU:HG	1:L:280:VAL:HG22	2.01	0.43
1:E:83:LYS:HA	1:E:113:PRO:HG2	2.00	0.43
1:G:75:PRO:HB3	1:H:62:TRP:HZ2	1.84	0.43
1:I:52:ASN:O	1:I:70:ASP:HA	2.19	0.43
1:B:54:THR:HG22	1:B:56:LYS:HD3	2.00	0.43
1:L:69:ASP:O	1:L:101:LYS:HG3	2.18	0.43
1:F:218:ARG:NH2	6:F:554:HOH:O	2.50	0.43
1:E:75:PRO:HB3	1:F:62:TRP:HZ2	1.84	0.43
1:J:3:HIS:CE1	1:J:5:LEU:HD12	2.52	0.43
1:A:226:CYS:SG	1:A:282:ALA:HB1	2.59	0.43
1:B:42:LEU:HG	1:B:43:ILE:N	2.33	0.43
1:C:81:ASN:HA	1:C:81:ASN:HD22	1.40	0.43
1:B:21:GLN:HG2	1:C:24:VAL:HG21	2.01	0.43
1:H:21:GLN:CD	1:H:21:GLN:H	2.20	0.43
1:B:62:TRP:H	1:B:65:ILE:HD12	1.84	0.43
1:C:253:ASP:OD1	1:C:253:ASP:N	2.51	0.43
1:B:275:ASP:N	1:B:275:ASP:OD2	2.39	0.43
1:B:208:THR:O	1:D:190:LEU:HA	2.19	0.43
1:K:180:PHE:HE2	1:K:198:ASP:HB3	1.84	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:219:GLY:O	1:H:220:GLU:HB2	2.19	0.43
3:H:401:TYD:O1B	1:J:187:ARG:NH1	2.52	0.42
1:H:217:VAL:O	1:J:187:ARG:NH2	2.52	0.42
1:I:112:LEU:HB3	1:I:113:PRO:CD	2.48	0.42
1:L:72:PHE:CD2	1:L:72:PHE:C	2.91	0.42
1:K:32:GLY:HA3	1:K:51:ASP:OD1	2.19	0.42
1:J:219:GLY:HA2	1:J:221:HIS:CE1	2.54	0.42
1:A:218:ARG:HB3	1:A:218:ARG:HE	1.44	0.42
1:E:269:GLN:HB3	1:E:269:GLN:HE21	1.72	0.42
1:F:197:LYS:HB2	1:F:197:LYS:HE3	1.68	0.42
1:F:182:LEU:CD1	1:F:191:SER:HB3	2.49	0.42
1:H:3:HIS:CE1	1:H:5:LEU:HG	2.53	0.42
1:C:301:MET:O	1:C:304:ASN:HB2	2.20	0.42
1:K:72:PHE:HZ	2:L:401:COA:H22	1.79	0.42
1:I:233:VAL:HG11	1:L:233:VAL:HG11	2.02	0.42
1:H:270:TYR:CE1	1:H:271:LYS:HE3	2.55	0.42
1:F:135:ASP:O	1:F:136:ASN:HB2	2.19	0.42
1:F:168:GLN:HB3	1:F:168:GLN:HE21	1.64	0.42
1:I:115:ILE:HD13	1:I:115:ILE:HA	1.85	0.42
1:H:187:ARG:HG2	1:J:216:GLU:OE1	2.19	0.42
1:G:15:ASP:HB3	1:G:16:ASN:HD22	1.85	0.42
1:B:199:ILE:HG23	1:B:229:PHE:CD2	2.54	0.42
1:A:206:TYR:CE2	1:E:193:GLY:HA3	2.54	0.42
1:H:227:LYS:HG2	1:H:260:TYR:OH	2.19	0.42
1:J:215[A]:LYS:HB3	1:J:215[A]:LYS:HE3	1.73	0.42
1:H:230:LEU:HB2	1:H:259:ILE:CG2	2.49	0.42
1:G:150:VAL:O	1:G:151:GLU:HB2	2.19	0.42
1:F:81:ASN:HA	1:F:113:PRO:HB3	2.01	0.42
1:I:96:LYS:NZ	1:I:98:ILE:HD11	2.33	0.42
1:G:68:GLN:HB3	6:G:572:HOH:O	2.19	0.42
1:A:243:ASP:OD2	1:A:243:ASP:C	2.58	0.42
1:F:264:MET:CE	1:F:292:ILE:CD1	2.96	0.42
1:J:242:ASP:HB3	1:J:266:TRP:HB3	2.00	0.42
1:G:8:VAL:HG12	1:G:10:SER:H	1.85	0.42
1:F:242:ASP:HB3	1:F:266:TRP:HB3	2.01	0.42
1:L:294:ASP:HB3	1:L:297:THR:HB	2.02	0.42
1:I:187:ARG:NH2	1:L:217:VAL:O	2.53	0.42
1:D:15:ASP:OD2	1:D:33:ARG:NE	2.37	0.41
1:D:187:ARG:CG	1:D:187:ARG:NH1	2.81	0.41
1:B:24:VAL:HB	1:B:42:LEU:HD12	2.02	0.41
1:C:73:ILE:HG21	1:C:73:ILE:HD13	1.84	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:190:LEU:HD21	1:E:192:VAL:HG22	2.01	0.41
1:G:226:CYS:HA	1:G:284:HIS:CD2	2.56	0.41
1:A:33:ARG:O	1:A:34:ASN:CB	2.67	0.41
1:D:22:PHE:CE2	1:E:22:PHE:HA	2.56	0.41
1:C:255:ILE:HD11	1:F:210:PHE:CZ	2.55	0.41
1:H:60:GLN:HB2	1:H:62:TRP:NE1	2.36	0.41
1:H:206:TYR:HA	1:H:280:VAL:O	2.20	0.41
1:D:213:PRO:CB	1:D:215:LYS:HE2	2.51	0.41
1:F:60:GLN:HB2	1:F:62:TRP:CZ2	2.55	0.41
1:L:247:ARG:HG3	1:L:247:ARG:NH1	2.35	0.41
1:E:294:ASP:HB2	1:E:297:THR:CB	2.51	0.41
1:A:232:CYS:SG	1:A:237:CYS:HB2	2.61	0.41
1:B:105:ILE:HA	1:B:123:VAL:HB	2.02	0.41
1:A:21:GLN:N	1:A:21:GLN:HE21	2.07	0.41
1:K:138:ILE:CD1	1:K:150:VAL:HG23	2.50	0.41
1:J:206:TYR:HA	1:J:280:VAL:O	2.21	0.41
1:I:133:VAL:HA	1:I:134:PRO:HD3	1.91	0.41
1:G:183:VAL:O	1:G:189:ASN:HA	2.21	0.41
1:A:186:LEU:HD12	1:A:186:LEU:HA	1.94	0.41
1:G:146:ILE:HD12	1:G:217:VAL:HG21	2.03	0.41
1:I:219:GLY:O	1:I:220:GLU:HB2	2.21	0.41
1:F:215:LYS:CE	1:F:215:LYS:H	2.17	0.41
1:C:60:GLN:CG	1:C:62:TRP:CZ2	2.98	0.41
1:G:123:VAL:HG11	1:G:129:ILE:HD11	2.02	0.41
1:G:247:ARG:HH21	1:G:247:ARG:HD2	1.76	0.41
1:K:138:ILE:CD1	1:K:150:VAL:CG2	2.98	0.41
1:J:215[A]:LYS:H	1:J:215[A]:LYS:CD	2.32	0.41
1:B:36:ASN:ND2	6:B:508:HOH:O	2.54	0.41
1:J:206:TYR:C	1:J:206:TYR:CD1	2.93	0.41
1:L:214:ASN:HB3	6:L:547:HOH:O	2.20	0.41
1:D:133:VAL:HA	1:D:134:PRO:HD3	1.93	0.41
1:G:190:LEU:HA	1:K:208:THR:O	2.20	0.41
1:B:218:ARG:HB3	1:B:218:ARG:HE	1.76	0.41
1:H:56:LYS:HD2	1:H:56:LYS:HA	1.88	0.41
1:J:202:THR:HA	1:J:203:PRO:HD3	1.77	0.41
1:D:120:ASN:O	1:E:86:ARG:NH2	2.54	0.41
1:G:18:LYS:N	1:G:18:LYS:HD3	2.36	0.41
1:D:24:VAL:HG22	1:F:21:GLN:HG3	2.02	0.40
1:L:112:LEU:HB3	1:L:113:PRO:HD2	2.01	0.40
1:I:13:ILE:HG23	1:I:17:THR:HG21	2.02	0.40
1:F:178:HIS:N	1:F:178:HIS:CD2	2.89	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:255:ILE:N	1:I:255:ILE:HD12	2.36	0.40
1:L:226:CYS:SG	1:L:282:ALA:HB1	2.61	0.40
1:I:67:ILE:HG22	1:I:67:ILE:O	2.20	0.40
1:E:176:SER:OG	1:E:260:TYR:HB3	2.21	0.40
1:G:44:GLU:HB3	1:G:45:ASN:H	1.77	0.40
1:C:255:ILE:HD12	1:C:255:ILE:N	2.36	0.40
1:L:42:LEU:O	1:L:60:GLN:HA	2.22	0.40
1:A:255:ILE:CD1	1:E:210:PHE:CZ	3.05	0.40
1:D:208:THR:HA	1:D:278:LEU:O	2.21	0.40
1:L:172:VAL:HG21	1:L:241:VAL:HG23	2.03	0.40
1:L:183:VAL:O	1:L:189:ASN:HA	2.21	0.40
1:E:61:ILE:HD12	1:E:67:ILE:HD11	2.04	0.40
1:G:187:ARG:NH2	1:K:217:VAL:O	2.50	0.40
1:B:178:HIS:N	1:B:178:HIS:CD2	2.90	0.40
1:I:24:VAL:O	1:I:42:LEU:HA	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:G:566:HOH:O	6:J:526:HOH:O[1_545]	1.99	0.21

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	279/312 (89%)	269 (96%)	9 (3%)	1 (0%)	39	42
1	B	284/312 (91%)	270 (95%)	14 (5%)	0	100	100
1	C	280/312 (90%)	270 (96%)	10 (4%)	0	100	100
1	D	277/312 (89%)	263 (95%)	13 (5%)	1 (0%)	39	42

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	E	280/312 (90%)	266 (95%)	13 (5%)	1 (0%)	39	42
1	F	288/312 (92%)	268 (93%)	20 (7%)	0	100	100
1	G	278/312 (89%)	267 (96%)	10 (4%)	1 (0%)	39	42
1	H	272/312 (87%)	252 (93%)	19 (7%)	1 (0%)	39	42
1	I	279/312 (89%)	261 (94%)	16 (6%)	2 (1%)	26	25
1	J	270/312 (86%)	258 (96%)	9 (3%)	3 (1%)	17	14
1	K	280/312 (90%)	261 (93%)	16 (6%)	3 (1%)	17	14
1	L	281/312 (90%)	260 (92%)	19 (7%)	2 (1%)	26	25
All	All	3348/3744 (89%)	3165 (94%)	168 (5%)	15 (0%)	39	42

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	197	LYS
1	H	14	GLY
1	K	3	HIS
1	J	297	THR
1	E	197	LYS
1	G	20	TRP
1	I	14	GLY
1	J	4	LYS
1	L	14	GLY
1	I	50	GLY
1	K	50	GLY
1	K	164	GLU
1	L	4	LYS
1	D	151	GLU
1	J	200	PRO

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	246/272 (90%)	220 (89%)	26 (11%)	8	7
1	B	251/272 (92%)	230 (92%)	21 (8%)	14	13
1	C	245/272 (90%)	224 (91%)	21 (9%)	13	12
1	D	244/272 (90%)	218 (89%)	26 (11%)	8	7
1	E	247/272 (91%)	220 (89%)	27 (11%)	8	7
1	F	252/272 (93%)	231 (92%)	21 (8%)	14	13
1	G	245/272 (90%)	225 (92%)	20 (8%)	14	13
1	H	239/272 (88%)	211 (88%)	28 (12%)	7	5
1	I	245/272 (90%)	228 (93%)	17 (7%)	19	20
1	J	237/272 (87%)	206 (87%)	31 (13%)	5	4
1	K	247/272 (91%)	225 (91%)	22 (9%)	12	11
1	L	246/272 (90%)	217 (88%)	29 (12%)	6	5
All	All	2944/3264 (90%)	2655 (90%)	289 (10%)	10	9

All (289) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	34	ASN
1	A	36	ASN
1	A	46	ASP
1	A	81	ASN
1	A	104	SER
1	A	116	LEU
1	A	150	VAL
1	A	161	ASN
1	A	164	GLU
1	A	168	GLN
1	A	171	LYS
1	A	173	LYS
1	A	186	LEU
1	A	196	GLU
1	A	215	LYS
1	A	218	ARG
1	A	234	SER
1	A	236	ASN
1	A	245	GLU
1	A	255	ILE
1	A	269	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	270	TYR
1	A	296	SER
1	A	300	GLN
1	A	302	ARG
1	B	4	LYS
1	B	21	GLN
1	B	40	ASN
1	B	42	LEU
1	B	56	LYS
1	B	84	GLN
1	B	115	ILE
1	B	164	GLU
1	B	165	LEU
1	B	168	GLN
1	B	171	LYS
1	B	173	LYS
1	B	182	LEU
1	B	187	ARG
1	B	191	SER
1	B	194	GLU
1	B	197	LYS
1	B	233	VAL
1	B	248	GLU
1	B	270	TYR
1	B	275	ASP
1	C	4	LYS
1	C	21	GLN
1	C	34	ASN
1	C	60	GLN
1	C	70	ASP
1	C	81	ASN
1	C	104	SER
1	C	116	LEU
1	C	164	GLU
1	C	171	LYS
1	C	186	LEU
1	C	196	GLU
1	C	197	LYS
1	C	202	THR
1	C	233	VAL
1	C	234	SER
1	C	247	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	254	SER
1	C	255	ILE
1	C	270	TYR
1	C	304	ASN
1	D	11	GLN
1	D	15	ASP
1	D	16	ASN
1	D	34	ASN
1	D	37	ILE
1	D	42	LEU
1	D	60	GLN
1	D	115	ILE
1	D	120	ASN
1	D	165	LEU
1	D	166	LYS
1	D	168	GLN
1	D	173	LYS
1	D	179	LYS
1	D	184	ASN
1	D	186	LEU
1	D	187	ARG
1	D	196	GLU
1	D	202	THR
1	D	215	LYS
1	D	269	GLN
1	D	270	TYR
1	D	279	LEU
1	D	293	ARG
1	D	296	SER
1	D	304	ASN
1	E	1	MET
1	E	4	LYS
1	E	21	GLN
1	E	34	ASN
1	E	70	ASP
1	E	82	ASP
1	E	94	TYR
1	E	115	ILE
1	E	120	ASN
1	E	131	LYS
1	E	140	ILE
1	E	151	GLU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	162	ASN
1	E	165	LEU
1	E	173	LYS
1	E	184	ASN
1	E	186	LEU
1	E	196	GLU
1	E	198	ASP
1	E	233	VAL
1	E	248	GLU
1	E	269	GLN
1	E	270	TYR
1	E	274	LYS
1	E	288	SER
1	E	294	ASP
1	E	299	LYS
1	F	21	GLN
1	F	36	ASN
1	F	60	GLN
1	F	84	GLN
1	F	86	ARG
1	F	88	LYS
1	F	115	ILE
1	F	140	ILE
1	F	163	PHE
1	F	164	GLU
1	F	168	GLN
1	F	173	LYS
1	F	183	VAL
1	F	196	GLU
1	F	205	ARG
1	F	215	LYS
1	F	234	SER
1	F	254	SER
1	F	269	GLN
1	F	270	TYR
1	F	296	SER
1	G	21	GLN
1	G	52	ASN
1	G	60	GLN
1	G	116	LEU
1	G	131	LYS
1	G	161	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	G	164	GLU
1	G	166	LYS
1	G	171	LYS
1	G	173	LYS
1	G	184	ASN
1	G	196	GLU
1	G	197	LYS
1	G	205	ARG
1	G	215	LYS
1	G	234	SER
1	G	270	TYR
1	G	274	LYS
1	G	296	SER
1	G	305	LEU
1	H	4	LYS
1	H	11	GLN
1	H	12	ASN
1	H	36	ASN
1	H	56	LYS
1	H	60	GLN
1	H	96	LYS
1	H	101	LYS
1	H	115	ILE
1	H	122	MET
1	H	140	ILE
1	H	150	VAL
1	H	168	GLN
1	H	171	LYS
1	H	173	LYS
1	H	186	LEU
1	H	189	ASN
1	H	190	LEU
1	H	192	VAL
1	H	237	CYS
1	H	245	GLU
1	H	269	GLN
1	H	270	TYR
1	H	274	LYS
1	H	279	LEU
1	H	288	SER
1	H	296	SER
1	H	301	MET

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	I	18	LYS
1	I	81	ASN
1	I	163	PHE
1	I	165	LEU
1	I	166	LYS
1	I	167	LEU
1	I	168	GLN
1	I	177	LEU
1	I	186	LEU
1	I	224	LYS
1	I	255	ILE
1	I	265	THR
1	I	269	GLN
1	I	270	TYR
1	I	293	ARG
1	I	296	SER
1	I	302	ARG
1	J	4	LYS
1	J	9	GLN
1	J	21	GLN
1	J	33	ARG
1	J	37	ILE
1	J	40	ASN
1	J	56	LYS
1	J	60	GLN
1	J	81	ASN
1	J	96	LYS
1	J	104	SER
1	J	115	ILE
1	J	116	LEU
1	J	140	ILE
1	J	165	LEU
1	J	168	GLN
1	J	171	LYS
1	J	178	HIS
1	J	179	LYS
1	J	192	VAL
1	J	196	GLU
1	J	197	LYS
1	J	198	ASP
1	J	202	THR
1	J	215[A]	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	J	215[B]	LYS
1	J	234	SER
1	J	259	ILE
1	J	269	GLN
1	J	270	TYR
1	J	296	SER
1	K	4	LYS
1	K	10	SER
1	K	11	GLN
1	K	34	ASN
1	K	41	SER
1	K	60	GLN
1	K	116	LEU
1	K	131	LYS
1	K	165	LEU
1	K	167	LEU
1	K	171	LYS
1	K	179	LYS
1	K	186	LEU
1	K	191	SER
1	K	215[A]	LYS
1	K	215[B]	LYS
1	K	234	SER
1	K	270	TYR
1	K	274	LYS
1	K	293	ARG
1	K	296	SER
1	K	299	LYS
1	L	4	LYS
1	L	11	GLN
1	L	16	ASN
1	L	18	LYS
1	L	21	GLN
1	L	34	ASN
1	L	41	SER
1	L	57	SER
1	L	60	GLN
1	L	104	SER
1	L	119	GLU
1	L	120	ASN
1	L	131	LYS
1	L	140	ILE

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	L	171	LYS
1	L	173	LYS
1	L	196	GLU
1	L	202	THR
1	L	215[A]	LYS
1	L	215[B]	LYS
1	L	218	ARG
1	L	233	VAL
1	L	254	SER
1	L	269	GLN
1	L	270	TYR
1	L	274	LYS
1	L	293	ARG
1	L	294	ASP
1	L	296	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (64) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	60	GLN
1	A	81	ASN
1	A	189	ASN
1	A	236	ASN
1	A	300	GLN
1	B	168	GLN
1	B	189	ASN
1	B	221	HIS
1	C	66	HIS
1	C	81	ASN
1	C	184	ASN
1	C	221	HIS
1	D	184	ASN
1	D	189	ASN
1	D	221	HIS
1	D	236	ASN
1	D	304	ASN
1	E	21	GLN
1	E	162	ASN
1	E	168	GLN
1	E	184	ASN
1	E	189	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	E	269	GLN
1	F	40	ASN
1	F	168	GLN
1	F	189	ASN
1	F	221	HIS
1	F	246	ASN
1	G	16	ASN
1	G	60	GLN
1	G	161	ASN
1	G	168	GLN
1	G	221	HIS
1	G	284	HIS
1	H	16	ASN
1	H	34	ASN
1	H	36	ASN
1	H	66	HIS
1	H	76	ASN
1	H	81	ASN
1	H	168	GLN
1	H	221	HIS
1	H	236	ASN
1	H	284	HIS
1	I	81	ASN
1	I	168	GLN
1	I	189	ASN
1	I	221	HIS
1	I	300	GLN
1	I	304	ASN
1	J	40	ASN
1	J	60	GLN
1	J	81	ASN
1	J	168	GLN
1	J	184	ASN
1	J	221	HIS
1	J	269	GLN
1	K	60	GLN
1	K	136	ASN
1	K	184	ASN
1	K	189	ASN
1	K	236	ASN
1	L	52	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 ⓘ

Of 38 ligands modelled in this entry, 5 are monoatomic - leaving 33 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	COA	A	401	-	40,50,50	0.84	2 (5%)	50,75,75	2.22	14 (28%)
3	TYD	A	402	-	19,26,26	0.65	0	27,40,40	2.22	4 (14%)
4	TDR	A	403	-	5,9,9	1.16	0	7,12,12	7.31	5 (71%)
2	COA	B	401	-	40,50,50	0.75	1 (2%)	50,75,75	1.93	13 (26%)
3	TYD	B	402	-	19,26,26	0.49	0	27,40,40	2.05	5 (18%)
4	TDR	B	403	-	5,9,9	0.98	0	7,12,12	6.30	5 (71%)
2	COA	C	401	-	40,50,50	0.84	2 (5%)	50,75,75	2.51	12 (24%)
3	TYD	C	402	-	19,26,26	0.58	0	27,40,40	2.10	6 (22%)
4	TDR	C	403	-	5,9,9	1.02	0	7,12,12	5.45	6 (85%)
2	COA	D	401	-	40,50,50	0.70	1 (2%)	50,75,75	1.93	11 (22%)
3	TYD	D	402	-	19,26,26	0.65	0	27,40,40	1.91	6 (22%)
4	TDR	D	403	-	5,9,9	1.09	0	7,12,12	5.74	6 (85%)
2	COA	E	401	-	40,50,50	0.69	1 (2%)	50,75,75	2.23	12 (24%)
3	TYD	E	402	-	19,26,26	0.54	0	27,40,40	2.13	7 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	TDR	E	403	-	5,9,9	0.76	0	7,12,12	5.79	6 (85%)
2	COA	F	401	-	40,50,50	0.72	1 (2%)	50,75,75	2.10	12 (24%)
3	TYD	F	402	-	19,26,26	0.49	0	27,40,40	1.87	5 (18%)
4	TDR	F	403	-	5,9,9	0.84	0	7,12,12	6.20	6 (85%)
2	COA	G	401	-	40,50,50	0.77	1 (2%)	50,75,75	2.26	13 (26%)
3	TYD	G	402	-	19,26,26	0.57	0	27,40,40	1.96	8 (29%)
2	COA	G	403	-	40,50,50	0.70	0	50,75,75	1.98	12 (24%)
3	TYD	H	401	-	19,26,26	0.63	0	27,40,40	2.15	5 (18%)
2	COA	I	401	-	40,50,50	0.79	1 (2%)	50,75,75	1.92	14 (28%)
3	TYD	I	402	-	19,26,26	0.60	0	27,40,40	1.78	5 (18%)
2	COA	J	401	-	40,50,50	0.62	0	50,75,75	2.47	13 (26%)
3	TYD	J	402	-	19,26,26	0.64	0	27,40,40	2.15	5 (18%)
4	TDR	J	403	-	5,9,9	0.95	0	7,12,12	5.81	6 (85%)
2	COA	K	401	-	40,50,50	0.68	1 (2%)	50,75,75	1.91	10 (20%)
3	TYD	K	402	-	19,26,26	0.55	0	27,40,40	2.29	6 (22%)
4	TDR	K	403	-	5,9,9	0.70	0	7,12,12	6.35	5 (71%)
2	COA	L	401	-	40,50,50	0.72	1 (2%)	50,75,75	2.14	11 (22%)
3	TYD	L	402	-	19,26,26	0.61	0	27,40,40	2.02	4 (14%)
4	TDR	L	403	-	5,9,9	0.57	0	7,12,12	6.48	7 (100%)

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	COA	A	401	-	-	0/44/64/64	0/3/3/3
3	TYD	A	402	-	-	0/12/28/28	0/2/2/2
4	TDR	A	403	-	-	0/0/0/0	0/1/1/1
2	COA	B	401	-	-	0/44/64/64	0/3/3/3
3	TYD	B	402	-	-	0/12/28/28	0/2/2/2
4	TDR	B	403	-	-	0/0/0/0	0/1/1/1
2	COA	C	401	-	-	0/44/64/64	0/3/3/3
3	TYD	C	402	-	-	0/12/28/28	0/2/2/2
4	TDR	C	403	-	-	0/0/0/0	0/1/1/1
2	COA	D	401	-	-	0/44/64/64	0/3/3/3
3	TYD	D	402	-	-	0/12/28/28	0/2/2/2
4	TDR	D	403	-	-	0/0/0/0	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	COA	E	401	-	-	0/44/64/64	0/3/3/3
3	TYD	E	402	-	-	0/12/28/28	0/2/2/2
4	TDR	E	403	-	-	0/0/0/0	0/1/1/1
2	COA	F	401	-	-	0/44/64/64	0/3/3/3
3	TYD	F	402	-	-	0/12/28/28	0/2/2/2
4	TDR	F	403	-	-	0/0/0/0	0/1/1/1
2	COA	G	401	-	-	0/44/64/64	0/3/3/3
3	TYD	G	402	-	-	0/12/28/28	0/2/2/2
2	COA	G	403	-	-	0/44/64/64	0/3/3/3
3	TYD	H	401	-	-	0/12/28/28	0/2/2/2
2	COA	I	401	-	-	0/44/64/64	0/3/3/3
3	TYD	I	402	-	-	0/12/28/28	0/2/2/2
2	COA	J	401	-	-	0/44/64/64	0/3/3/3
3	TYD	J	402	-	-	0/12/28/28	0/2/2/2
4	TDR	J	403	-	-	0/0/0/0	0/1/1/1
2	COA	K	401	-	-	0/44/64/64	0/3/3/3
3	TYD	K	402	-	-	0/12/28/28	0/2/2/2
4	TDR	K	403	-	-	0/0/0/0	0/1/1/1
2	COA	L	401	-	-	0/44/64/64	0/3/3/3
3	TYD	L	402	-	-	0/12/28/28	0/2/2/2
4	TDR	L	403	-	-	0/0/0/0	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	COA	O4B-C1B	2.14	1.43	1.41
2	G	401	COA	O4B-C1B	2.15	1.43	1.41
2	C	401	COA	C2A-N3A	2.19	1.36	1.32
2	E	401	COA	O4B-C1B	2.35	1.44	1.41
2	B	401	COA	O4B-C1B	2.37	1.44	1.41
2	A	401	COA	O4B-C1B	2.38	1.44	1.41
2	F	401	COA	O4B-C1B	2.43	1.44	1.41
2	K	401	COA	O4B-C1B	2.44	1.44	1.41
2	I	401	COA	O4B-C1B	2.46	1.44	1.41
2	L	401	COA	O4B-C1B	2.80	1.44	1.41
2	A	401	COA	C2A-N3A	2.96	1.37	1.32
2	C	401	COA	O4B-C1B	3.47	1.45	1.41

All (265) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	403	TDR	N1-C2-N3	-15.58	118.39	128.33

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	COA	N3A-C2A-N1A	-12.71	119.16	128.89
4	K	403	TDR	N1-C2-N3	-11.81	120.80	128.33
2	J	401	COA	N3A-C2A-N1A	-11.71	119.93	128.89
4	L	403	TDR	N1-C2-N3	-11.61	120.92	128.33
4	E	403	TDR	N1-C2-N3	-10.96	121.34	128.33
4	B	403	TDR	N1-C2-N3	-10.93	121.36	128.33
4	J	403	TDR	N1-C2-N3	-10.63	121.55	128.33
2	E	401	COA	N3A-C2A-N1A	-9.97	121.26	128.89
4	F	403	TDR	N1-C2-N3	-9.57	122.23	128.33
4	D	403	TDR	N1-C2-N3	-9.47	122.29	128.33
2	G	401	COA	N3A-C2A-N1A	-9.36	121.72	128.89
2	L	401	COA	N3A-C2A-N1A	-9.23	121.83	128.89
2	G	403	COA	N3A-C2A-N1A	-8.81	122.14	128.89
2	A	401	COA	N3A-C2A-N1A	-8.74	122.20	128.89
2	F	401	COA	N3A-C2A-N1A	-8.46	122.42	128.89
4	F	403	TDR	C5-C4-N3	-8.42	115.76	125.14
4	C	403	TDR	N1-C2-N3	-8.34	123.01	128.33
2	D	401	COA	N3A-C2A-N1A	-8.22	122.60	128.89
4	B	403	TDR	C5-C6-N1	-7.30	118.72	125.23
4	A	403	TDR	C5-C6-N1	-7.23	118.78	125.23
2	K	401	COA	N3A-C2A-N1A	-7.10	123.46	128.89
4	D	403	TDR	C5-C4-N3	-7.02	117.32	125.14
2	B	401	COA	N3A-C2A-N1A	-6.78	123.70	128.89
2	I	401	COA	N3A-C2A-N1A	-6.72	123.75	128.89
4	C	403	TDR	C5-C4-N3	-6.72	117.65	125.14
3	A	402	TYD	C5-C4-N3	-6.65	117.74	125.14
3	K	402	TYD	C5-C4-N3	-6.54	117.85	125.14
4	L	403	TDR	C5-C6-N1	-6.06	119.82	125.23
4	K	403	TDR	C5-C4-N3	-6.05	118.40	125.14
4	B	403	TDR	C5-C4-N3	-5.95	118.51	125.14
4	J	403	TDR	C5-C4-N3	-5.81	118.67	125.14
2	G	401	COA	CEP-CBP-CCP	-5.70	101.11	108.50
3	L	402	TYD	C5-C4-N3	-5.67	118.82	125.14
3	H	401	TYD	C5-C4-N3	-5.67	118.82	125.14
4	C	403	TDR	C5-C6-N1	-5.55	120.28	125.23
3	E	402	TYD	C5-C4-N3	-5.38	119.15	125.14
4	K	403	TDR	C5-C6-N1	-5.26	120.54	125.23
4	L	403	TDR	C5-C4-N3	-5.25	119.30	125.14
4	E	403	TDR	C5-C4-N3	-5.18	119.36	125.14
2	K	401	COA	C7P-C6P-C5P	-5.10	103.90	112.31
2	L	401	COA	C2P-C3P-N4P	-5.05	102.39	112.37
3	F	402	TYD	C5-C4-N3	-4.89	119.69	125.14

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	COA	C2P-C3P-N4P	-4.75	103.00	112.37
3	D	402	TYD	C5-C4-N3	-4.63	119.98	125.14
3	G	402	TYD	C5-C4-N3	-4.60	120.02	125.14
2	A	401	COA	C2P-C3P-N4P	-4.54	103.40	112.37
3	C	402	TYD	C5-C4-N3	-4.51	120.11	125.14
3	J	402	TYD	C5-C4-N3	-4.49	120.14	125.14
3	I	402	TYD	C5-C4-N3	-4.40	120.23	125.14
3	B	402	TYD	C5-C4-N3	-4.37	120.27	125.14
2	E	401	COA	O3B-P3B-O7A	-4.14	96.78	107.11
2	I	401	COA	O3B-P3B-O7A	-4.11	96.84	107.11
2	J	401	COA	P2A-O3A-P1A	-4.09	121.25	132.73
2	K	401	COA	C4A-C5A-N7A	-3.85	105.94	109.48
2	J	401	COA	O5P-C5P-N4P	-3.83	115.33	122.94
2	C	401	COA	O3B-P3B-O7A	-3.80	97.61	107.11
2	A	401	COA	C4A-C5A-N7A	-3.76	106.02	109.48
4	J	403	TDR	C5-C6-N1	-3.72	121.91	125.23
3	C	402	TYD	C3'-C2'-C1'	-3.69	93.52	102.40
2	J	401	COA	O6A-CCP-CBP	-3.59	104.78	110.55
2	E	401	COA	P2A-O3A-P1A	-3.49	122.94	132.73
2	J	401	COA	C2B-C1B-N9A	-3.45	109.03	114.29
2	G	401	COA	O5P-C5P-N4P	-3.42	116.14	122.94
4	D	403	TDR	C5-C6-N1	-3.42	122.18	125.23
2	G	401	COA	P2A-O3A-P1A	-3.34	123.34	132.73
2	F	401	COA	C1B-N9A-C4A	-3.31	121.94	126.94
2	C	401	COA	C2P-C3P-N4P	-3.29	105.88	112.37
2	A	401	COA	C1B-N9A-C4A	-3.25	122.04	126.94
2	B	401	COA	C7P-C6P-C5P	-3.23	106.98	112.31
3	H	401	TYD	O3A-PA-O5'	-3.16	94.55	102.94
2	A	401	COA	O3B-P3B-O7A	-3.15	99.24	107.11
2	F	401	COA	C4A-C5A-N7A	-3.13	106.60	109.48
2	B	401	COA	C4A-C5A-N7A	-3.13	106.60	109.48
3	K	402	TYD	C2'-C1'-N1	-3.12	106.58	114.16
2	E	401	COA	C2P-C3P-N4P	-3.11	106.23	112.37
2	I	401	COA	C2P-C3P-N4P	-3.09	106.27	112.37
2	F	401	COA	C2P-C3P-N4P	-3.06	106.32	112.37
2	K	401	COA	C2P-C3P-N4P	-3.05	106.34	112.37
2	F	401	COA	O5P-C5P-N4P	-2.99	116.99	122.94
2	L	401	COA	O3B-P3B-O7A	-2.99	99.65	107.11
2	E	401	COA	CDP-CBP-CCP	-2.98	104.64	108.50
2	I	401	COA	CEP-CBP-CCP	-2.93	104.70	108.50
4	E	403	TDR	C5-C6-N1	-2.92	122.62	125.23
2	A	401	COA	O5P-C5P-N4P	-2.88	117.22	122.94

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	401	COA	C7P-C6P-C5P	-2.84	107.63	112.31
2	L	401	COA	O5P-C5P-N4P	-2.83	117.32	122.94
2	G	401	COA	C4A-C5A-N7A	-2.82	106.88	109.48
2	L	401	COA	P2A-O3A-P1A	-2.80	124.87	132.73
2	D	401	COA	C2P-C3P-N4P	-2.75	106.94	112.37
4	F	403	TDR	C5-C6-N1	-2.75	122.78	125.23
2	J	401	COA	C2B-C3B-C4B	-2.74	98.14	103.29
2	B	401	COA	CDP-CBP-CAP	-2.74	104.34	109.34
2	D	401	COA	CDP-CBP-CAP	-2.74	104.34	109.34
3	E	402	TYD	O3A-PA-O5'	-2.73	95.69	102.94
2	C	401	COA	P2A-O3A-P1A	-2.69	125.19	132.73
2	D	401	COA	C4A-C5A-N7A	-2.68	107.01	109.48
2	G	403	COA	C4A-C5A-N7A	-2.68	107.01	109.48
2	J	401	COA	C2P-C3P-N4P	-2.62	107.21	112.37
2	C	401	COA	CEP-CBP-CCP	-2.52	105.23	108.50
2	K	401	COA	O3B-P3B-O7A	-2.51	100.84	107.11
3	D	402	TYD	O3'-C3'-C2'	-2.51	102.44	110.74
2	D	401	COA	O3B-P3B-O7A	-2.51	100.85	107.11
3	E	402	TYD	C2'-C1'-N1	-2.50	108.07	114.16
2	G	401	COA	C2P-C3P-N4P	-2.48	107.47	112.37
3	G	402	TYD	C2'-C1'-N1	-2.47	108.14	114.16
2	A	401	COA	O3B-C3B-C4B	-2.41	100.52	109.99
3	L	402	TYD	C2'-C1'-N1	-2.37	108.40	114.16
2	L	401	COA	O3B-C3B-C4B	-2.37	100.70	109.99
2	E	401	COA	C1B-N9A-C4A	-2.36	123.39	126.94
2	B	401	COA	C6P-C7P-N8P	-2.31	106.80	111.88
2	J	401	COA	C7P-C6P-C5P	-2.31	108.50	112.31
3	F	402	TYD	O5'-PA-O1A	-2.30	100.70	109.62
3	I	402	TYD	O3'-C3'-C2'	-2.30	103.14	110.74
3	B	402	TYD	O5'-PA-O1A	-2.28	100.78	109.62
2	I	401	COA	O3A-P1A-O5B	-2.23	97.02	102.94
2	D	401	COA	CAP-C9P-N8P	-2.22	111.54	116.47
2	K	401	COA	O3B-C3B-C4B	-2.22	101.28	109.99
2	I	401	COA	C4A-C5A-N7A	-2.19	107.47	109.48
2	L	401	COA	C4A-C5A-N7A	-2.19	107.47	109.48
2	B	401	COA	P2A-O3A-P1A	-2.15	126.68	132.73
2	J	401	COA	O4B-C1B-N9A	-2.14	103.62	108.10
2	J	401	COA	C1B-N9A-C4A	-2.12	123.73	126.94
2	G	403	COA	O3B-P3B-O7A	-2.10	101.87	107.11
2	K	401	COA	C1B-N9A-C4A	-2.09	123.79	126.94
2	I	401	COA	O3B-C3B-C2B	-2.08	103.42	111.51
4	L	403	TDR	CM5-C5-C6	-2.07	117.51	120.65

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	COA	O5B-P1A-O1A	-2.06	101.61	109.62
2	I	401	COA	O5P-C5P-C6P	-2.01	118.51	121.98
3	E	402	TYD	O2A-PA-O3A	2.00	114.17	105.09
2	G	401	COA	O6A-CCP-CBP	2.02	113.80	110.55
3	H	401	TYD	O3B-PB-O2B	2.03	115.11	107.38
3	E	402	TYD	O3B-PB-O2B	2.05	115.17	107.38
2	I	401	COA	O5A-P2A-O4A	2.05	123.62	112.53
2	G	403	COA	O6A-CCP-CBP	2.05	113.85	110.55
2	G	403	COA	CDP-CBP-CCP	2.07	111.18	108.50
2	G	401	COA	O9A-P3B-O7A	2.07	117.24	110.58
2	I	401	COA	C7P-N8P-C9P	2.13	126.74	122.53
2	C	401	COA	CAP-C9P-N8P	2.13	121.20	116.47
2	C	401	COA	O2B-C2B-C3B	2.14	117.33	111.16
2	I	401	COA	C2B-C1B-N9A	2.15	117.58	114.29
2	B	401	COA	O8A-P3B-O7A	2.17	117.56	110.58
2	F	401	COA	C3P-N4P-C5P	2.18	127.08	122.79
3	F	402	TYD	O4'-C1'-N1	2.20	111.53	107.72
2	E	401	COA	CEP-CBP-CDP	2.21	113.72	109.28
2	G	403	COA	O3A-P1A-O5B	2.22	108.82	102.94
4	F	403	TDR	C6-N1-C2	2.22	119.04	115.47
2	F	401	COA	O8A-P3B-O7A	2.24	117.80	110.58
2	D	401	COA	O8A-P3B-O7A	2.25	117.83	110.58
2	E	401	COA	C2B-C1B-N9A	2.26	117.74	114.29
2	B	401	COA	O5A-P2A-O4A	2.26	124.80	112.53
2	G	403	COA	CEP-CBP-CAP	2.27	113.49	109.34
3	D	402	TYD	O4'-C1'-N1	2.27	111.65	107.72
2	I	401	COA	O2A-P1A-O3A	2.28	115.43	105.09
2	F	401	COA	O9A-P3B-O7A	2.28	117.93	110.58
3	G	402	TYD	O3B-PB-O2B	2.28	116.07	107.38
2	A	401	COA	CEP-CBP-CCP	2.28	111.46	108.50
2	B	401	COA	C3P-N4P-C5P	2.32	127.36	122.79
2	A	401	COA	O4B-C4B-C5B	2.33	117.64	109.32
2	A	401	COA	O9A-P3B-O7A	2.33	118.09	110.58
2	E	401	COA	C2A-N1A-C6A	2.34	122.95	118.77
3	I	402	TYD	C2'-C3'-C4'	2.37	107.69	102.77
2	C	401	COA	O8A-P3B-O7A	2.38	118.25	110.58
3	B	402	TYD	C3'-C2'-C1'	2.39	108.15	102.40
3	A	402	TYD	C5M-C5-C4	2.39	123.14	120.05
3	J	402	TYD	O3A-PA-O5'	2.40	109.30	102.94
3	H	401	TYD	O2A-PA-O3A	2.42	116.05	105.09
2	G	403	COA	P3B-O3B-C3B	2.42	127.37	121.56
2	G	403	COA	C3P-N4P-C5P	2.43	127.56	122.79

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	I	401	COA	O9A-P3B-O7A	2.43	118.39	110.58
3	K	402	TYD	O2A-PA-O3A	2.43	116.14	105.09
2	L	401	COA	P3B-O3B-C3B	2.44	127.41	121.56
2	A	401	COA	C6P-C5P-N4P	2.46	120.73	116.46
2	G	401	COA	P3B-O3B-C3B	2.47	127.48	121.56
3	G	402	TYD	O3'-C3'-C2'	2.49	118.97	110.74
2	F	401	COA	O5A-P2A-O3A	2.52	116.52	105.09
2	B	401	COA	C7P-N8P-C9P	2.53	127.53	122.53
2	L	401	COA	C7P-N8P-C9P	2.60	127.67	122.53
2	E	401	COA	C3P-N4P-C5P	2.62	127.94	122.79
4	F	403	TDR	CM5-C5-C4	2.62	123.44	120.05
2	G	401	COA	C7P-N8P-C9P	2.66	127.79	122.53
3	G	402	TYD	O4'-C4'-C5'	2.67	118.87	109.32
2	G	403	COA	O2A-P1A-O1A	2.67	127.02	112.53
3	J	402	TYD	C5M-C5-C4	2.69	123.52	120.05
2	G	401	COA	O4B-C1B-N9A	2.70	113.75	108.10
2	D	401	COA	CEP-CBP-CAP	2.73	114.33	109.34
2	J	401	COA	C4B-O4B-C1B	2.76	112.75	109.72
2	K	401	COA	O5A-P2A-O4A	2.76	127.51	112.53
2	J	401	COA	O9A-P3B-O7A	2.78	119.52	110.58
2	B	401	COA	O9A-P3B-O7A	2.80	119.58	110.58
3	K	402	TYD	O3B-PB-O1B	2.91	119.95	110.58
4	E	403	TDR	CM5-C5-C4	2.92	123.82	120.05
2	D	401	COA	C3P-N4P-C5P	2.94	128.56	122.79
3	C	402	TYD	O3A-PA-O5'	2.95	110.76	102.94
2	A	401	COA	C7P-N8P-C9P	2.95	128.37	122.53
2	L	401	COA	CDP-CBP-CCP	2.97	112.35	108.50
3	C	402	TYD	C5M-C5-C4	2.97	123.88	120.05
4	D	403	TDR	C6-N1-C2	2.99	120.28	115.47
3	A	402	TYD	O4'-C1'-N1	3.00	112.91	107.72
2	K	401	COA	C7P-N8P-C9P	3.01	128.49	122.53
2	D	401	COA	CDP-CBP-CCP	3.05	112.45	108.50
3	G	402	TYD	C5M-C5-C4	3.10	124.05	120.05
4	E	403	TDR	C6-N1-C2	3.10	120.46	115.47
2	K	401	COA	O9A-P3B-O7A	3.12	120.61	110.58
2	C	401	COA	O9A-P3B-O7A	3.13	120.67	110.58
3	D	402	TYD	O3A-PA-O5'	3.14	111.28	102.94
4	C	403	TDR	CM5-C5-C4	3.25	124.25	120.05
2	A	401	COA	O8A-P3B-O7A	3.25	121.05	110.58
3	G	402	TYD	O4'-C1'-N1	3.27	113.38	107.72
2	G	401	COA	C4B-O4B-C1B	3.29	113.33	109.72
2	E	401	COA	C7P-N8P-C9P	3.29	129.05	122.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	J	403	TDR	CM5-C5-C4	3.41	124.45	120.05
2	C	401	COA	C7P-N8P-C9P	3.41	129.28	122.53
3	I	402	TYD	C4-N3-C2	3.41	118.20	115.25
4	A	403	TDR	C4-N3-C2	3.45	118.23	115.25
2	A	401	COA	C3P-N4P-C5P	3.56	129.79	122.79
3	C	402	TYD	C4-N3-C2	3.57	118.33	115.25
2	G	401	COA	C6P-C5P-N4P	3.60	122.71	116.46
4	J	403	TDR	C6-N1-C2	3.64	121.33	115.47
4	C	403	TDR	C6-N1-C2	3.69	121.40	115.47
3	F	402	TYD	C5M-C5-C4	3.69	124.81	120.05
4	D	403	TDR	CM5-C5-C4	3.70	124.82	120.05
4	A	403	TDR	CM5-C5-C4	3.72	124.84	120.05
2	F	401	COA	C6P-C5P-N4P	3.96	123.34	116.46
2	G	403	COA	C7P-N8P-C9P	3.97	130.39	122.53
3	D	402	TYD	C5M-C5-C4	3.98	125.19	120.05
3	K	402	TYD	O4'-C1'-N1	4.01	114.67	107.72
2	L	401	COA	O9A-P3B-O7A	4.01	123.50	110.58
2	G	403	COA	O9A-P3B-O7A	4.07	123.67	110.58
2	B	401	COA	CDP-CBP-CCP	4.10	113.82	108.50
2	D	401	COA	C7P-N8P-C9P	4.12	130.68	122.53
3	G	402	TYD	C4-N3-C2	4.13	118.82	115.25
4	K	403	TDR	C6-N1-C2	4.19	122.20	115.47
3	L	402	TYD	O4'-C1'-N1	4.42	115.36	107.72
3	I	402	TYD	C5M-C5-C4	4.42	125.75	120.05
3	D	402	TYD	C4-N3-C2	4.47	119.11	115.25
2	E	401	COA	O9A-P3B-O7A	4.64	125.52	110.58
4	B	403	TDR	C6-N1-C2	4.78	123.16	115.47
3	E	402	TYD	C4-N3-C2	4.83	119.42	115.25
4	L	403	TDR	C6-N1-C2	4.96	123.44	115.47
2	J	401	COA	C7P-N8P-C9P	5.07	132.57	122.53
4	L	403	TDR	CM5-C5-C4	5.12	126.66	120.05
3	E	402	TYD	O4'-C1'-N1	5.16	116.65	107.72
3	B	402	TYD	O4'-C1'-N1	5.20	116.72	107.72
3	F	402	TYD	C4-N3-C2	5.26	119.80	115.25
3	B	402	TYD	C4-N3-C2	5.38	119.90	115.25
3	L	402	TYD	C4-N3-C2	5.62	120.11	115.25
3	C	402	TYD	O4'-C1'-N1	5.79	117.75	107.72
3	J	402	TYD	O4'-C1'-N1	5.80	117.76	107.72
4	C	403	TDR	C4-N3-C2	6.01	120.44	115.25
3	J	402	TYD	C4-N3-C2	6.02	120.45	115.25
2	I	401	COA	C3P-N4P-C5P	6.05	134.69	122.79
2	F	401	COA	C7P-N8P-C9P	6.06	134.52	122.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	401	COA	C3P-N4P-C5P	6.10	134.79	122.79
4	L	403	TDR	C4-N3-C2	6.28	120.68	115.25
4	B	403	TDR	C4-N3-C2	6.74	121.07	115.25
3	K	402	TYD	C4-N3-C2	6.92	121.23	115.25
4	J	403	TDR	C4-N3-C2	7.13	121.41	115.25
3	A	402	TYD	C4-N3-C2	7.19	121.46	115.25
4	A	403	TDR	C6-N1-C2	7.21	127.07	115.47
3	H	401	TYD	C4-N3-C2	7.23	121.50	115.25
4	D	403	TDR	C4-N3-C2	7.46	121.69	115.25
4	K	403	TDR	C4-N3-C2	7.64	121.85	115.25
4	E	403	TDR	C4-N3-C2	7.77	121.96	115.25
4	F	403	TDR	C4-N3-C2	9.34	123.32	115.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

15 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	403	TDR	1	0
2	B	401	COA	1	0
2	D	401	COA	1	0
3	D	402	TYD	2	0
3	E	402	TYD	4	0
3	F	402	TYD	1	0
3	G	402	TYD	1	0
2	G	403	COA	1	0
3	H	401	TYD	1	0
2	I	401	COA	2	0
2	J	401	COA	4	0
2	K	401	COA	3	0
2	L	401	COA	3	0
3	L	402	TYD	1	0
4	L	403	TDR	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	285/312 (91%)	0.08	10 (3%) 48 46	12, 27, 46, 67	0
1	B	290/312 (92%)	0.19	17 (5%) 26 25	12, 28, 51, 65	0
1	C	285/312 (91%)	0.09	6 (2%) 67 65	14, 28, 47, 66	0
1	D	283/312 (90%)	0.25	15 (5%) 30 29	18, 33, 53, 75	0
1	E	286/312 (91%)	0.21	13 (4%) 37 36	17, 32, 53, 67	0
1	F	294/312 (94%)	0.35	22 (7%) 17 17	20, 33, 54, 67	0
1	G	283/312 (90%)	0.11	8 (2%) 56 55	17, 31, 56, 63	0
1	H	278/312 (89%)	0.63	31 (11%) 7 6	27, 47, 65, 74	0
1	I	285/312 (91%)	0.30	15 (5%) 30 29	18, 34, 58, 65	0
1	J	275/312 (88%)	0.52	29 (10%) 8 7	18, 40, 63, 70	0
1	K	285/312 (91%)	0.27	19 (6%) 21 20	16, 29, 55, 81	0
1	L	286/312 (91%)	0.24	15 (5%) 31 30	20, 32, 58, 65	0
All	All	3415/3744 (91%)	0.27	200 (5%) 26 25	12, 33, 58, 81	0

All (200) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	165	LEU	9.0
1	E	94	TYR	7.0
1	F	165	LEU	6.1
1	K	167	LEU	5.8
1	C	95	LEU	5.6
1	E	161	ASN	5.5
1	I	95	LEU	5.4
1	K	165	LEU	5.2
1	H	186	LEU	5.0
1	J	279	LEU	4.8
1	H	11	GLN	4.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	K	168	GLN	4.6
1	D	305	LEU	4.6
1	K	186	LEU	4.4
1	K	169	MET	4.4
1	H	33	ARG	4.3
1	D	165	LEU	4.2
1	J	184	ASN	4.1
1	J	230	LEU	4.0
1	I	16	ASN	4.0
1	J	164	GLU	4.0
1	L	161	ASN	4.0
1	A	161	ASN	3.9
1	K	166	LYS	3.9
1	K	164	GLU	3.9
1	J	186	LEU	3.8
1	C	186	LEU	3.8
1	B	280	VAL	3.8
1	H	169	MET	3.7
1	B	305	LEU	3.6
1	H	95	LEU	3.6
1	G	16	ASN	3.6
1	B	164	GLU	3.5
1	F	166	LYS	3.5
1	F	89	ILE	3.5
1	J	280	VAL	3.5
1	L	1	MET	3.5
1	B	186	LEU	3.4
1	B	279	LEU	3.4
1	B	289	ASP	3.4
1	E	280	VAL	3.4
1	H	280	VAL	3.3
1	H	15	ASP	3.3
1	L	307	HIS	3.3
1	E	279	LEU	3.3
1	K	280	VAL	3.3
1	J	287	ASP	3.3
1	F	33	ARG	3.3
1	D	279	LEU	3.2
1	J	165	LEU	3.2
1	L	280	VAL	3.2
1	D	306	GLU	3.2
1	J	286	TYR	3.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	H	164	GLU	3.2
1	K	59	VAL	3.1
1	J	225	GLU	3.1
1	H	165	LEU	3.1
1	H	230	LEU	3.1
1	H	279	LEU	3.1
1	K	95	LEU	3.1
1	B	184	ASN	3.1
1	H	300	GLN	3.1
1	A	279	LEU	3.0
1	D	230	LEU	3.0
1	I	186	LEU	3.0
1	I	303	GLN	3.0
1	G	279	LEU	3.0
1	E	300	GLN	3.0
1	F	307	HIS	3.0
1	F	88	LYS	2.9
1	F	186	LEU	2.9
1	J	167	LEU	2.9
1	K	57	SER	2.9
1	D	280	VAL	2.9
1	C	307	HIS	2.9
1	G	231	ILE	2.9
1	D	164	GLU	2.9
1	F	167	LEU	2.9
1	H	173	LYS	2.9
1	G	230	LEU	2.8
1	H	184	ASN	2.8
1	J	285	TYR	2.8
1	C	171	LYS	2.8
1	A	95	LEU	2.8
1	F	164	GLU	2.8
1	F	184	ASN	2.8
1	H	16	ASN	2.8
1	H	1	MET	2.8
1	G	36	ASN	2.8
1	K	77	VAL	2.8
1	D	300	GLN	2.8
1	J	185	ASP	2.8
1	J	281	PHE	2.8
1	F	59	VAL	2.7
1	J	264	MET	2.7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	K	279	LEU	2.7
1	J	231	ILE	2.7
1	I	15	ASP	2.7
1	A	303	GLN	2.7
1	L	59	VAL	2.7
1	J	289	ASP	2.6
1	H	278	LEU	2.6
1	F	309	HIS	2.6
1	H	58	GLY	2.6
1	B	281	PHE	2.6
1	D	197	LYS	2.6
1	B	230	LEU	2.6
1	E	58	GLY	2.6
1	E	59	VAL	2.6
1	F	12	ASN	2.6
1	L	11	GLN	2.6
1	E	95	LEU	2.5
1	H	59	VAL	2.5
1	I	184	ASN	2.5
1	H	18	LYS	2.5
1	L	165	LEU	2.5
1	D	281	PHE	2.5
1	J	173	LYS	2.5
1	K	40	ASN	2.5
1	H	28	GLY	2.4
1	D	259	ILE	2.4
1	C	184	ASN	2.4
1	D	303	GLN	2.4
1	F	15	ASP	2.4
1	B	207	PHE	2.4
1	G	280	VAL	2.4
1	H	77	VAL	2.4
1	J	166	LYS	2.4
1	K	33	ARG	2.4
1	A	82	ASP	2.3
1	J	288	SER	2.3
1	H	231	ILE	2.3
1	B	185	ASP	2.3
1	I	164	GLU	2.3
1	L	164	GLU	2.3
1	J	259	ILE	2.3
1	D	304	ASN	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	I	274	LYS	2.3
1	F	41	SER	2.3
1	F	300	GLN	2.3
1	K	11	GLN	2.3
1	H	281	PHE	2.3
1	A	184	ASN	2.3
1	I	6	ALA	2.3
1	L	41	SER	2.3
1	G	274	LYS	2.3
1	J	34	ASN	2.3
1	B	245	GLU	2.3
1	L	96	LYS	2.2
1	H	229	PHE	2.2
1	E	230	LEU	2.2
1	E	231	ILE	2.2
1	H	168	GLN	2.2
1	F	305	LEU	2.2
1	I	78	THR	2.2
1	A	280	VAL	2.2
1	A	233	VAL	2.2
1	I	77	VAL	2.2
1	H	185	ASP	2.2
1	F	279	LEU	2.2
1	D	184	ASN	2.2
1	D	289	ASP	2.2
1	J	294	ASP	2.2
1	B	40	ASN	2.2
1	B	304	ASN	2.2
1	J	183	VAL	2.1
1	F	40	ASN	2.1
1	A	278	LEU	2.1
1	H	42	LEU	2.1
1	K	58	GLY	2.1
1	G	233	VAL	2.1
1	B	16	ASN	2.1
1	B	162	ASN	2.1
1	A	281	PHE	2.1
1	L	230	LEU	2.1
1	F	78	THR	2.1
1	E	184	ASN	2.1
1	I	187	ARG	2.1
1	J	196	GLU	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	L	306	GLU	2.1
1	F	230	LEU	2.1
1	J	1	MET	2.1
1	I	163	PHE	2.1
1	B	206	TYR	2.1
1	K	230	LEU	2.1
1	H	171	LYS	2.1
1	K	41	SER	2.1
1	J	172	VAL	2.1
1	I	34	ASN	2.1
1	L	231	ILE	2.1
1	C	58	GLY	2.0
1	H	17	THR	2.0
1	J	229	PHE	2.0
1	L	33	ARG	2.0
1	L	279	LEU	2.0
1	E	84	GLN	2.0
1	H	285	TYR	2.0
1	E	289	ASP	2.0
1	J	233	VAL	2.0
1	F	285	TYR	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
4	TDR	D	403	9/9	0.74	0.20	2.72	43,47,49,50	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
4	TDR	J	403	9/9	0.76	0.25	2.47	58,62,64,65	0
4	TDR	L	403	9/9	0.71	0.20	2.08	71,72,73,74	0
4	TDR	K	403	9/9	0.76	0.20	1.35	69,72,74,74	0
4	TDR	A	403	9/9	0.84	0.17	1.23	31,41,43,44	0
4	TDR	C	403	9/9	0.75	0.18	1.23	51,55,57,59	0
2	COA	I	401	48/48	0.94	0.14	0.47	27,43,62,71	0
3	TYD	D	402	25/25	0.87	0.18	0.36	47,71,75,77	0
2	COA	D	401	48/48	0.95	0.13	0.25	20,41,56,64	0
4	TDR	B	403	9/9	0.83	0.17	0.24	41,43,47,47	0
3	TYD	G	402	25/25	0.86	0.17	0.22	40,58,72,72	0
3	TYD	A	402	25/25	0.88	0.16	0.14	39,63,74,75	0
3	TYD	C	402	25/25	0.90	0.14	0.03	31,56,66,68	0
3	TYD	J	402	25/25	0.82	0.19	0.00	69,81,92,93	0
3	TYD	L	402	25/25	0.90	0.14	-0.07	46,63,71,72	0
4	TDR	F	403	9/9	0.85	0.14	-0.09	52,54,56,56	0
5	MG	J	404	1/1	0.99	0.20	-0.11	26,26,26,26	0
2	COA	G	403	48/48	0.95	0.12	-0.12	35,42,57,70	0
2	COA	K	401	48/48	0.96	0.12	-0.29	21,37,64,70	0
3	TYD	E	402	25/25	0.91	0.13	-0.34	31,49,61,63	0
2	COA	E	401	48/48	0.94	0.13	-0.34	20,37,49,59	0
2	COA	A	401	48/48	0.95	0.12	-0.34	17,29,42,55	0
2	COA	G	401	48/48	0.95	0.12	-0.35	26,36,41,53	0
4	TDR	E	403	9/9	0.85	0.13	-0.40	41,46,48,49	0
5	MG	D	404	1/1	0.99	0.20	-0.41	21,21,21,21	0
5	MG	C	404	1/1	0.97	0.19	-0.43	20,20,20,20	0
3	TYD	K	402	25/25	0.92	0.12	-0.44	22,39,55,57	0
3	TYD	H	401	25/25	0.88	0.15	-0.46	44,61,73,74	0
3	TYD	I	402	25/25	0.91	0.11	-0.52	22,40,66,68	0
3	TYD	B	402	25/25	0.91	0.12	-0.55	34,57,71,73	0
2	COA	J	401	48/48	0.95	0.12	-0.58	21,36,48,60	0
2	COA	L	401	48/48	0.95	0.11	-0.61	15,33,45,53	0
3	TYD	F	402	25/25	0.88	0.13	-0.71	35,56,79,79	0
2	COA	B	401	48/48	0.97	0.10	-0.85	9,24,33,42	0
2	COA	F	401	48/48	0.96	0.10	-0.89	21,35,43,49	0
2	COA	C	401	48/48	0.96	0.10	-1.06	14,32,42,45	0
5	MG	G	404	1/1	0.98	0.14	-2.08	27,27,27,27	0
5	MG	B	404	1/1	0.99	0.22	-	26,26,26,26	0

6.5 Other polymers ⓘ

There are no such residues in this entry.