



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:20 PM GMT

PDB ID : 3TGX
Title : IL-21:IL21R complex
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Paludan, S.R.; Hjort, S.A.; Bondensgaard, K.; Hartmann, R.
Deposited on : 2011-08-18
Resolution : 2.80 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

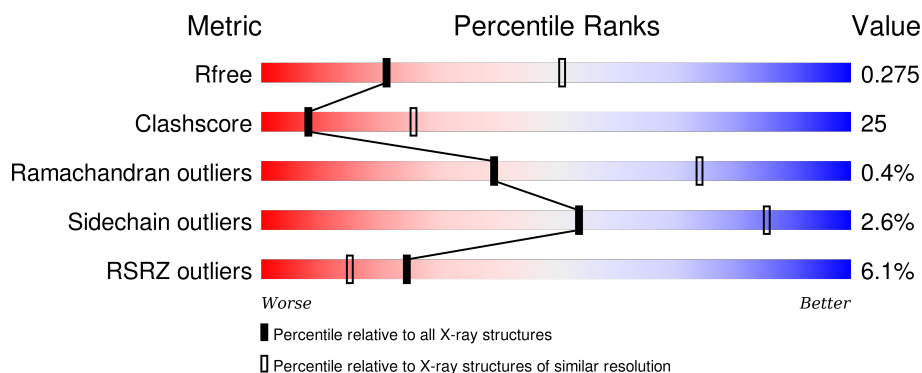
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	219	<div> <div>72%</div> <div>22%</div> <div>• 5%</div> </div>
1	C	219	<div> <div>66%</div> <div>27%</div> <div>• 5%</div> </div>
1	E	219	<div> <div>5%</div> <div>63%</div> <div>31%</div> <div>5%</div> </div>
1	G	219	<div> <div>3%</div> <div>67%</div> <div>26%</div> <div>• 5%</div> </div>
1	I	219	<div> <div>5%</div> <div>66%</div> <div>27%</div> <div>• 5%</div> </div>

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Mol	Chain	Length	Quality of chain
1	K	219	
1	M	219	
1	O	219	
2	B	134	
2	D	134	
2	F	134	
2	H	134	
2	J	134	
2	L	134	
2	N	134	
2	P	134	

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
11	NAG	M	303	-	-	X	-
12	BMA	M	308	-	-	X	-
13	FUL	O	301	-	-	-	X
3	MAN	A	301	-	-	X	-
4	NI	O	308	-	-	-	X
6	FUL	A	307	-	-	-	X
6	NAG	A	309	-	-	X	-
6	FUL	E	301	-	-	-	X
6	NAG	E	304	-	-	X	-
7	BMA	A	310	-	-	X	-
7	MAN	A	312	-	-	X	-
7	MAN	A	313	-	-	-	X
7	BMA	C	311	-	-	X	-
7	MAN	C	314	-	-	-	X
7	BMA	E	306	-	-	X	-
7	BMA	G	310	-	-	X	-
7	MAN	G	313	-	-	-	X
7	BMA	I	309	-	-	X	-

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	MAN	I	312	-	-	-	X
8	FUL	C	308	-	-	-	X
8	FUL	G	307	-	-	-	X
8	FUL	I	306	-	-	-	X
8	FUL	K	301	-	-	-	X
9	NAG	C	309	-	-	X	-
9	NAG	C	310	-	-	X	-
9	NAG	G	308	-	-	X	-
9	NAG	G	309	-	-	X	-
9	NAG	I	307	-	-	X	-
9	NAG	I	308	-	-	X	-

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 21830 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 Interleukin-21 receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	S	0	0	0
			1687	1071	277	328	11			
1	C	209	Total	C	N	O	S	0	0	0
			1696	1076	278	331	11			
1	E	207	Total	C	N	O	S	0	0	0
			1681	1068	276	326	11			
1	G	209	Total	C	N	O	S	0	0	0
			1696	1076	278	331	11			
1	I	209	Total	C	N	O	S	0	0	0
			1696	1076	278	331	11			
1	K	209	Total	C	N	O	S	0	0	0
			1696	1076	278	331	11			
1	M	208	Total	C	N	O	S	0	0	0
			1687	1071	277	328	11			
1	O	208	Total	C	N	O	S	0	0	0
			1687	1071	277	328	11			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	78	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
A	85	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
A	106	ASP	ASN	ENGINEERED MUTATION	UNP Q9HBE5
A	116	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
A	214	HIS	-	EXPRESSION TAG	UNP Q9HBE5
A	215	HIS	-	EXPRESSION TAG	UNP Q9HBE5
A	216	HIS	-	EXPRESSION TAG	UNP Q9HBE5
A	217	HIS	-	EXPRESSION TAG	UNP Q9HBE5
A	218	HIS	-	EXPRESSION TAG	UNP Q9HBE5
A	219	HIS	-	EXPRESSION TAG	UNP Q9HBE5
C	78	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
C	85	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
C	106	ASP	ASN	ENGINEERED MUTATION	UNP Q9HBE5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	116	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
C	214	HIS	-	EXPRESSION TAG	UNP Q9HBE5
C	215	HIS	-	EXPRESSION TAG	UNP Q9HBE5
C	216	HIS	-	EXPRESSION TAG	UNP Q9HBE5
C	217	HIS	-	EXPRESSION TAG	UNP Q9HBE5
C	218	HIS	-	EXPRESSION TAG	UNP Q9HBE5
C	219	HIS	-	EXPRESSION TAG	UNP Q9HBE5
E	78	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
E	85	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
E	106	ASP	ASN	ENGINEERED MUTATION	UNP Q9HBE5
E	116	GLN	ASN	ENGINEERED MUTATION'	UNP Q9HBE5
E	214	HIS	-	EXPRESSION TAG	UNP Q9HBE5
E	215	HIS	-	EXPRESSION TAG	UNP Q9HBE5
E	216	HIS	-	EXPRESSION TAG	UNP Q9HBE5
E	217	HIS	-	EXPRESSION TAG	UNP Q9HBE5
E	218	HIS	-	EXPRESSION TAG	UNP Q9HBE5
E	219	HIS	-	EXPRESSION TAG	UNP Q9HBE5
G	78	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
G	85	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
G	106	ASP	ASN	ENGINEERED MUTATION	UNP Q9HBE5
G	116	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
G	214	HIS	-	EXPRESSION TAG	UNP Q9HBE5
G	215	HIS	-	EXPRESSION TAG	UNP Q9HBE5
G	216	HIS	-	EXPRESSION TAG	UNP Q9HBE5
G	217	HIS	-	EXPRESSION TAG	UNP Q9HBE5
G	218	HIS	-	EXPRESSION TAG	UNP Q9HBE5
G	219	HIS	-	EXPRESSION TAG	UNP Q9HBE5
I	78	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
I	85	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
I	106	ASP	ASN	ENGINEERED MUTATION	UNP Q9HBE5
I	116	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
I	214	HIS	-	EXPRESSION TAG	UNP Q9HBE5
I	215	HIS	-	EXPRESSION TAG	UNP Q9HBE5
I	216	HIS	-	EXPRESSION TAG	UNP Q9HBE5
I	217	HIS	-	EXPRESSION TAG	UNP Q9HBE5
I	218	HIS	-	EXPRESSION TAG	UNP Q9HBE5
I	219	HIS	-	EXPRESSION TAG	UNP Q9HBE5
K	78	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
K	85	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
K	106	ASP	ASN	ENGINEERED MUTATION	UNP Q9HBE5
K	116	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
K	214	HIS	-	EXPRESSION TAG	UNP Q9HBE5

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Chain	Residue	Modelled	Actual	Comment	Reference
K	215	HIS	-	EXPRESSION TAG	UNP Q9HBE5
K	216	HIS	-	EXPRESSION TAG	UNP Q9HBE5
K	217	HIS	-	EXPRESSION TAG	UNP Q9HBE5
K	218	HIS	-	EXPRESSION TAG	UNP Q9HBE5
K	219	HIS	-	EXPRESSION TAG	UNP Q9HBE5
M	78	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
M	85	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
M	106	ASP	ASN	ENGINEERED MUTATION	UNP Q9HBE5
M	116	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
M	214	HIS	-	EXPRESSION TAG	UNP Q9HBE5
M	215	HIS	-	EXPRESSION TAG	UNP Q9HBE5
M	216	HIS	-	EXPRESSION TAG	UNP Q9HBE5
M	217	HIS	-	EXPRESSION TAG	UNP Q9HBE5
M	218	HIS	-	EXPRESSION TAG	UNP Q9HBE5
M	219	HIS	-	EXPRESSION TAG	UNP Q9HBE5
O	78	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
O	85	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
O	106	ASP	ASN	ENGINEERED MUTATION	UNP Q9HBE5
O	116	GLN	ASN	ENGINEERED MUTATION	UNP Q9HBE5
O	214	HIS	-	EXPRESSION TAG	UNP Q9HBE5
O	215	HIS	-	EXPRESSION TAG	UNP Q9HBE5
O	216	HIS	-	EXPRESSION TAG	UNP Q9HBE5
O	217	HIS	-	EXPRESSION TAG	UNP Q9HBE5
O	218	HIS	-	EXPRESSION TAG	UNP Q9HBE5
O	219	HIS	-	EXPRESSION TAG	UNP Q9HBE5

- Molecule 2 is a protein called Interleukin-21.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	115	Total	C	N	O	S	0	0	0
			944	595	171	171	7			
2	D	117	Total	C	N	O	S	0	0	0
			951	598	172	174	7			
2	F	113	Total	C	N	O	S	0	0	0
			923	581	165	170	7			
2	H	116	Total	C	N	O	S	0	0	0
			957	603	174	173	7			
2	J	116	Total	C	N	O	S	0	0	0
			940	592	167	174	7			
2	L	110	Total	C	N	O	S	0	0	0
			902	570	160	165	7			
2	N	107	Total	C	N	O	S	0	0	0
			875	553	154	161	7			

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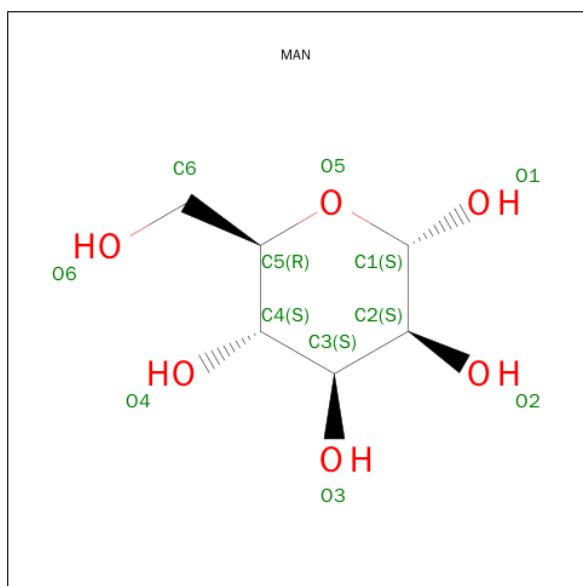
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	110	Total	C	N	O	S	0	0	0
			902	570	160	165	7			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	0	MET	-	EXPRESSION TAG	UNP Q9HBE4
D	0	MET	-	EXPRESSION TAG	UNP Q9HBE4
F	0	MET	-	EXPRESSION TAG	UNP Q9HBE4
H	0	MET	-	EXPRESSION TAG	UNP Q9HBE4
J	0	MET	-	EXPRESSION TAG	UNP Q9HBE4
L	0	MET	-	EXPRESSION TAG	UNP Q9HBE4
N	0	MET	-	EXPRESSION TAG	UNP Q9HBE4
P	0	MET	-	EXPRESSION TAG	UNP Q9HBE4

- Molecule 3 is SUGAR (ALPHA-D-MANNOSE) (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		
3	C	1	Total	C	O	0	0
			11	6	5		
3	E	1	Total	C	O	0	0
			11	6	5		
3	G	1	Total	C	O	0	0
			11	6	5		

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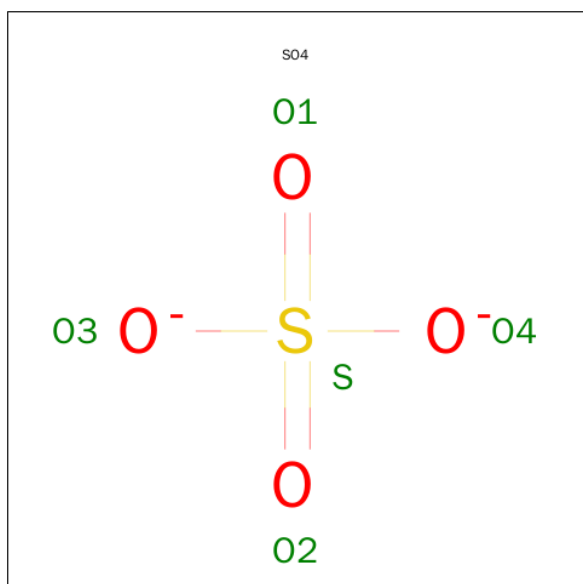
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	I	1	Total	C	O	0	0
			11	6	5		
3	K	1	Total	C	O	0	0
			11	6	5		
3	M	1	Total	C	O	0	0
			11	6	5		
3	O	1	Total	C	O	0	0
			11	6	5		

- Molecule 4 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	G	1	Total	Ni	0	0
			1	1		
4	O	1	Total	Ni	0	0
			1	1		
4	A	1	Total	Ni	0	0
			1	1		
4	E	1	Total	Ni	0	0
			1	1		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	A	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	C	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	E	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	G	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		
5	H	1	Total	O	S	0	0
			5	4	1		
5	I	1	Total	O	S	0	0
			5	4	1		
5	I	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	I	1	Total	O	S	0	0
			5	4	1		
5	I	1	Total	O	S	0	0
			5	4	1		
5	K	1	Total	O	S	0	0
			5	4	1		
5	K	1	Total	O	S	0	0
			5	4	1		
5	K	1	Total	O	S	0	0
			5	4	1		
5	K	1	Total	O	S	0	0
			5	4	1		
5	L	1	Total	O	S	0	0
			5	4	1		
5	M	1	Total	O	S	0	0
			5	4	1		
5	M	1	Total	O	S	0	0
			5	4	1		
5	M	1	Total	O	S	0	0
			5	4	1		
5	M	1	Total	O	S	0	0
			5	4	1		
5	O	1	Total	O	S	0	0
			5	4	1		
5	O	1	Total	O	S	0	0
			5	4	1		
5	O	1	Total	O	S	0	0
			5	4	1		
5	O	1	Total	O	S	0	0
			5	4	1		

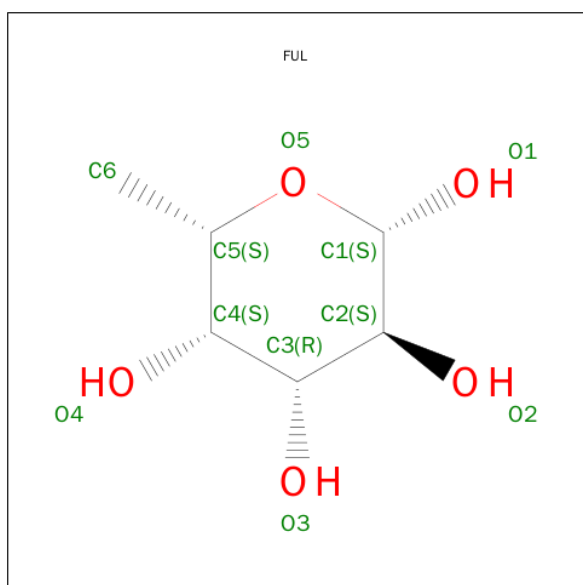
- Molecule 6 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	3	Total	C	N	O	0	0
			38	22	2	14		
6	E	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 7 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	4	Total	C	O	0	0
			44	24	20		
7	C	4	Total	C	O	0	0
			44	24	20		
7	E	4	Total	C	O	0	0
			44	24	20		
7	G	4	Total	C	O	0	0
			44	24	20		
7	I	4	Total	C	O	0	0
			44	24	20		

- Molecule 8 is SUGAR (BETA-L-FUCOSE) (three-letter code: FUL) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	C	1	Total	C	O	0	0
			10	6	4		
8	G	1	Total	C	O	0	0
			10	6	4		
8	I	1	Total	C	O	0	0
			10	6	4		
8	K	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	C	2	Total	C	N	O	0	0
			28	16	2	10		
9	G	2	Total	C	N	O	0	0
			28	16	2	10		
9	I	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 10 is a polymer of unknown type called SUGAR (5-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	K	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 11 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	M	3	Total	C	N	O	0	0
			38	22	2	14		

- Molecule 12 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
12	M	3	Total	C	O	0	0
			33	18	15		

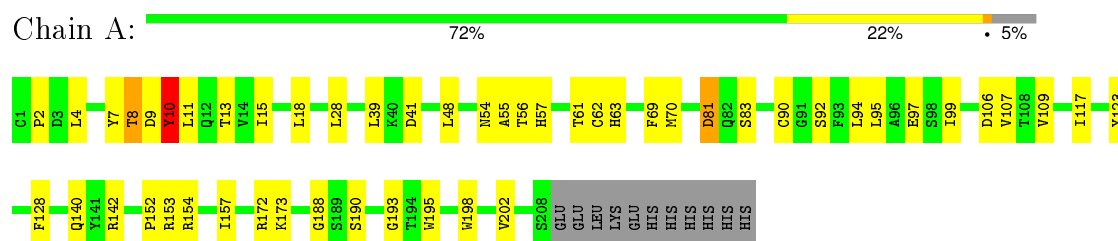
- Molecule 13 is a polymer of unknown type called SUGAR (6-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
13	O	6	Total	C	N	O	0	0
			71	40	2	29		

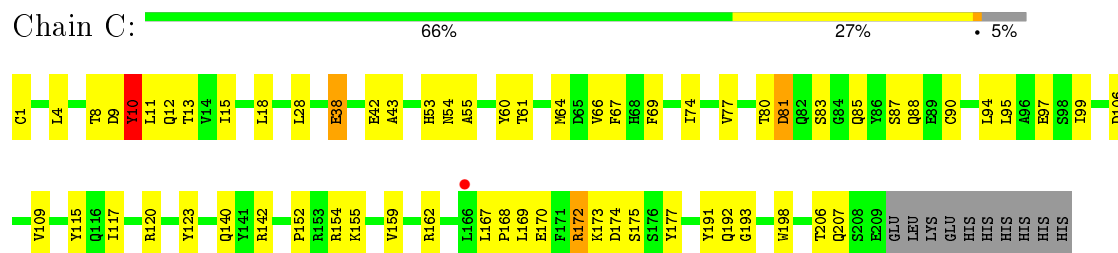
3 Residue-property plots

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.

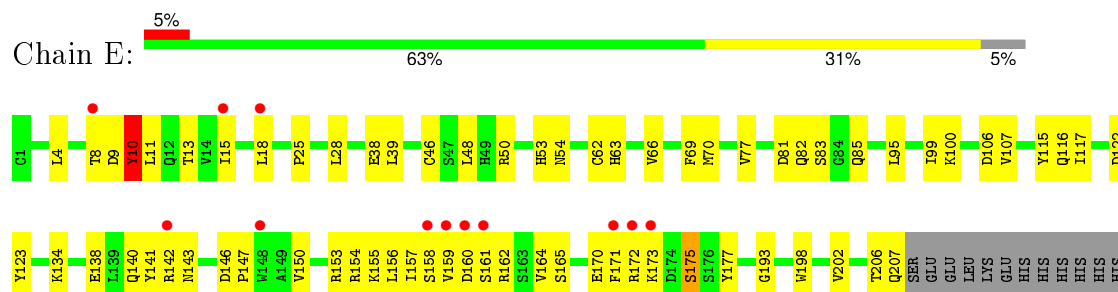
• Molecule 1: Interleukin-21 receptor



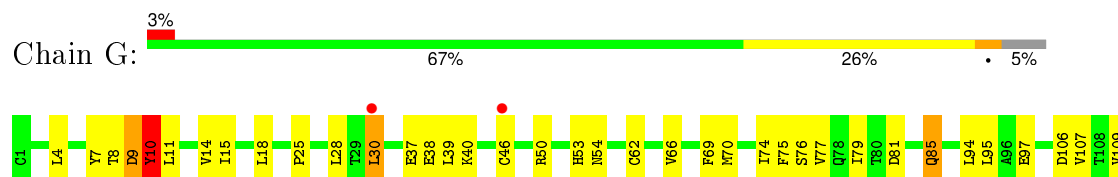
• Molecule 1: Interleukin-21 receptor

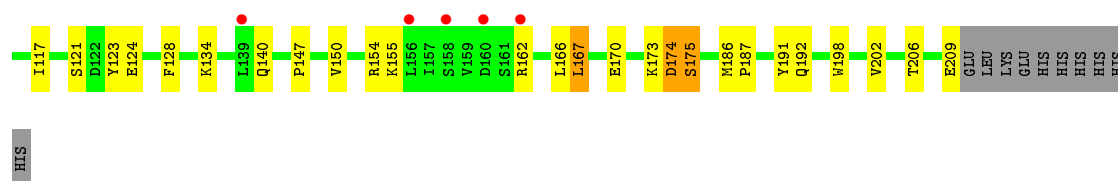


• Molecule 1: Interleukin-21 receptor

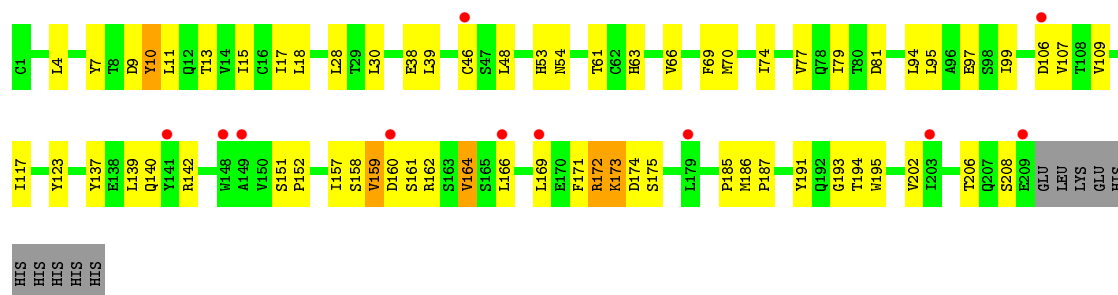


• Molecule 1: Interleukin-21 receptor

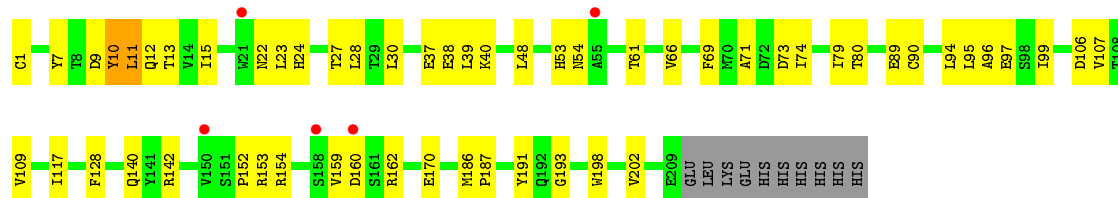




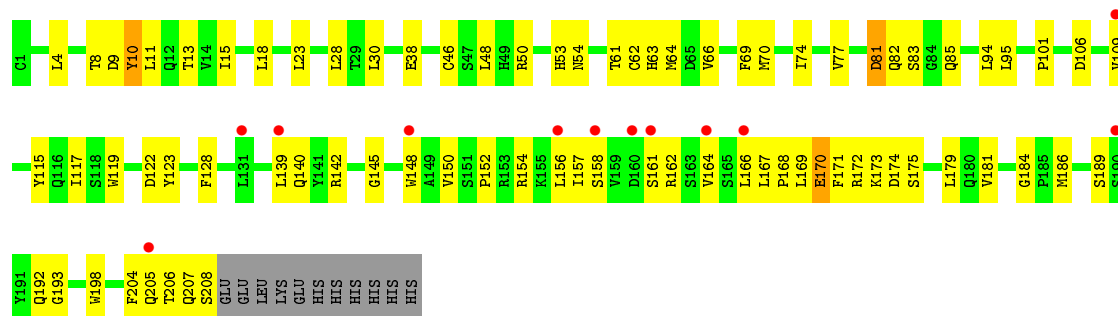
- Molecule 1: Interleukin-21 receptor



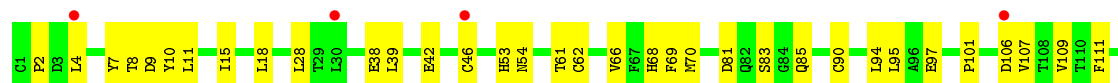
- Molecule 1: Interleukin-21 receptor

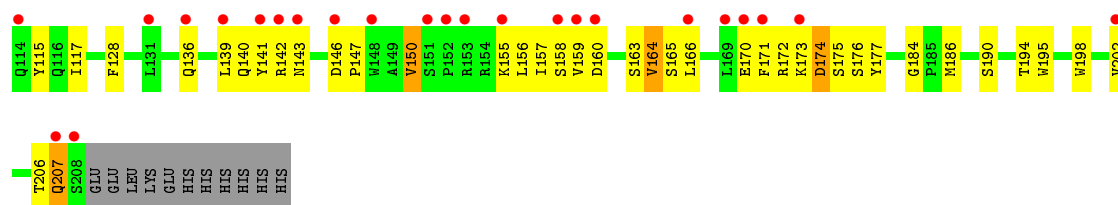


- Molecule 1: Interleukin-21 receptor

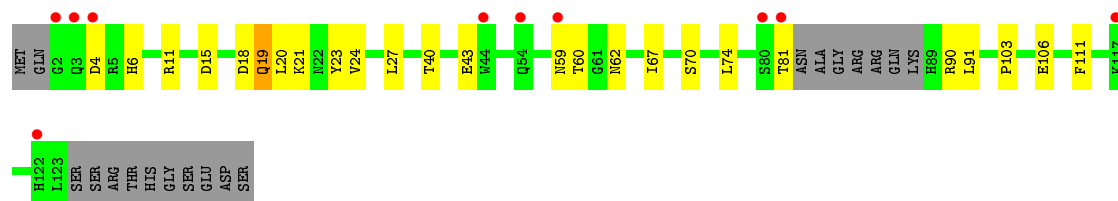


- Molecule 1: Interleukin-21 receptor

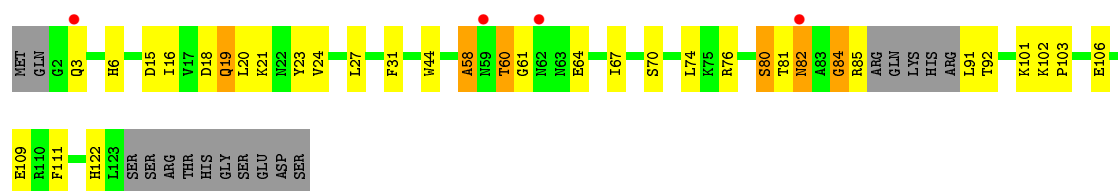




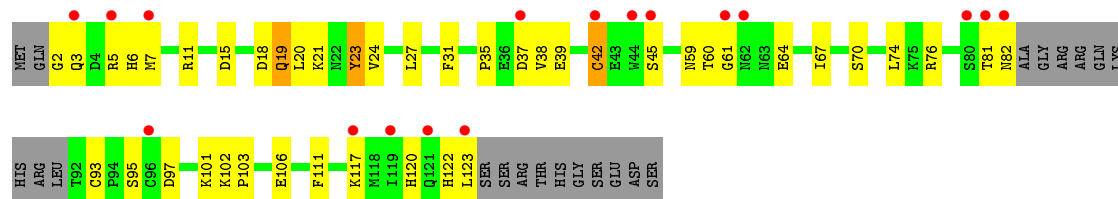
• Molecule 2: Interleukin-21



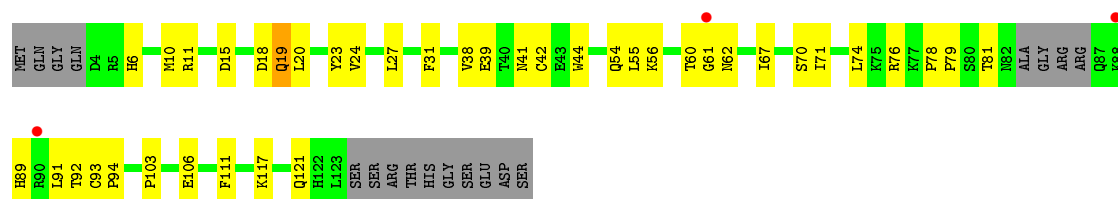
• Molecule 2: Interleukin-21



• Molecule 2: Interleukin-21

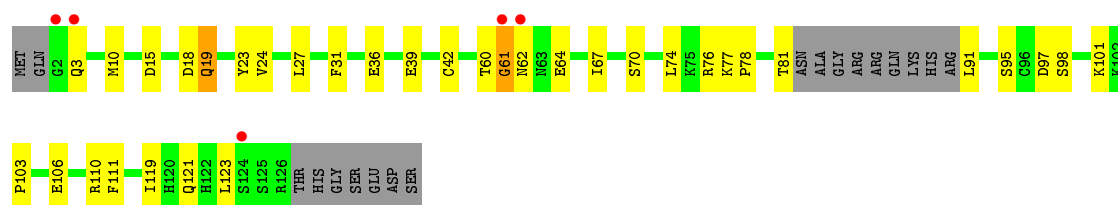


• Molecule 2: Interleukin-21

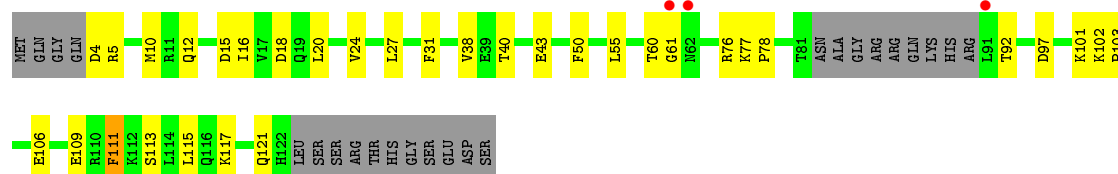


• Molecule 2: Interleukin-21

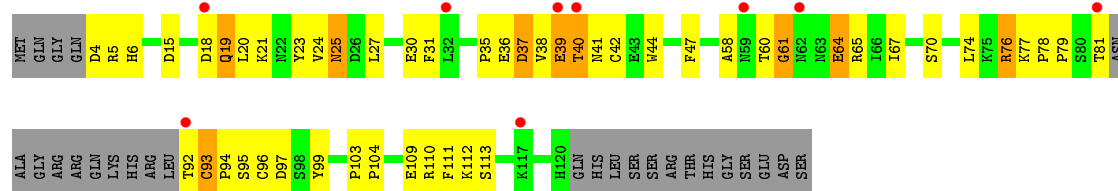
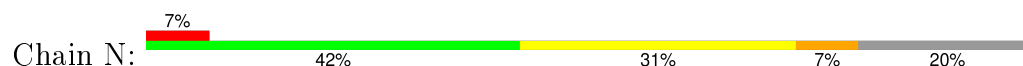




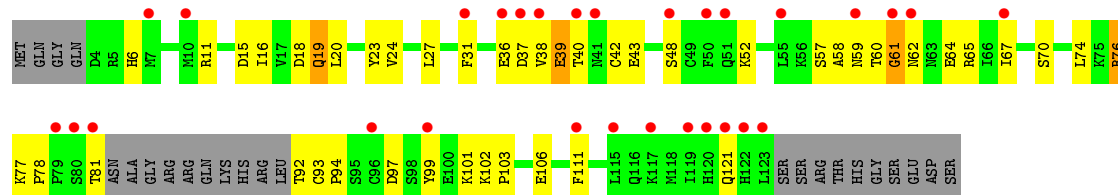
• Molecule 2: Interleukin-21



• Molecule 2: Interleukin-21



• Molecule 2: Interleukin-21



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.23Å 151.12Å 364.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	80.22 – 2.80 80.22 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.7 (80.22-2.80) 99.7 (80.22-2.80)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 2.82Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.7.2_869)	Depositor
R, R_{free}	0.242 , 0.273 0.247 , 0.275	Depositor DCC
R_{free} test set	5633 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	53.7	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 64.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	2 of 112643 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	21830	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.03% 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: NI, BMA, NAG, FUC, FUL, MAN, SO4

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	1/1737 (0.1%)	0.62	3/2367 (0.1%)
1	C	0.85	7/1746 (0.4%)	0.68	3/2379 (0.1%)
1	E	0.57	2/1731 (0.1%)	0.64	2/2359 (0.1%)
1	G	0.65	4/1746 (0.2%)	0.64	4/2379 (0.2%)
1	I	0.41	1/1746 (0.1%)	0.58	4/2379 (0.2%)
1	K	0.61	1/1746 (0.1%)	0.64	6/2379 (0.3%)
1	M	0.38	0/1737	0.59	2/2367 (0.1%)
1	O	0.40	2/1737 (0.1%)	0.62	1/2367 (0.0%)
2	B	0.47	0/963	0.49	0/1294
2	D	0.53	0/969	0.62	1/1302 (0.1%)
2	F	0.85	6/941 (0.6%)	0.58	0/1265
2	H	0.30	0/976	0.45	0/1311
2	J	0.46	0/958	0.54	1/1288 (0.1%)
2	L	0.29	0/920	0.45	0/1237
2	N	0.44	0/892	0.55	1/1199 (0.1%)
2	P	0.48	0/920	0.62	1/1237 (0.1%)
All	All	0.56	24/21465 (0.1%)	0.60	29/29109 (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	A	0	1
1	C	0	1
1	K	0	1
1	O	0	1
2	D	0	2
2	N	0	1
2	P	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
All	All	0	8

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	42	CYS	CB-SG	-10.35	1.64	1.82
2	F	23	TYR	CD1-CE1	-7.96	1.27	1.39
1	C	191	TYR	CD2-CE2	-7.56	1.28	1.39
2	F	23	TYR	CD2-CE2	-7.16	1.28	1.39
1	C	10	TYR	CE1-CZ	-6.90	1.29	1.38
1	C	191	TYR	CE2-CZ	-6.29	1.30	1.38
2	F	23	TYR	CE2-CZ	-6.17	1.30	1.38
1	K	10	TYR	CE2-CZ	-6.08	1.30	1.38
1	G	14	VAL	CB-CG2	-5.96	1.40	1.52
1	G	10	TYR	CE2-CZ	-5.94	1.30	1.38
1	C	10	TYR	CD1-CE1	-5.85	1.30	1.39
1	C	191	TYR	CD1-CE1	-5.84	1.30	1.39
1	A	10	TYR	CE1-CZ	-5.76	1.31	1.38
2	F	93	CYS	CB-SG	5.57	1.91	1.82
1	E	10	TYR	CD2-CE2	-5.39	1.31	1.39
1	E	10	TYR	CE2-CZ	-5.34	1.31	1.38
1	G	10	TYR	CD2-CE2	-5.33	1.31	1.39
2	F	23	TYR	CE1-CZ	-5.28	1.31	1.38
1	O	111	PHE	CD2-CE2	5.20	1.49	1.39
1	I	10	TYR	CD2-CE2	-5.14	1.31	1.39
1	G	10	TYR	CG-CD1	-5.10	1.32	1.39
1	C	10	TYR	CD2-CE2	-5.05	1.31	1.39
1	O	164	VAL	CA-CB	-5.02	1.44	1.54
1	C	192	GLN	C-O	-5.02	1.13	1.23

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	10	TYR	CA-CB-CG	7.84	128.30	113.40
1	K	11	LEU	CA-CB-CG	7.80	133.25	115.30
1	C	10	TYR	CA-CB-CG	6.72	126.16	113.40
1	E	10	TYR	CA-CB-CG	6.70	126.13	113.40
1	G	10	TYR	N-CA-CB	-6.51	98.88	110.60
1	I	10	TYR	CA-CB-CG	6.32	125.41	113.40
1	G	30	LEU	CA-CB-CG	6.06	129.25	115.30
1	A	10	TYR	CA-CB-CG	6.04	124.87	113.40
2	J	61	GLY	N-CA-C	-5.90	98.34	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	82	ASN	N-CA-C	-5.86	95.17	111.00
1	G	10	TYR	CA-CB-CG	5.81	124.43	113.40
2	P	61	GLY	N-CA-C	-5.76	98.70	113.10
1	I	169	LEU	CA-CB-CG	5.76	128.54	115.30
1	C	10	TYR	N-CA-CB	-5.76	100.24	110.60
1	K	12	GLN	C-N-CA	5.73	136.03	121.70
1	A	10	TYR	N-CA-CB	-5.65	100.43	110.60
1	K	10	TYR	CB-CG-CD1	5.50	124.30	121.00
2	N	41	ASN	N-CA-C	-5.41	96.41	111.00
1	K	30	LEU	CA-CB-CG	5.40	127.72	115.30
1	M	10	TYR	CA-CB-CG	5.34	123.55	113.40
1	K	106	ASP	CB-CG-OD2	5.26	123.03	118.30
1	G	106	ASP	CB-CG-OD2	5.23	123.01	118.30
1	I	106	ASP	CB-CG-OD2	5.22	123.00	118.30
1	E	106	ASP	CB-CG-OD2	5.22	123.00	118.30
1	A	106	ASP	CB-CG-OD2	5.19	122.97	118.30
1	O	106	ASP	CB-CG-OD2	5.18	122.96	118.30
1	C	106	ASP	CB-CG-OD2	5.17	122.96	118.30
1	I	10	TYR	N-CA-CB	-5.16	101.32	110.60
1	M	106	ASP	CB-CG-OD2	5.14	122.92	118.30

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	8	THR	Peptide
1	C	172	ARG	Peptide
2	D	58	ALA	Peptide
2	D	60	THR	Peptide
1	K	13	THR	Mainchain
2	N	61	GLY	Peptide
1	O	174	ASP	Peptide
2	P	39	GLU	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	1687	0	1582	56	0
1	C	1696	0	1588	86	0
1	E	1681	0	1575	98	0
1	G	1696	0	1590	74	0
1	I	1696	0	1590	69	0
1	K	1696	0	1590	51	0
1	M	1687	0	1584	124	1
1	O	1687	0	1584	87	0
2	B	944	0	952	30	0
2	D	951	0	959	57	0
2	F	923	0	926	45	0
2	H	957	0	968	38	0
2	J	940	0	944	23	0
2	L	902	0	910	24	0
2	N	875	0	884	54	1
2	P	902	0	910	63	0
3	A	11	0	10	7	0
3	C	11	0	10	0	0
3	E	11	0	10	0	0
3	G	11	0	10	1	0
3	I	11	0	10	4	0
3	K	11	0	10	0	0
3	M	11	0	10	0	0
3	O	11	0	10	1	0
4	A	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	O	1	0	0	0	0
5	A	20	0	0	0	0
5	C	30	0	0	1	0
5	E	20	0	0	0	0
5	G	20	0	0	0	0
5	H	10	0	0	0	0
5	I	20	0	0	0	0
5	K	25	0	0	1	0
5	L	5	0	0	0	0
5	M	20	0	0	0	0
5	O	25	0	0	0	0
6	A	38	0	34	12	0
6	E	38	0	34	10	0
7	A	44	0	37	14	0
7	C	44	0	37	11	0
7	E	44	0	37	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	G	44	0	37	12	0
7	I	44	0	37	11	0
8	C	10	0	10	4	0
8	G	10	0	10	4	0
8	I	10	0	10	4	0
8	K	10	0	10	0	0
9	C	28	0	24	15	0
9	G	28	0	24	17	0
9	I	28	0	24	18	0
10	K	61	0	51	11	0
11	M	38	0	34	13	0
12	M	33	0	28	12	0
13	O	71	0	61	8	0
All	All	21830	0	20755	1041	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 25.

All (1041) 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:I:195:TRP:CD1	3:I:301:MAN:C1	1.77	1.64
1:E:172:ARG:HB3	1:E:173:LYS:CG	1.30	1.55
1:E:172:ARG:HD3	1:E:173:LYS:CE	1.39	1.52
1:I:195:TRP:HD1	3:I:301:MAN:C1	0.90	1.51
1:M:54:ASN:HD21	11:M:302:NAG:C1	1.24	1.49
1:A:54:ASN:HD21	6:A:308:NAG:C1	1.29	1.45
1:M:13:THR:HG22	1:M:63:HIS:ND1	1.28	1.42
1:I:13:THR:HG22	1:I:63:HIS:ND1	1.28	1.42
1:I:54:ASN:HD21	9:I:307:NAG:C1	1.32	1.41
1:A:13:THR:HG22	1:A:63:HIS:ND1	1.34	1.41
1:A:54:ASN:ND2	6:A:308:NAG:C1	1.83	1.41
1:M:167:LEU:CD1	1:M:169:LEU:HG	1.49	1.40
2:P:6:HIS:CD2	2:P:81:THR:CG2	2.07	1.38
1:E:13:THR:HG22	1:E:63:HIS:ND1	1.31	1.37
2:F:3:GLN:OE1	2:F:82:ASN:ND2	1.56	1.37
1:M:169:LEU:HD12	1:M:170:GLU:N	1.36	1.35
1:C:167:LEU:HD13	1:C:169:LEU:CB	1.56	1.34
1:K:38:GLU:OE1	2:L:76:ARG:HG3	1.27	1.30
1:M:174:ASP:HA	1:M:206:THR:O	1.18	1.29
1:M:54:ASN:ND2	11:M:302:NAG:C1	1.92	1.28

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:155:LYS:NZ	1:G:170:GLU:OE2	1.64	1.27
1:I:54:ASN:ND2	9:I:307:NAG:C1	1.94	1.27
1:K:1:CYS:CB	1:K:90:CYS:SG	2.23	1.26
1:E:172:ARG:CD	1:E:173:LYS:HE2	1.64	1.25
1:E:172:ARG:CB	1:E:173:LYS:HG3	1.66	1.25
1:I:13:THR:HG22	1:I:63:HIS:CE1	1.72	1.25
2:P:6:HIS:CD2	2:P:81:THR:HG22	1.70	1.24
11:M:303:NAG:H4	12:M:308:BMA:O2	1.33	1.23
3:A:301:MAN:O4	7:A:312:MAN:H2	1.35	1.23
2:P:6:HIS:CG	2:P:81:THR:HG22	1.73	1.22
1:M:174:ASP:O	1:M:205:GLN:NE2	1.71	1.22
1:E:13:THR:HG22	1:E:63:HIS:CE1	1.74	1.21
10:K:308:NAG:C4	10:K:310:BMA:O2	1.89	1.21
1:A:13:THR:HG22	1:A:63:HIS:CE1	1.75	1.21
1:E:142:ARG:NH2	1:M:148:TRP:CD2	2.07	1.21
1:M:13:THR:HG22	1:M:63:HIS:CE1	1.76	1.21
1:K:54:ASN:HD21	10:K:307:NAG:C1	1.54	1.20
3:A:301:MAN:O4	7:A:312:MAN:C2	1.90	1.20
1:I:13:THR:CG2	1:I:63:HIS:CE1	2.24	1.20
1:C:167:LEU:CD1	1:C:169:LEU:HB2	1.70	1.20
1:G:30:LEU:HD11	1:G:75:PHE:CD2	1.77	1.20
1:O:176:SER:O	1:O:177:TYR:HD2	1.24	1.17
1:O:158:SER:HB3	1:O:159:VAL:CG2	1.74	1.17
1:E:172:ARG:CB	1:E:173:LYS:CG	2.22	1.17
1:E:13:THR:CG2	1:E:63:HIS:CE1	2.28	1.17
2:N:70:SER:O	2:N:74:LEU:HD13	1.45	1.15
1:G:30:LEU:CD1	1:G:75:PHE:HD2	1.57	1.15
1:E:159:VAL:HG13	1:E:160:ASP:N	1.58	1.15
1:G:155:LYS:NZ	1:G:170:GLU:CD	2.00	1.15
2:D:84:GLY:O	2:D:85:ARG:HG3	1.47	1.14
1:O:158:SER:HB3	1:O:159:VAL:HG23	1.25	1.14
8:I:306:FUL:C1	9:I:307:NAG:C6	2.26	1.12
1:M:139:LEU:CD2	1:M:181:VAL:HG22	1.79	1.12
8:C:308:FUL:C1	9:C:309:NAG:C6	2.26	1.12
8:G:307:FUL:C1	9:G:308:NAG:C6	2.26	1.11
1:K:37:GLU:HB3	1:K:40:LYS:HE2	1.32	1.11
1:K:54:ASN:ND2	10:K:307:NAG:C1	2.14	1.10
2:H:6:HIS:CD2	2:H:81:THR:CG2	2.33	1.10
1:O:173:LYS:O	1:O:206:THR:HG23	1.49	1.10
1:I:13:THR:CG2	1:I:63:HIS:ND1	2.13	1.09
1:A:13:THR:CG2	1:A:63:HIS:CE1	2.34	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:9:ASP:HB3	1:E:11:LEU:H	1.10	1.09
1:M:169:LEU:CD1	1:M:170:GLU:N	2.15	1.08
1:M:167:LEU:HD13	1:M:169:LEU:HG	1.33	1.08
1:O:176:SER:O	1:O:177:TYR:CD2	2.06	1.08
1:E:159:VAL:HG13	1:E:160:ASP:H	1.01	1.08
1:M:167:LEU:CD1	1:M:169:LEU:CG	2.32	1.08
1:K:9:ASP:HB3	1:K:11:LEU:H	1.08	1.08
1:M:13:THR:CG2	1:M:63:HIS:CE1	2.37	1.07
2:D:60:THR:HG22	2:D:61:GLY:HA3	1.32	1.07
2:H:6:HIS:CD2	2:H:81:THR:HG22	1.90	1.07
1:O:9:ASP:HB3	1:O:11:LEU:H	1.19	1.07
2:D:60:THR:HB	2:D:64:GLU:OE2	1.54	1.06
1:E:13:THR:CG2	1:E:63:HIS:ND1	2.17	1.06
1:E:172:ARG:CD	1:E:173:LYS:CE	2.27	1.05
1:C:167:LEU:O	1:C:167:LEU:HD12	1.56	1.05
1:G:9:ASP:HB3	1:G:11:LEU:H	1.13	1.05
11:M:303:NAG:C4	12:M:308:BMA:O2	2.04	1.05
1:A:9:ASP:HB3	1:A:11:LEU:H	1.17	1.05
1:M:13:THR:CG2	1:M:63:HIS:ND1	2.19	1.04
1:E:159:VAL:CG1	1:E:160:ASP:H	1.69	1.04
2:H:6:HIS:CG	2:H:81:THR:HG22	1.92	1.04
1:G:155:LYS:HZ2	1:G:170:GLU:CD	1.60	1.03
1:C:9:ASP:HB3	1:C:11:LEU:H	1.23	1.03
1:G:46:CYS:SG	1:G:62:CYS:HB2	1.99	1.03
1:A:13:THR:CG2	1:A:63:HIS:ND1	2.22	1.03
2:D:16:ILE:O	2:D:20:LEU:CD1	2.07	1.03
2:D:60:THR:HG22	2:D:61:GLY:CA	1.89	1.02
1:M:9:ASP:HB3	1:M:11:LEU:H	1.21	1.02
10:K:308:NAG:H4	10:K:310:BMA:O2	1.12	1.01
2:N:39:GLU:HA	2:N:39:GLU:OE2	1.56	1.01
1:M:174:ASP:CA	1:M:206:THR:O	2.08	1.01
2:N:70:SER:O	2:N:74:LEU:CD1	2.08	1.01
1:M:169:LEU:HD12	1:M:170:GLU:CA	1.90	1.00
1:E:117:ILE:HB	1:E:164:VAL:HG12	1.43	1.00
1:E:117:ILE:HB	1:E:164:VAL:CG1	1.91	1.00
1:M:174:ASP:CB	1:M:208:SER:HA	1.91	1.00
2:P:38:VAL:HG12	2:P:39:GLU:H	1.25	0.99
2:P:40:THR:O	2:P:43:GLU:CD	2.01	0.99
1:E:172:ARG:HB3	1:E:173:LYS:HG2	1.40	0.99
9:I:308:NAG:HO4	7:I:309:BMA:C1	1.67	0.99
1:I:9:ASP:HB3	1:I:11:LEU:H	1.26	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:11:LEU:HD22	1:O:128:PHE:CG	1.98	0.98
2:P:61:GLY:CA	2:P:62:ASN:OD1	2.11	0.98
2:P:19:GLN:HG3	2:P:20:LEU:N	1.78	0.97
2:D:60:THR:O	2:D:64:GLU:HG3	1.64	0.97
2:D:16:ILE:O	2:D:20:LEU:HD12	1.63	0.97
1:K:9:ASP:HB3	1:K:11:LEU:N	1.80	0.96
11:M:303:NAG:H4	12:M:308:BMA:HO2	1.25	0.96
9:I:308:NAG:H4	7:I:309:BMA:O2	1.66	0.96
2:P:40:THR:O	2:P:43:GLU:CG	2.13	0.96
9:G:309:NAG:H4	7:G:310:BMA:O2	1.66	0.96
6:E:304:NAG:H4	7:E:306:BMA:O2	1.66	0.96
1:C:167:LEU:HD11	1:C:170:GLU:HG3	1.48	0.96
2:N:6:HIS:CD2	2:N:81:THR:HG22	2.01	0.96
9:C:310:NAG:HO4	7:C:311:BMA:C1	1.65	0.95
8:C:308:FUL:C2	9:C:309:NAG:O6	2.15	0.95
2:P:40:THR:O	2:P:43:GLU:HG3	1.66	0.95
1:I:13:THR:HG21	1:I:63:HIS:CE1	2.02	0.94
9:C:310:NAG:H4	7:C:311:BMA:O2	1.66	0.94
1:M:174:ASP:HB2	1:M:208:SER:HA	1.49	0.94
6:A:309:NAG:H4	7:A:310:BMA:O2	1.66	0.94
6:E:304:NAG:HO4	7:E:306:BMA:C1	1.62	0.94
8:G:307:FUL:C2	9:G:308:NAG:O6	2.15	0.93
8:I:306:FUL:C2	9:I:307:NAG:O6	2.15	0.93
1:I:159:VAL:HG23	1:I:160:ASP:N	1.83	0.93
9:G:309:NAG:HO4	7:G:310:BMA:C1	1.64	0.93
1:G:9:ASP:HB3	1:G:11:LEU:N	1.84	0.93
1:G:30:LEU:CD1	1:G:75:PHE:CD2	2.44	0.92
6:A:309:NAG:HO4	7:A:310:BMA:C1	1.69	0.91
2:P:6:HIS:CD2	2:P:81:THR:HG23	2.04	0.91
1:M:173:LYS:O	1:M:206:THR:HG23	1.70	0.91
2:P:61:GLY:HA3	2:P:62:ASN:OD1	1.70	0.91
2:P:94:PRO:HB2	2:P:99:TYR:HE2	1.32	0.91
2:D:60:THR:CG2	2:D:61:GLY:N	2.32	0.90
1:G:30:LEU:HD11	1:G:75:PHE:HD2	1.11	0.90
1:C:167:LEU:C	1:C:167:LEU:HD12	1.92	0.90
2:P:94:PRO:CB	2:P:99:TYR:HE2	1.85	0.89
1:O:54:ASN:ND2	13:O:302:NAG:C1	2.34	0.89
1:O:11:LEU:HD22	1:O:128:PHE:CD2	2.07	0.89
1:E:13:THR:HG21	1:E:63:HIS:CE1	2.06	0.89
2:D:60:THR:CG2	2:D:61:GLY:HA3	2.02	0.89
1:O:166:LEU:HB3	1:O:170:GLU:OE1	1.72	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:6:HIS:NE2	2:P:81:THR:HG21	1.87	0.88
1:M:167:LEU:HD11	1:M:169:LEU:HG	1.53	0.88
2:D:60:THR:O	2:D:64:GLU:CG	2.22	0.87
2:N:93:CYS:HB3	2:N:94:PRO:CD	2.05	0.87
1:M:115:TYR:OH	1:M:206:THR:OG1	1.90	0.87
2:B:90:ARG:CZ	2:B:90:ARG:HB2	2.04	0.87
2:F:2:GLY:O	2:F:6:HIS:N	2.05	0.87
2:H:6:HIS:CD2	2:H:81:THR:HG23	2.07	0.87
1:M:169:LEU:HD12	1:M:169:LEU:C	1.95	0.86
2:N:60:THR:HG22	2:N:61:GLY:H	1.40	0.86
2:H:6:HIS:NE2	2:H:81:THR:CG2	2.37	0.86
2:F:2:GLY:O	2:F:5:ARG:N	2.08	0.86
2:N:18:ASP:OD1	2:N:112:LYS:HD2	1.76	0.86
1:M:167:LEU:HD11	1:M:169:LEU:CG	2.04	0.86
2:P:6:HIS:NE2	2:P:81:THR:CG2	2.38	0.86
1:O:142:ARG:NH2	1:O:147:PRO:O	2.08	0.86
1:O:142:ARG:HH12	1:O:146:ASP:HB2	1.41	0.86
2:P:38:VAL:HG12	2:P:39:GLU:N	1.90	0.85
1:G:30:LEU:HD12	1:G:76:SER:O	1.75	0.85
1:A:188:GLY:O	2:D:92:THR:OG1	1.93	0.85
1:C:54:ASN:HD21	9:C:309:NAG:C1	1.88	0.85
1:A:54:ASN:ND2	6:A:308:NAG:O5	2.09	0.85
9:C:310:NAG:C4	7:C:311:BMA:C1	2.55	0.84
6:E:304:NAG:C4	7:E:306:BMA:C1	2.55	0.84
10:K:308:NAG:H4	10:K:310:BMA:HO2	0.93	0.84
1:E:157:ILE:HG22	1:E:158:SER:N	1.91	0.84
1:E:172:ARG:CB	1:E:173:LYS:HG2	1.99	0.84
1:C:167:LEU:HD12	1:C:169:LEU:N	1.92	0.84
1:M:154:ARG:HH22	12:M:311:MAN:H61	1.42	0.84
9:I:308:NAG:C4	7:I:309:BMA:C1	2.55	0.84
2:N:37:ASP:O	2:N:38:VAL:HG23	1.77	0.84
9:G:309:NAG:C4	7:G:310:BMA:C1	2.55	0.84
1:C:167:LEU:HD13	1:C:169:LEU:CA	2.08	0.84
1:O:173:LYS:O	1:O:206:THR:CG2	2.26	0.84
1:M:174:ASP:HB3	1:M:208:SER:HA	1.60	0.83
2:D:20:LEU:H	2:D:20:LEU:HD12	1.43	0.83
2:P:15:ASP:HA	2:P:18:ASP:OD1	1.78	0.83
6:A:309:NAG:C4	7:A:310:BMA:C1	2.55	0.83
1:I:13:THR:HG21	1:I:63:HIS:HE1	1.40	0.83
1:O:158:SER:CB	1:O:159:VAL:HG23	2.08	0.83
2:D:60:THR:CG2	2:D:61:GLY:CA	2.56	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:167:LEU:HD13	1:M:169:LEU:CG	2.04	0.82
1:O:38:GLU:OE1	2:P:76:ARG:HG2	1.80	0.82
1:C:167:LEU:CD1	1:C:170:GLU:N	2.42	0.82
13:O:303:NAG:H4	13:O:304:BMA:O2	1.78	0.82
1:O:54:ASN:HD21	13:O:302:NAG:C1	1.92	0.82
1:E:9:ASP:HB3	1:E:11:LEU:N	1.90	0.82
1:E:141:TYR:CD2	1:E:171:PHE:CE1	2.68	0.82
1:C:167:LEU:CD1	1:C:169:LEU:N	2.42	0.82
2:P:39:GLU:O	2:P:42:CYS:N	2.12	0.82
1:M:109:VAL:HG21	1:M:204:PHE:CE2	2.15	0.82
1:G:30:LEU:HD21	1:G:75:PHE:CD2	2.15	0.82
1:M:139:LEU:HD22	1:M:181:VAL:HG22	1.59	0.81
1:G:30:LEU:HD11	1:G:75:PHE:CB	2.10	0.81
2:N:93:CYS:HB3	2:N:94:PRO:HD2	1.62	0.81
1:E:15:ILE:HD11	1:E:100:LYS:HD3	1.62	0.81
2:D:60:THR:HG22	2:D:61:GLY:N	1.91	0.81
1:E:172:ARG:HD3	1:E:173:LYS:HE3	1.57	0.81
1:O:46:CYS:SG	1:O:62:CYS:HB2	2.20	0.81
1:G:30:LEU:HD11	1:G:75:PHE:HB2	1.61	0.81
2:N:19:GLN:HG3	2:N:20:LEU:N	1.94	0.81
1:K:1:CYS:HG	1:K:90:CYS:CB	1.93	0.81
2:P:92:THR:HG22	2:P:93:CYS:N	1.96	0.81
1:O:175:SER:O	1:O:206:THR:HG22	1.81	0.80
2:D:84:GLY:O	2:D:85:ARG:CG	2.29	0.80
2:N:6:HIS:NE2	2:N:81:THR:HG22	1.95	0.80
1:K:154:ARG:HH22	10:K:312:MAN:H61	1.46	0.80
1:E:13:THR:HG21	1:E:63:HIS:HE1	1.44	0.80
2:P:6:HIS:CD2	2:P:81:THR:HG21	2.17	0.80
1:C:167:LEU:HD11	1:C:170:GLU:N	1.97	0.80
1:I:30:LEU:HD11	1:I:46:CYS:SG	2.22	0.80
1:C:167:LEU:HD13	1:C:169:LEU:HB2	0.82	0.80
1:G:121:SER:HB2	1:G:162:ARG:HE	1.45	0.79
1:M:167:LEU:HD12	1:M:169:LEU:HG	1.59	0.79
1:O:159:VAL:HG12	1:O:160:ASP:HB3	1.63	0.79
3:A:301:MAN:O4	7:A:312:MAN:O2	1.92	0.79
1:M:157:ILE:HG12	1:M:164:VAL:HG11	1.64	0.79
1:G:155:LYS:HZ1	1:G:170:GLU:CD	1.77	0.79
1:O:158:SER:HB3	1:O:159:VAL:HG22	1.64	0.79
2:N:60:THR:CG2	2:N:61:GLY:H	1.95	0.79
1:O:163:SER:O	1:O:164:VAL:HG12	1.81	0.79
1:O:141:TYR:OH	1:O:155:LYS:NZ	2.16	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:N:58:ALA:O	2:N:64:GLU:OE2	2.02	0.78
1:A:81:ASP:OD2	1:A:83:SER:OG	1.98	0.78
1:G:30:LEU:HD11	1:G:75:PHE:CG	2.18	0.78
2:J:119:ILE:O	2:J:123:LEU:HG	1.83	0.78
1:O:11:LEU:CD2	1:O:128:PHE:CG	2.65	0.78
2:P:61:GLY:HA2	2:P:62:ASN:OD1	1.84	0.78
1:G:7:TYR:O	1:G:15:ILE:HG22	1.84	0.78
1:A:154:ARG:HH22	7:A:312:MAN:H61	1.49	0.77
8:G:307:FUL:C1	9:G:308:NAG:H62	2.14	0.77
1:A:13:THR:HG21	1:A:63:HIS:CE1	2.17	0.77
1:O:158:SER:CB	1:O:159:VAL:CG2	2.59	0.77
8:I:306:FUL:C1	9:I:307:NAG:H62	2.14	0.77
1:M:11:LEU:HD22	1:M:128:PHE:CD2	2.20	0.77
1:M:173:LYS:O	1:M:207:GLN:HB2	1.83	0.77
1:O:176:SER:C	1:O:177:TYR:HD2	1.88	0.77
1:M:169:LEU:HD12	1:M:170:GLU:HA	1.67	0.77
1:I:9:ASP:HB3	1:I:11:LEU:N	1.99	0.77
1:K:38:GLU:OE1	2:L:76:ARG:CG	2.22	0.76
1:I:159:VAL:HG23	1:I:160:ASP:H	1.48	0.76
1:C:167:LEU:CD1	1:C:169:LEU:CA	2.64	0.76
2:L:60:THR:HG22	2:L:61:GLY:H	1.48	0.76
2:F:123:LEU:HD12	2:F:123:LEU:N	1.98	0.76
2:N:37:ASP:O	2:N:38:VAL:CG2	2.33	0.76
8:C:308:FUL:C1	9:C:309:NAG:H62	2.14	0.76
2:P:38:VAL:CG1	2:P:39:GLU:H	1.99	0.76
1:E:142:ARG:NH2	1:M:148:TRP:CE2	2.53	0.76
2:F:103:PRO:HG2	2:F:106:GLU:OE1	1.86	0.76
1:E:172:ARG:CG	1:E:173:LYS:HG2	2.16	0.76
1:G:46:CYS:SG	1:G:62:CYS:CB	2.74	0.76
1:E:115:TYR:OH	1:E:207:GLN:OE1	2.03	0.76
2:D:81:THR:HB	2:D:85:ARG:NH1	1.99	0.76
2:N:60:THR:HG22	2:N:61:GLY:N	2.00	0.76
1:E:141:TYR:CD2	1:E:171:PHE:HE1	2.04	0.76
1:C:167:LEU:O	1:C:167:LEU:CD1	2.34	0.75
2:F:38:VAL:HG12	2:F:39:GLU:O	1.86	0.75
1:K:1:CYS:SG	1:K:90:CYS:CB	2.71	0.75
1:G:30:LEU:HD13	1:G:75:PHE:HD2	1.52	0.75
1:C:54:ASN:ND2	9:C:309:NAG:C1	2.50	0.75
2:F:120:HIS:O	2:F:123:LEU:HD12	1.86	0.74
1:E:172:ARG:CD	1:E:173:LYS:HE3	2.13	0.74
2:F:81:THR:HG23	2:F:81:THR:O	1.86	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:115:TYR:HH	1:O:206:THR:HG1	0.77	0.74
1:M:30:LEU:HD11	1:M:46:CYS:SG	2.28	0.74
1:O:163:SER:C	1:O:164:VAL:CG1	2.55	0.74
1:M:140:GLN:OE1	1:M:198:TRP:CZ2	2.40	0.74
1:M:169:LEU:O	1:M:171:PHE:N	2.20	0.73
2:B:90:ARG:NH1	2:B:90:ARG:CB	2.52	0.73
1:M:9:ASP:HB3	1:M:11:LEU:N	2.01	0.73
2:P:19:GLN:CG	2:P:20:LEU:N	2.51	0.73
11:M:301:FUC:C1	11:M:301:FUC:O4	2.30	0.73
1:M:140:GLN:CD	1:M:198:TRP:CZ2	2.62	0.73
1:K:39:LEU:HD13	1:K:69:PHE:HE1	1.54	0.73
2:P:36:GLU:O	2:P:37:ASP:OD1	2.05	0.73
1:M:13:THR:HG21	1:M:63:HIS:CE1	2.21	0.73
1:E:142:ARG:NH2	1:M:148:TRP:CE3	2.57	0.73
2:N:92:THR:O	2:N:92:THR:HG23	1.89	0.73
1:G:9:ASP:CB	1:G:11:LEU:H	1.96	0.72
1:C:155:LYS:HE3	1:C:170:GLU:OE2	1.88	0.72
1:O:94:LEU:HD23	1:O:97:GLU:HG3	1.71	0.72
1:E:172:ARG:HD3	1:E:173:LYS:HE2	0.74	0.72
2:F:122:HIS:O	2:F:123:LEU:O	2.07	0.72
1:C:174:ASP:H	1:C:206:THR:HG23	1.55	0.72
6:A:309:NAG:C4	7:A:310:BMA:O2	2.38	0.72
1:K:23:LEU:HD12	1:K:24:HIS:N	2.04	0.72
6:E:304:NAG:C4	7:E:306:BMA:O2	2.38	0.72
2:L:97:ASP:OD1	2:L:101:LYS:NZ	2.21	0.72
1:M:156:LEU:CD2	1:M:158:SER:OG	2.37	0.72
1:A:13:THR:HG21	1:A:63:HIS:HE1	1.54	0.72
1:E:172:ARG:HB3	1:E:173:LYS:HG3	0.72	0.71
1:C:115:TYR:HH	1:C:206:THR:HG1	1.32	0.71
1:C:9:ASP:HB3	1:C:11:LEU:N	2.01	0.71
2:N:39:GLU:OE2	2:N:39:GLU:CA	2.37	0.71
1:E:141:TYR:CE2	1:E:171:PHE:CE1	2.77	0.71
1:O:101:PRO:HG2	1:O:184:GLY:HA2	1.73	0.71
9:I:308:NAG:C4	7:I:309:BMA:O2	2.38	0.71
9:G:309:NAG:C4	7:G:310:BMA:O2	2.38	0.71
1:C:167:LEU:HD12	1:C:170:GLU:H	1.55	0.71
1:G:166:LEU:HB3	1:G:170:GLU:OE1	1.89	0.71
1:O:159:VAL:CG1	1:O:160:ASP:HB3	2.20	0.71
2:D:85:ARG:HB2	2:D:85:ARG:HH11	1.54	0.71
1:O:38:GLU:OE1	2:P:76:ARG:CG	2.39	0.71
2:B:90:ARG:HB2	2:B:90:ARG:NH1	2.05	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:38:GLU:OE1	2:H:76:ARG:HG2	1.91	0.71
2:L:43:GLU:OE2	2:L:121:GLN:NE2	2.24	0.71
1:M:140:GLN:NE2	1:M:198:TRP:CE2	2.59	0.70
6:E:304:NAG:H4	7:E:306:BMA:HO2	1.54	0.70
2:D:3:GLN:CG	2:D:82:ASN:HB2	2.21	0.70
2:P:94:PRO:CB	2:P:99:TYR:CE2	2.71	0.70
2:D:20:LEU:N	2:D:20:LEU:HD12	2.05	0.70
1:O:163:SER:C	1:O:164:VAL:HG13	2.12	0.70
1:I:39:LEU:HD13	1:I:69:PHE:HE1	1.55	0.70
1:I:18:LEU:CD2	1:I:28:LEU:HD11	2.22	0.70
2:N:39:GLU:HG3	2:N:40:THR:HB	1.74	0.70
1:A:39:LEU:HD13	1:A:69:PHE:HE1	1.54	0.70
1:M:175:SER:O	1:M:206:THR:HG22	1.91	0.70
2:N:6:HIS:CD2	2:N:81:THR:CG2	2.74	0.70
9:C:310:NAG:C4	7:C:311:BMA:O2	2.38	0.70
1:C:173:LYS:O	1:C:174:ASP:HB3	1.93	0.69
1:A:54:ASN:C	1:A:54:ASN:OD1	2.30	0.69
2:D:102:LYS:NZ	2:D:106:GLU:OE1	2.16	0.69
2:B:90:ARG:HG2	2:B:91:LEU:HD12	1.73	0.69
1:G:173:LYS:O	1:G:174:ASP:HB3	1.92	0.69
1:M:167:LEU:HD11	1:M:169:LEU:CD1	2.22	0.69
2:D:3:GLN:HG3	2:D:82:ASN:HB2	1.73	0.69
1:O:155:LYS:HE2	1:O:170:GLU:OE2	1.91	0.69
1:O:9:ASP:HB3	1:O:11:LEU:N	2.03	0.69
1:K:153:ARG:NH2	1:K:170:GLU:O	2.25	0.69
1:M:13:THR:HG21	1:M:63:HIS:HE1	1.58	0.68
1:A:15:ILE:HG13	1:A:61:THR:HG22	1.75	0.68
1:K:15:ILE:HG13	1:K:61:THR:HG22	1.76	0.68
2:F:2:GLY:O	2:F:5:ARG:CA	2.41	0.68
1:E:147:PRO:HG2	1:E:150:VAL:HG23	1.75	0.68
1:E:164:VAL:HG22	1:E:165:SER:N	2.09	0.68
1:I:15:ILE:HG13	1:I:61:THR:HG22	1.76	0.68
1:O:115:TYR:OH	1:O:207:GLN:NE2	2.26	0.67
1:M:169:LEU:CG	1:M:170:GLU:N	2.56	0.67
1:O:139:LEU:HG	1:O:157:ILE:HD11	1.75	0.67
2:B:90:ARG:CG	2:B:90:ARG:O	2.42	0.67
1:C:167:LEU:CD1	1:C:170:GLU:H	2.03	0.67
1:E:82:GLN:OE1	2:N:65:ARG:NH2	2.27	0.67
2:F:39:GLU:OE2	2:F:42:CYS:SG	2.53	0.67
2:D:85:ARG:CB	2:D:85:ARG:NH1	2.58	0.66
1:I:30:LEU:CD1	1:I:46:CYS:SG	2.84	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:10:TYR:O	1:A:10:TYR:CD2	2.48	0.66
1:G:30:LEU:CD2	1:G:75:PHE:CD2	2.78	0.66
1:E:38:GLU:HG3	2:F:76:ARG:NH1	2.09	0.66
1:M:207:GLN:O	1:M:208:SER:C	2.30	0.66
2:P:92:THR:HG22	2:P:93:CYS:H	1.58	0.66
2:B:59:ASN:O	2:B:60:THR:HG23	1.95	0.66
2:H:60:THR:HG22	2:H:61:GLY:H	1.60	0.66
2:N:6:HIS:NE2	2:N:81:THR:CG2	2.59	0.66
1:E:18:LEU:CD2	1:E:28:LEU:HD11	2.26	0.66
1:M:18:LEU:CD2	1:M:28:LEU:HD11	2.25	0.65
2:B:90:ARG:O	2:B:90:ARG:HG3	1.95	0.65
1:E:38:GLU:HG3	2:F:76:ARG:HH11	1.61	0.65
1:E:157:ILE:CG2	1:E:158:SER:N	2.59	0.65
1:O:163:SER:O	1:O:164:VAL:CG1	2.44	0.65
2:J:103:PRO:HG2	2:J:106:GLU:OE1	1.97	0.65
2:D:85:ARG:HB2	2:D:85:ARG:NH1	2.11	0.65
1:I:160:ASP:OD1	1:I:162:ARG:NH1	2.30	0.65
1:C:155:LYS:CE	1:C:170:GLU:OE2	2.45	0.64
2:D:81:THR:HB	2:D:85:ARG:HH11	1.59	0.64
2:B:103:PRO:HG2	2:B:106:GLU:OE1	1.96	0.64
1:C:154:ARG:HH22	7:C:313:MAN:H61	1.62	0.64
2:F:3:GLN:O	2:F:7:MET:HB2	1.97	0.64
1:M:139:LEU:HD23	1:M:181:VAL:HG22	1.76	0.64
2:H:6:HIS:CE1	2:H:81:THR:HG22	2.32	0.64
1:M:30:LEU:CD1	1:M:46:CYS:SG	2.85	0.64
1:O:15:ILE:HG13	1:O:61:THR:HG22	1.78	0.64
1:M:167:LEU:HD13	1:M:169:LEU:CD2	2.27	0.64
1:C:38:GLU:HG3	2:D:76:ARG:HH11	1.62	0.64
1:M:169:LEU:CD1	1:M:170:GLU:H	2.09	0.64
1:C:167:LEU:CD1	1:C:169:LEU:H	2.09	0.63
1:G:121:SER:CB	1:G:162:ARG:HE	2.11	0.63
2:N:21:LYS:HZ1	2:N:109:GLU:HB2	1.63	0.63
2:H:117:LYS:HE2	2:H:121:GLN:HE22	1.62	0.63
1:C:9:ASP:CG	1:C:13:THR:OG1	2.36	0.63
2:F:3:GLN:OE1	2:F:82:ASN:CG	2.35	0.63
1:I:174:ASP:OD2	1:I:208:SER:OG	2.17	0.63
1:M:172:ARG:HB2	1:M:173:LYS:HD2	1.81	0.63
1:C:120:ARG:HA	1:C:162:ARG:HH12	1.64	0.63
2:P:48:SER:OG	2:P:52:LYS:NZ	2.32	0.63
1:O:18:LEU:CD2	1:O:28:LEU:HD11	2.28	0.63
2:F:123:LEU:CD1	2:F:123:LEU:N	2.61	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:167:LEU:HD11	1:M:169:LEU:HD11	1.81	0.62
1:C:38:GLU:HG3	2:D:76:ARG:NH1	2.14	0.62
1:C:15:ILE:HG13	1:C:61:THR:HG22	1.81	0.62
2:H:6:HIS:CE1	2:H:81:THR:CG2	2.82	0.62
1:C:120:ARG:HA	1:C:162:ARG:NH1	2.14	0.62
2:L:103:PRO:HG2	2:L:106:GLU:OE1	1.99	0.62
1:O:39:LEU:HD13	1:O:69:PHE:HE1	1.63	0.62
1:E:83:SER:OG	1:E:85:GLN:HG2	2.00	0.62
2:H:15:ASP:HA	2:H:18:ASP:HB2	1.82	0.62
1:I:54:ASN:CG	9:I:307:NAG:C1	2.68	0.62
2:F:2:GLY:O	2:F:5:ARG:HB2	1.99	0.61
2:F:123:LEU:HD12	2:F:123:LEU:H	1.63	0.61
1:C:9:ASP:HB2	1:C:13:THR:OG1	2.00	0.61
2:H:70:SER:O	2:H:74:LEU:HG	2.00	0.61
1:K:37:GLU:OE2	1:K:40:LYS:CE	2.48	0.61
1:E:143:ASN:ND2	1:E:146:ASP:OD1	2.30	0.61
2:D:60:THR:HG23	2:D:61:GLY:N	2.13	0.61
1:G:18:LEU:CD2	1:G:28:LEU:HD11	2.31	0.61
2:B:19:GLN:NE2	2:B:70:SER:OG	2.33	0.61
1:M:169:LEU:O	1:M:170:GLU:C	2.36	0.60
1:G:30:LEU:CD1	1:G:75:PHE:HB2	2.30	0.60
1:I:142:ARG:NH2	7:I:312:MAN:O3	2.25	0.60
2:F:18:ASP:O	2:F:21:LYS:HB2	2.01	0.60
1:K:9:ASP:CB	1:K:11:LEU:H	1.99	0.60
1:A:18:LEU:CD2	1:A:28:LEU:HD11	2.31	0.60
1:E:15:ILE:CD1	1:E:100:LYS:HD3	2.32	0.60
2:L:15:ASP:HA	2:L:18:ASP:HB2	1.83	0.60
1:A:154:ARG:HH22	7:A:312:MAN:C6	2.16	0.59
1:E:142:ARG:NH2	1:M:148:TRP:CG	2.42	0.59
1:E:154:ARG:HH22	7:E:308:MAN:H61	1.65	0.59
1:A:41:ASP:O	1:A:41:ASP:OD1	2.20	0.59
1:K:1:CYS:HB3	1:K:90:CYS:SG	2.37	0.59
1:A:154:ARG:NH2	7:A:312:MAN:H61	2.18	0.59
2:N:44:TRP:O	2:N:47:PHE:HB3	2.03	0.59
2:B:90:ARG:CZ	2:B:90:ARG:CB	2.77	0.59
2:F:42:CYS:HB2	2:F:45:SER:CB	2.33	0.59
1:G:173:LYS:HD2	1:G:209:GLU:HB2	1.84	0.59
2:J:36:GLU:OE1	2:J:110:ARG:CZ	2.51	0.59
1:E:53:HIS:HD2	1:E:54:ASN:O	1.86	0.59
2:B:15:ASP:HA	2:B:18:ASP:HB2	1.85	0.59
1:O:115:TYR:CZ	1:O:207:GLN:NE2	2.71	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:9:ASP:CB	1:E:11:LEU:H	1.99	0.58
1:M:11:LEU:HD22	1:M:128:PHE:CG	2.38	0.58
2:H:11:ARG:O	2:H:11:ARG:NH2	2.32	0.58
2:P:103:PRO:HG2	2:P:106:GLU:OE1	2.02	0.58
1:O:141:TYR:CD2	1:O:171:PHE:CE1	2.92	0.58
1:E:156:LEU:O	1:E:157:ILE:HD13	2.04	0.58
2:B:59:ASN:O	2:B:60:THR:CG2	2.51	0.58
1:K:99:ILE:O	1:K:193:GLY:HA3	2.04	0.58
1:G:167:LEU:H	1:G:167:LEU:HD12	1.69	0.58
2:H:6:HIS:ND1	2:H:81:THR:HG22	2.18	0.58
1:K:22:ASN:OD1	1:K:23:LEU:N	2.37	0.58
10:K:308:NAG:C3	10:K:310:BMA:O2	2.52	0.57
1:K:1:CYS:N	5:K:306:SO4:O2	2.38	0.57
2:P:24:VAL:HA	2:P:27:LEU:HD12	1.87	0.57
1:E:164:VAL:O	1:E:164:VAL:HG13	2.03	0.57
1:C:10:TYR:O	1:C:10:TYR:CD2	2.57	0.57
8:I:306:FUL:O2	9:I:307:NAG:O6	2.23	0.57
2:P:94:PRO:HB3	2:P:99:TYR:CE2	2.40	0.57
1:G:39:LEU:HD13	1:G:69:PHE:HE1	1.68	0.57
2:B:19:GLN:HG3	2:B:20:LEU:N	2.18	0.57
2:B:90:ARG:HB3	2:B:90:ARG:HH11	1.70	0.57
2:P:59:ASN:C	2:P:60:THR:HG23	2.25	0.57
1:E:172:ARG:HD3	1:E:173:LYS:CD	2.30	0.57
2:J:91:LEU:O	2:J:91:LEU:HG	2.05	0.57
1:O:158:SER:CB	1:O:159:VAL:HG22	2.28	0.56
1:C:109:VAL:HG22	1:C:117:ILE:HG13	1.86	0.56
1:M:154:ARG:HH22	12:M:311:MAN:C6	2.16	0.56
1:E:159:VAL:CG1	1:E:160:ASP:N	2.31	0.56
1:M:139:LEU:CD2	1:M:181:VAL:CG2	2.70	0.56
1:G:9:ASP:O	1:G:123:TYR:OH	2.23	0.56
1:K:39:LEU:HD13	1:K:69:PHE:CE1	2.39	0.56
1:G:18:LEU:HD21	1:G:28:LEU:HD11	1.86	0.56
1:I:53:HIS:HD2	1:I:54:ASN:O	1.88	0.56
2:F:59:ASN:HA	2:F:64:GLU:OE2	2.04	0.56
1:C:167:LEU:C	1:C:167:LEU:CD1	2.62	0.56
2:B:4:ASP:OD1	2:B:4:ASP:N	2.36	0.56
1:O:171:PHE:HD1	1:O:177:TYR:CE1	2.23	0.56
2:J:36:GLU:OE1	2:J:110:ARG:NE	2.39	0.56
8:G:307:FUL:O2	9:G:308:NAG:O6	2.23	0.56
8:C:308:FUL:O2	9:C:309:NAG:O6	2.23	0.56
1:E:141:TYR:CZ	1:E:171:PHE:CZ	2.93	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:ARG:HG2	1:C:173:LYS:HB2	1.87	0.56
1:C:174:ASP:N	1:C:206:THR:HG23	2.20	0.56
1:C:167:LEU:HD13	1:C:169:LEU:N	2.16	0.56
1:I:94:LEU:HD23	1:I:97:GLU:CD	2.27	0.56
1:E:10:TYR:CD1	1:E:10:TYR:O	2.59	0.56
1:O:107:VAL:O	1:O:202:VAL:HG21	2.05	0.56
1:I:142:ARG:HG3	1:I:152:PRO:HB3	1.88	0.55
1:C:159:VAL:HG11	2:J:121:GLN:HA	1.88	0.55
1:M:4:LEU:HD21	1:M:77:VAL:HB	1.87	0.55
1:I:185:PRO:HG2	1:I:193:GLY:N	2.22	0.55
1:G:10:TYR:CD1	1:G:10:TYR:O	2.60	0.55
1:M:115:TYR:HH	1:M:206:THR:HG1	1.26	0.55
2:P:94:PRO:HB2	2:P:99:TYR:CE2	2.24	0.55
2:J:70:SER:O	2:J:74:LEU:HG	2.06	0.55
1:O:11:LEU:HD21	1:O:128:PHE:HB3	1.87	0.55
1:G:37:GLU:HG2	1:G:40:LYS:HE3	1.87	0.55
1:O:165:SER:O	1:O:166:LEU:HD23	2.07	0.55
2:N:70:SER:O	2:N:74:LEU:HD12	2.05	0.55
6:A:309:NAG:H4	7:A:310:BMA:C2	2.37	0.55
1:M:167:LEU:HD12	1:M:170:GLU:H	1.71	0.55
2:F:3:GLN:HB3	2:F:82:ASN:ND2	2.22	0.55
1:I:161:SER:O	1:I:162:ARG:HB2	2.07	0.55
1:G:173:LYS:CD	1:G:209:GLU:HB2	2.37	0.55
9:I:308:NAG:H4	7:I:309:BMA:C2	2.37	0.55
1:A:9:ASP:HB3	1:A:11:LEU:N	2.03	0.55
1:C:154:ARG:HH22	7:C:313:MAN:C6	2.18	0.55
1:G:155:LYS:HZ3	1:G:166:LEU:HD22	1.71	0.55
2:N:37:ASP:C	2:N:38:VAL:HG23	2.27	0.55
2:F:15:ASP:HA	2:F:18:ASP:HB2	1.88	0.55
1:I:195:TRP:NE1	3:I:301:MAN:C1	2.59	0.54
2:D:20:LEU:O	2:D:21:LYS:C	2.43	0.54
1:K:109:VAL:HG22	1:K:117:ILE:HG13	1.88	0.54
1:O:42:GLU:OE2	1:O:68:HIS:ND1	2.36	0.54
2:D:3:GLN:HG2	2:D:82:ASN:HB2	1.88	0.54
2:D:58:ALA:O	2:D:64:GLU:OE2	2.25	0.54
2:L:4:ASP:CG	2:L:5:ARG:H	2.10	0.54
1:I:109:VAL:HG22	1:I:117:ILE:HG13	1.90	0.54
2:D:15:ASP:HA	2:D:18:ASP:HB2	1.88	0.54
1:O:4:LEU:HD23	1:O:90:CYS:O	2.08	0.54
1:M:140:GLN:CD	1:M:198:TRP:CE2	2.81	0.54
2:B:90:ARG:NH1	2:B:90:ARG:HB3	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:E:304:NAG:H4	7:E:306:BMA:C2	2.37	0.54
1:E:157:ILE:O	1:E:158:SER:OG	2.21	0.54
1:C:174:ASP:CG	1:C:174:ASP:O	2.46	0.54
1:A:2:PRO:HB3	1:M:85:GLN:HG3	1.89	0.54
9:G:309:NAG:H4	7:G:310:BMA:C2	2.37	0.54
2:N:6:HIS:CE1	2:N:81:THR:HG22	2.42	0.54
2:B:90:ARG:CB	2:B:90:ARG:HH11	2.19	0.54
1:E:4:LEU:HD21	1:E:77:VAL:HB	1.89	0.54
2:N:35:PRO:HA	2:N:99:TYR:HD1	1.72	0.54
9:C:310:NAG:H4	7:C:311:BMA:C2	2.37	0.54
1:O:11:LEU:HD22	1:O:128:PHE:CD1	2.43	0.54
1:M:18:LEU:HD21	1:M:28:LEU:HD11	1.91	0.53
2:N:21:LYS:HZ3	2:N:109:GLU:N	2.06	0.53
1:M:167:LEU:CD1	1:M:169:LEU:CD2	2.85	0.53
1:E:99:ILE:O	1:E:193:GLY:HA3	2.08	0.53
9:I:308:NAG:H4	7:I:309:BMA:HO2	1.71	0.53
1:O:11:LEU:CD2	1:O:128:PHE:CD2	2.88	0.53
1:I:137:TYR:OH	1:I:162:ARG:NH1	2.37	0.53
2:F:42:CYS:HB2	2:F:45:SER:HB3	1.89	0.53
1:M:186:MET:O	1:M:189:SER:OG	2.22	0.53
1:M:142:ARG:NH1	1:M:150:VAL:O	2.41	0.53
2:D:85:ARG:CZ	2:D:85:ARG:HB3	2.39	0.53
2:P:38:VAL:CG1	2:P:39:GLU:OE1	2.57	0.53
2:H:20:LEU:CD2	2:H:74:LEU:HD11	2.38	0.53
1:K:54:ASN:CG	10:K:307:NAG:C1	2.77	0.53
1:C:142:ARG:HG3	1:C:152:PRO:HB3	1.90	0.53
1:A:142:ARG:HG3	1:A:152:PRO:HB3	1.90	0.53
1:A:54:ASN:OD1	1:A:55:ALA:N	2.41	0.53
2:B:40:THR:O	2:B:43:GLU:HG3	2.09	0.53
1:M:140:GLN:OE1	1:M:154:ARG:CZ	2.57	0.53
11:M:303:NAG:HO4	12:M:308:BMA:C1	2.12	0.53
2:P:59:ASN:O	2:P:60:THR:CG2	2.57	0.53
1:C:9:ASP:CB	1:C:13:THR:OG1	2.57	0.53
1:K:160:ASP:OD2	1:K:162:ARG:NH1	2.42	0.53
1:E:164:VAL:CG2	1:E:165:SER:N	2.71	0.52
1:K:154:ARG:NH2	10:K:312:MAN:H61	2.19	0.52
1:E:154:ARG:HH22	7:E:308:MAN:C6	2.20	0.52
2:P:6:HIS:CE1	2:P:81:THR:HG21	2.42	0.52
1:M:140:GLN:HG2	1:M:198:TRP:CZ3	2.45	0.52
1:I:159:VAL:CG2	1:I:160:ASP:N	2.56	0.52
1:K:71:ALA:HB1	1:K:96:ALA:HB2	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:174:ASP:HB3	1:M:208:SER:CA	2.37	0.52
1:I:7:TYR:HB2	1:I:15:ILE:HG22	1.92	0.52
1:C:80:THR:HG23	1:C:87:SER:HB3	1.92	0.52
1:I:195:TRP:CD1	3:I:301:MAN:C2	2.83	0.52
1:M:169:LEU:CD1	1:M:169:LEU:C	2.66	0.52
1:K:94:LEU:HD22	1:K:97:GLU:HG3	1.92	0.52
1:M:54:ASN:ND2	11:M:302:NAG:C2	2.68	0.52
2:D:3:GLN:NE2	2:D:122:HIS:HE1	2.07	0.52
1:I:9:ASP:CB	1:I:11:LEU:H	2.11	0.52
2:L:60:THR:HG22	2:L:61:GLY:N	2.22	0.52
1:O:136:GLN:HB3	1:O:186:MET:SD	2.50	0.52
2:P:101:LYS:HD2	2:P:101:LYS:H	1.73	0.52
13:O:302:NAG:H61	13:O:303:NAG:N2	2.25	0.52
1:O:7:TYR:HB2	1:O:15:ILE:HG22	1.92	0.52
2:N:25:ASN:OD1	2:N:25:ASN:N	2.42	0.52
1:C:167:LEU:HD12	1:C:169:LEU:H	1.67	0.52
1:I:185:PRO:HG2	1:I:193:GLY:H	1.75	0.52
1:M:167:LEU:HD11	1:M:170:GLU:HG3	1.91	0.51
2:N:15:ASP:HA	2:N:18:ASP:HB2	1.92	0.51
1:C:206:THR:HG1	1:C:207:GLN:H	1.58	0.51
1:G:154:ARG:HH22	7:G:312:MAN:H61	1.75	0.51
1:M:169:LEU:CG	1:M:170:GLU:H	2.23	0.51
1:G:30:LEU:HD12	1:G:76:SER:C	2.30	0.51
2:D:81:THR:O	2:D:82:ASN:C	2.43	0.51
2:P:19:GLN:HG3	2:P:20:LEU:CA	2.40	0.51
2:J:31:PHE:CE1	2:J:103:PRO:HD3	2.44	0.51
1:K:71:ALA:HA	1:K:95:LEU:HD22	1.92	0.51
1:C:167:LEU:CD1	1:C:169:LEU:C	2.77	0.51
1:E:142:ARG:HG2	1:E:143:ASN:N	2.24	0.51
1:E:116:GLN:OE1	1:E:165:SER:OG	2.28	0.51
1:E:28:LEU:HB2	1:E:48:LEU:HB2	1.90	0.51
11:M:302:NAG:H61	11:M:303:NAG:N2	2.26	0.51
1:O:117:ILE:HD13	1:O:166:LEU:HG	1.92	0.51
1:M:142:ARG:HG2	1:M:152:PRO:HB3	1.91	0.51
1:A:4:LEU:HD23	1:A:90:CYS:O	2.09	0.51
1:I:172:ARG:NH1	1:I:173:LYS:HG3	2.25	0.51
1:C:9:ASP:O	1:C:123:TYR:OH	2.27	0.51
1:M:169:LEU:C	1:M:171:PHE:N	2.64	0.51
1:M:169:LEU:O	1:M:171:PHE:O	2.29	0.51
1:G:97:GLU:HG2	1:G:192:GLN:HE21	1.76	0.51
2:D:24:VAL:HA	2:D:27:LEU:HD12	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:167:LEU:C	1:M:167:LEU:HD12	2.32	0.51
2:P:16:ILE:O	2:P:20:LEU:HB2	2.11	0.51
1:I:30:LEU:HD23	1:I:48:LEU:HD21	1.92	0.51
1:M:46:CYS:SG	1:M:64:MET:SD	3.08	0.51
1:G:121:SER:CB	1:G:162:ARG:NE	2.74	0.51
2:N:38:VAL:HG12	2:N:39:GLU:N	2.26	0.51
1:E:141:TYR:CE2	1:E:171:PHE:CZ	2.99	0.51
2:J:97:ASP:N	2:J:97:ASP:OD1	2.41	0.51
2:D:19:GLN:HG3	2:D:20:LEU:N	2.25	0.50
1:M:119:TRP:HZ2	1:M:161:SER:O	1.94	0.50
1:G:54:ASN:HD21	9:G:308:NAG:C1	2.24	0.50
1:M:167:LEU:CD1	1:M:170:GLU:H	2.24	0.50
1:M:169:LEU:HG	1:M:170:GLU:H	1.76	0.50
2:F:2:GLY:O	2:F:5:ARG:CB	2.59	0.50
1:G:28:LEU:HD22	1:G:79:ILE:HG12	1.94	0.50
1:M:119:TRP:CZ2	1:M:162:ARG:HA	2.46	0.50
2:F:37:ASP:CG	2:F:117:LYS:NZ	2.65	0.50
1:K:53:HIS:HD2	1:K:54:ASN:O	1.93	0.50
2:P:40:THR:C	2:P:43:GLU:HG3	2.29	0.50
2:N:92:THR:O	2:N:93:CYS:O	2.30	0.50
1:I:39:LEU:HD13	1:I:69:PHE:CE1	2.42	0.50
1:I:172:ARG:CZ	1:I:173:LYS:HG3	2.42	0.50
1:M:38:GLU:HG3	2:N:76:ARG:HH11	1.76	0.50
2:F:81:THR:O	2:F:82:ASN:O	2.30	0.50
1:O:141:TYR:CD2	1:O:171:PHE:HE1	2.29	0.50
2:N:58:ALA:O	2:N:64:GLU:CD	2.50	0.50
1:C:175:SER:O	1:C:206:THR:HG22	2.11	0.50
1:I:117:ILE:HD13	1:I:166:LEU:HG	1.93	0.50
2:D:81:THR:CB	2:D:85:ARG:NH1	2.72	0.50
2:N:31:PHE:CE1	2:N:103:PRO:HD3	2.47	0.50
1:M:9:ASP:O	1:M:123:TYR:OH	2.30	0.50
1:G:174:ASP:OD1	1:G:174:ASP:O	2.29	0.50
2:N:4:ASP:OD1	2:N:5:ARG:N	2.45	0.49
1:M:139:LEU:HD11	1:M:164:VAL:HG21	1.93	0.49
2:F:38:VAL:HG12	2:F:39:GLU:N	2.26	0.49
1:M:23:LEU:O	1:M:50:ARG:NH1	2.41	0.49
1:G:4:LEU:HD21	1:G:77:VAL:HB	1.94	0.49
1:I:107:VAL:O	1:I:202:VAL:HG11	2.12	0.49
1:C:66:VAL:HA	1:C:69:PHE:HD2	1.77	0.49
1:C:8:THR:OG1	1:C:9:ASP:N	2.45	0.49
1:M:156:LEU:HD21	1:M:158:SER:OG	2.09	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:119:TRP:CE2	1:M:162:ARG:HA	2.47	0.49
2:J:62:ASN:C	2:J:64:GLU:H	2.16	0.49
1:O:190:SER:HB3	2:P:11:ARG:NH2	2.28	0.49
1:C:154:ARG:NH2	7:C:313:MAN:H61	2.26	0.49
11:M:303:NAG:O4	12:M:308:BMA:C2	2.58	0.49
1:O:166:LEU:HD13	1:O:170:GLU:OE1	2.13	0.49
2:H:54:GLN:HE21	2:H:56:LYS:NZ	2.11	0.49
1:A:94:LEU:HD23	1:A:97:GLU:HG3	1.95	0.49
2:B:6:HIS:CD2	2:B:81:THR:HB	2.47	0.49
1:O:172:ARG:O	1:O:175:SER:OG	2.14	0.49
2:N:60:THR:CG2	2:N:61:GLY:N	2.61	0.49
2:J:95:SER:O	2:J:98:SER:OG	2.21	0.49
1:K:28:LEU:HD22	1:K:79:ILE:HG12	1.94	0.49
1:I:9:ASP:O	1:I:123:TYR:OH	2.30	0.49
1:E:171:PHE:CD2	1:E:171:PHE:N	2.81	0.49
1:C:174:ASP:OD2	1:C:174:ASP:O	2.30	0.49
1:C:175:SER:HG	1:C:177:TYR:HE2	1.59	0.49
2:N:35:PRO:HA	2:N:99:TYR:CD1	2.47	0.49
2:P:23:TYR:HB3	2:P:67:ILE:HD11	1.95	0.49
1:C:53:HIS:HD2	1:C:54:ASN:O	1.95	0.49
2:L:27:LEU:HD13	2:L:55:LEU:HD11	1.95	0.49
2:D:3:GLN:HG3	2:D:82:ASN:CB	2.43	0.49
2:P:38:VAL:HG12	2:P:39:GLU:OE1	2.13	0.49
1:M:139:LEU:HD21	1:M:181:VAL:HG22	1.84	0.49
2:N:38:VAL:O	2:N:39:GLU:OE2	2.30	0.49
1:G:121:SER:CB	1:G:162:ARG:HH21	2.26	0.49
2:J:31:PHE:HB3	2:J:101:LYS:HB3	1.95	0.49
1:E:154:ARG:NH2	7:E:308:MAN:H61	2.27	0.49
1:E:66:VAL:HA	1:E:69:PHE:HD2	1.78	0.49
1:A:8:THR:OG1	1:A:9:ASP:N	2.46	0.48
1:I:185:PRO:HB3	1:I:191:TYR:O	2.14	0.48
1:C:1:CYS:HB3	1:C:90:CYS:HB3	1.67	0.48
1:E:122:ASP:OD1	1:M:53:HIS:HE1	1.96	0.48
1:I:18:LEU:HD21	1:I:28:LEU:HD11	1.94	0.48
2:B:59:ASN:C	2:B:60:THR:HG23	2.33	0.48
2:F:60:THR:N	2:F:64:GLU:OE2	2.31	0.48
1:C:42:GLU:HG3	1:C:43:ALA:N	2.28	0.48
1:G:147:PRO:HB2	1:G:150:VAL:HG23	1.95	0.48
1:K:1:CYS:CA	1:K:90:CYS:SG	2.99	0.48
6:A:309:NAG:C3	7:A:310:BMA:HO2	2.25	0.48
1:O:11:LEU:CD2	1:O:128:PHE:HB3	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:117:ILE:HB	1:I:164:VAL:HG12	1.96	0.48
7:G:312:MAN:H61	7:G:313:MAN:H2	1.60	0.48
2:F:24:VAL:HA	2:F:27:LEU:HD12	1.96	0.48
1:G:85:GLN:HG3	1:O:2:PRO:HB3	1.94	0.48
1:O:53:HIS:HD2	1:O:54:ASN:O	1.96	0.48
1:G:7:TYR:HB2	1:G:15:ILE:CG2	2.44	0.48
2:F:19:GLN:HG3	2:F:20:LEU:N	2.27	0.48
2:D:85:ARG:CZ	2:D:85:ARG:CB	2.90	0.48
1:E:48:LEU:HD23	1:E:62:CYS:HB3	1.96	0.48
12:M:308:BMA:C6	12:M:310:MAN:O2	2.61	0.48
1:C:18:LEU:CD2	1:C:28:LEU:HD11	2.44	0.48
2:P:97:ASP:N	2:P:97:ASP:OD1	2.33	0.48
1:E:172:ARG:HG2	1:E:173:LYS:HG2	1.93	0.48
1:G:155:LYS:NZ	1:G:166:LEU:HD22	2.28	0.48
1:O:70:MET:O	1:O:95:LEU:HD23	2.13	0.48
1:G:8:THR:OG1	1:G:9:ASP:N	2.39	0.48
2:P:39:GLU:O	2:P:42:CYS:HB2	2.14	0.48
2:B:91:LEU:N	2:B:91:LEU:HD12	2.29	0.48
2:L:31:PHE:HB3	2:L:101:LYS:HB3	1.96	0.48
2:J:60:THR:O	2:J:61:GLY:C	2.50	0.48
1:I:4:LEU:HD21	1:I:77:VAL:HB	1.95	0.48
9:G:308:NAG:H61	9:G:309:NAG:N2	2.29	0.48
1:E:170:GLU:HB2	1:E:171:PHE:CD2	2.49	0.48
1:I:38:GLU:OE1	2:J:76:ARG:HG2	2.14	0.48
2:H:31:PHE:CE1	2:H:103:PRO:HD3	2.48	0.47
6:E:303:NAG:H61	6:E:304:NAG:N2	2.29	0.47
2:D:81:THR:O	2:D:82:ASN:HB3	2.14	0.47
1:O:54:ASN:CG	13:O:302:NAG:C1	2.82	0.47
2:N:60:THR:HB	2:N:64:GLU:OE2	2.14	0.47
2:F:42:CYS:HB2	2:F:45:SER:HB2	1.95	0.47
2:P:31:PHE:HB3	2:P:101:LYS:HB3	1.95	0.47
2:F:31:PHE:HB3	2:F:101:LYS:HB3	1.95	0.47
2:D:60:THR:O	2:D:64:GLU:HG2	2.10	0.47
1:E:171:PHE:HD1	1:E:177:TYR:CE1	2.32	0.47
2:H:19:GLN:HB2	2:H:19:GLN:HE21	1.53	0.47
2:H:89:HIS:O	2:H:92:THR:N	2.43	0.47
1:I:17:ILE:HG21	9:I:308:NAG:H82	1.96	0.47
1:E:158:SER:HB3	1:E:159:VAL:HA	1.97	0.47
1:A:9:ASP:O	1:A:123:TYR:OH	2.33	0.47
1:G:46:CYS:HG	1:G:62:CYS:CB	2.28	0.47
1:O:46:CYS:SG	1:O:62:CYS:CB	2.99	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:7:TYR:HB2	1:K:15:ILE:HG22	1.97	0.47
1:G:140:GLN:HB2	1:G:198:TRP:CH2	2.49	0.47
2:P:6:HIS:CE1	2:P:81:THR:CG2	2.97	0.47
1:O:171:PHE:HD1	1:O:177:TYR:CD1	2.33	0.47
2:B:91:LEU:HD23	2:P:121:GLN:HB3	1.96	0.47
1:G:53:HIS:HD2	1:G:54:ASN:O	1.98	0.47
9:C:309:NAG:H61	9:C:310:NAG:N2	2.29	0.47
2:P:40:THR:O	2:P:43:GLU:OE2	2.31	0.47
1:G:38:GLU:OE1	2:H:76:ARG:NH1	2.47	0.47
1:A:39:LEU:HD13	1:A:69:PHE:CE1	2.43	0.47
1:E:18:LEU:HD21	1:E:28:LEU:HD11	1.96	0.47
2:B:20:LEU:HD12	2:B:20:LEU:HA	1.71	0.47
1:K:71:ALA:CB	1:K:191:TYR:CE1	2.97	0.47
1:A:172:ARG:HG3	1:A:173:LYS:N	2.30	0.47
2:F:70:SER:O	2:F:74:LEU:HG	2.15	0.47
2:N:93:CYS:CB	2:N:94:PRO:CD	2.79	0.47
2:N:21:LYS:NZ	2:N:109:GLU:HB2	2.27	0.47
1:O:136:GLN:OE1	1:O:156:LEU:HD11	2.15	0.47
1:G:70:MET:O	1:G:95:LEU:HD23	2.15	0.47
9:I:307:NAG:H61	9:I:308:NAG:N2	2.29	0.47
2:F:81:THR:CG2	2:F:81:THR:O	2.57	0.47
1:I:66:VAL:HA	1:I:69:PHE:HD2	1.79	0.47
1:K:28:LEU:HB2	1:K:48:LEU:HB2	1.95	0.47
1:E:107:VAL:O	1:E:202:VAL:HG11	2.15	0.47
2:N:30:GLU:O	2:N:104:PRO:HD3	2.14	0.47
1:I:172:ARG:HA	1:I:172:ARG:HD2	1.42	0.47
1:M:101:PRO:HG2	1:M:184:GLY:HA2	1.96	0.47
10:K:307:NAG:H61	10:K:308:NAG:N2	2.29	0.46
2:D:85:ARG:NH1	2:D:85:ARG:HB3	2.30	0.46
1:C:81:ASP:OD1	1:C:83:SER:OG	2.28	0.46
9:G:309:NAG:H4	7:G:310:BMA:HO2	1.75	0.46
2:N:93:CYS:HB3	2:N:94:PRO:HD3	1.93	0.46
1:O:142:ARG:NH1	1:O:143:ASN:O	2.48	0.46
1:C:1:CYS:SG	1:C:88:GLN:HG2	2.55	0.46
2:B:23:TYR:HB3	2:B:67:ILE:HD11	1.97	0.46
2:J:15:ASP:HA	2:J:18:ASP:HB2	1.98	0.46
2:D:19:GLN:HE21	2:D:19:GLN:HB2	1.33	0.46
1:M:30:LEU:HG	1:M:46:CYS:SG	2.55	0.46
1:A:10:TYR:O	1:A:10:TYR:HD2	1.97	0.46
1:M:81:ASP:OD2	1:M:83:SER:OG	2.32	0.46
1:E:134:LYS:HE3	2:F:11:ARG:HH22	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:6:HIS:CG	2:P:81:THR:CG2	2.57	0.46
1:I:142:ARG:HH22	7:I:312:MAN:HO3	1.58	0.46
1:K:107:VAL:O	1:K:202:VAL:HG11	2.15	0.46
12:M:310:MAN:H61	12:M:311:MAN:H2	1.45	0.46
6:A:308:NAG:H61	6:A:309:NAG:N2	2.29	0.46
1:M:169:LEU:HD11	1:M:170:GLU:HG3	1.97	0.46
2:N:24:VAL:HA	2:N:27:LEU:HD12	1.97	0.46
1:O:8:THR:OG1	1:O:9:ASP:N	2.48	0.46
1:O:142:ARG:NH1	1:O:146:ASP:HB2	2.19	0.46
1:G:175:SER:O	1:G:206:THR:OG1	2.29	0.46
1:M:172:ARG:HA	1:M:173:LYS:HA	1.53	0.46
1:C:8:THR:HG21	1:C:95:LEU:HD13	1.97	0.46
2:L:4:ASP:OD1	2:L:5:ARG:N	2.48	0.46
2:F:37:ASP:CG	2:F:117:LYS:HZ1	2.19	0.46
2:H:23:TYR:HB3	2:H:67:ILE:HD11	1.98	0.46
12:M:308:BMA:H62	12:M:310:MAN:O2	2.15	0.46
2:L:31:PHE:CE1	2:L:103:PRO:HD3	2.50	0.46
2:P:57:SER:HB3	2:P:67:ILE:HG21	1.98	0.46
1:M:74:ILE:HD13	1:M:94:LEU:HA	1.98	0.46
2:P:58:ALA:O	2:P:64:GLU:OE2	2.34	0.46
7:A:312:MAN:H61	7:A:313:MAN:H2	1.61	0.46
2:L:117:LYS:O	2:L:121:GLN:HG3	2.16	0.46
1:E:54:ASN:OD1	1:E:54:ASN:C	2.54	0.46
1:A:109:VAL:HG22	1:A:117:ILE:HG13	1.97	0.46
1:E:161:SER:O	1:E:162:ARG:CB	2.63	0.46
2:J:19:GLN:HE21	2:J:19:GLN:HB2	1.52	0.46
1:C:4:LEU:HD21	1:C:77:VAL:HB	1.96	0.46
1:E:155:LYS:HG2	1:E:156:LEU:O	2.16	0.45
1:I:28:LEU:HB2	1:I:48:LEU:HB2	1.99	0.45
2:J:60:THR:C	2:J:61:GLY:O	2.49	0.45
1:A:157:ILE:CD1	1:A:157:ILE:N	2.80	0.45
1:C:167:LEU:HD11	1:C:170:GLU:CG	2.33	0.45
1:I:151:SER:HA	1:I:152:PRO:HD2	1.84	0.45
1:G:37:GLU:HG2	1:G:40:LYS:CE	2.46	0.45
1:C:18:LEU:HD21	1:C:60:TYR:CE2	2.51	0.45
1:A:107:VAL:O	1:A:202:VAL:HG11	2.15	0.45
1:C:175:SER:OG	1:C:177:TYR:HE2	1.99	0.45
2:P:59:ASN:C	2:P:60:THR:CG2	2.84	0.45
6:E:304:NAG:C4	7:E:306:BMA:C2	2.95	0.45
1:C:167:LEU:O	1:C:167:LEU:CG	2.65	0.45
2:D:60:THR:HG23	2:D:61:GLY:CA	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:38:VAL:CG1	2:F:39:GLU:N	2.80	0.45
1:C:18:LEU:HD12	1:C:18:LEU:C	2.37	0.45
2:J:3:GLN:NE2	2:J:81:THR:O	2.50	0.45
2:H:24:VAL:HA	2:H:27:LEU:HD12	1.97	0.45
2:F:3:GLN:CB	2:F:82:ASN:ND2	2.79	0.45
1:M:139:LEU:CD1	1:M:164:VAL:HG21	2.47	0.45
1:I:30:LEU:HG	1:I:46:CYS:SG	2.56	0.45
2:B:90:ARG:C	2:B:91:LEU:HD12	2.36	0.45
1:O:140:GLN:HB2	1:O:198:TRP:CH2	2.52	0.45
1:C:74:ILE:HD13	1:C:94:LEU:HA	1.99	0.45
2:H:103:PRO:HG2	2:H:106:GLU:OE1	2.16	0.45
1:M:11:LEU:CD2	1:M:128:PHE:CG	2.99	0.45
1:A:7:TYR:HB2	1:A:15:ILE:HG22	1.99	0.45
1:O:8:THR:HG21	1:O:95:LEU:CD1	2.47	0.45
1:E:53:HIS:HE1	1:M:122:ASP:OD1	1.99	0.45
1:G:107:VAL:O	1:G:202:VAL:HG11	2.16	0.45
1:K:142:ARG:HG3	1:K:152:PRO:HB3	1.98	0.45
2:N:6:HIS:HD2	2:N:79:PRO:O	1.99	0.45
1:I:158:SER:O	1:I:159:VAL:HG22	2.17	0.45
13:O:303:NAG:C4	13:O:304:BMA:O2	2.60	0.45
2:D:70:SER:O	2:D:74:LEU:HG	2.15	0.45
2:D:23:TYR:HB3	2:D:67:ILE:HD11	1.98	0.45
10:K:310:BMA:C6	10:K:311:MAN:O2	2.64	0.45
1:A:8:THR:HG21	1:A:95:LEU:HD13	1.99	0.45
1:M:109:VAL:HG21	1:M:204:PHE:CD2	2.50	0.45
1:O:83:SER:CB	1:O:85:GLN:HG2	2.47	0.45
1:C:167:LEU:HA	1:C:168:PRO:HD3	1.70	0.44
1:O:158:SER:CA	1:O:159:VAL:CG2	2.95	0.44
1:M:8:THR:OG1	1:M:9:ASP:N	2.49	0.44
1:K:66:VAL:HA	1:K:69:PHE:HD2	1.82	0.44
2:L:50:PHE:HB3	2:L:111:PHE:CE2	2.52	0.44
2:D:31:PHE:HB3	2:D:101:LYS:HB3	1.99	0.44
9:C:310:NAG:C4	7:C:311:BMA:C2	2.95	0.44
1:E:138:GLU:HG3	1:E:156:LEU:HD23	1.98	0.44
2:H:6:HIS:NE2	2:H:81:THR:HG21	2.26	0.44
2:D:102:LYS:HD2	2:D:103:PRO:HD2	1.99	0.44
2:H:71:ILE:HA	2:H:74:LEU:HD12	1.99	0.44
1:I:139:LEU:HD12	1:I:140:GLN:H	1.82	0.44
1:K:186:MET:HA	1:K:187:PRO:HD3	1.83	0.44
1:K:11:LEU:HD22	1:K:128:PHE:CG	2.51	0.44
1:I:161:SER:O	1:I:162:ARG:CB	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:39:LEU:HD13	1:O:69:PHE:CE1	2.48	0.44
2:H:20:LEU:HD12	2:H:20:LEU:HA	1.79	0.44
1:A:94:LEU:HD23	1:A:97:GLU:CG	2.48	0.44
1:O:194:THR:OG1	1:O:195:TRP:N	2.51	0.44
1:E:172:ARG:HD2	1:E:173:LYS:HE3	1.92	0.44
2:H:41:ASN:HB3	2:H:89:HIS:HD2	1.83	0.44
1:G:186:MET:HA	1:G:187:PRO:HD3	1.87	0.44
1:M:192:GLN:OE1	1:M:193:GLY:N	2.44	0.44
2:B:24:VAL:HA	2:B:27:LEU:HD12	1.99	0.44
13:O:305:MAN:H61	13:O:306:MAN:H2	1.38	0.44
1:K:71:ALA:HB2	1:K:191:TYR:CE1	2.52	0.44
1:A:190:SER:OG	2:B:11:ARG:NH2	2.50	0.44
2:L:20:LEU:HA	2:L:20:LEU:HD12	1.80	0.44
1:M:54:ASN:ND2	11:M:302:NAG:N2	2.65	0.44
1:C:167:LEU:CD1	1:C:169:LEU:CB	2.47	0.44
2:D:106:GLU:HA	2:D:109:GLU:HG2	2.00	0.44
1:C:10:TYR:HE2	1:C:67:PHE:HA	1.83	0.44
1:E:175:SER:O	1:E:206:THR:HG22	2.17	0.44
1:E:8:THR:HG21	1:E:95:LEU:CD1	2.47	0.44
1:M:66:VAL:HA	1:M:69:PHE:HD2	1.83	0.44
2:F:81:THR:O	2:F:82:ASN:C	2.56	0.44
1:O:175:SER:OG	1:O:177:TYR:CE2	2.71	0.44
1:E:158:SER:CB	1:E:159:VAL:HA	2.48	0.44
2:F:37:ASP:OD1	2:F:117:LYS:NZ	2.51	0.44
1:A:157:ILE:N	1:A:157:ILE:HD12	2.32	0.44
2:L:12:GLN:O	2:L:16:ILE:HG13	2.18	0.44
1:A:54:ASN:HD22	6:A:308:NAG:C1	2.10	0.43
2:P:77:LYS:HA	2:P:78:PRO:HD3	1.91	0.43
3:A:301:MAN:HO4	7:A:312:MAN:C2	1.92	0.43
2:N:19:GLN:NE2	2:N:70:SER:OG	2.51	0.43
1:A:48:LEU:HD23	1:A:62:CYS:HB3	2.00	0.43
2:F:60:THR:HB	2:F:61:GLY:H	1.57	0.43
1:I:186:MET:HA	1:I:187:PRO:HD2	1.81	0.43
1:G:74:ILE:HD13	1:G:94:LEU:HA	2.00	0.43
1:G:54:ASN:ND2	9:G:308:NAG:C1	2.82	0.43
1:G:174:ASP:C	1:G:174:ASP:OD1	2.56	0.43
1:I:172:ARG:NH2	1:I:173:LYS:HD2	2.32	0.43
2:L:109:GLU:O	2:L:113:SER:OG	2.34	0.43
2:N:95:SER:OG	2:N:96:CYS:N	2.51	0.43
1:M:173:LYS:C	1:M:206:THR:HG23	2.35	0.43
1:A:195:TRP:NE1	3:A:301:MAN:H3	2.30	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:ARG:HG3	1:C:173:LYS:HE2	2.00	0.43
1:O:66:VAL:HA	1:O:69:PHE:HD2	1.83	0.43
1:C:140:GLN:HB2	1:C:198:TRP:CH2	2.53	0.43
2:D:81:THR:CB	2:D:85:ARG:HH11	2.29	0.43
1:I:158:SER:O	1:I:159:VAL:C	2.56	0.43
2:B:18:ASP:O	2:B:21:LYS:HB2	2.19	0.43
1:K:71:ALA:HB2	1:K:191:TYR:OH	2.18	0.43
1:M:156:LEU:HD23	1:M:158:SER:N	2.32	0.43
2:P:59:ASN:O	2:P:60:THR:HG23	2.19	0.43
1:K:74:ILE:HD13	1:K:94:LEU:HA	2.01	0.43
1:C:94:LEU:HD23	1:C:97:GLU:CD	2.38	0.43
1:K:140:GLN:HB2	1:K:198:TRP:CH2	2.53	0.43
1:K:73:ASP:OD1	2:L:76:ARG:NH2	2.52	0.43
1:C:115:TYR:OH	1:C:206:THR:OG1	2.12	0.43
2:N:95:SER:OG	2:N:97:ASP:OD1	2.32	0.43
1:I:70:MET:O	1:I:95:LEU:HD23	2.19	0.43
2:J:39:GLU:O	2:J:42:CYS:N	2.46	0.43
9:G:309:NAG:C4	7:G:310:BMA:C2	2.95	0.43
2:F:102:LYS:HD2	2:F:103:PRO:HD2	2.00	0.43
2:B:70:SER:O	2:B:74:LEU:HG	2.17	0.43
2:P:101:LYS:HD2	2:P:101:LYS:N	2.33	0.43
1:G:25:PRO:HD3	1:G:50:ARG:HH21	1.83	0.43
1:G:109:VAL:HG22	1:G:117:ILE:HG13	2.00	0.43
1:M:166:LEU:HD12	1:M:171:PHE:HZ	1.83	0.43
1:M:167:LEU:HA	1:M:168:PRO:HD3	1.76	0.43
1:K:11:LEU:HD22	1:K:128:PHE:CD2	2.54	0.43
2:N:6:HIS:HE2	2:N:44:TRP:HH2	1.66	0.43
2:B:91:LEU:HD22	2:P:121:GLN:HG2	2.00	0.43
1:O:147:PRO:O	1:O:150:VAL:HG13	2.19	0.43
1:E:141:TYR:CG	1:E:171:PHE:HE1	2.36	0.43
7:C:313:MAN:H61	7:C:314:MAN:H2	1.61	0.43
1:A:172:ARG:HG3	1:A:173:LYS:H	1.84	0.43
1:I:28:LEU:HD22	1:I:79:ILE:HG12	2.01	0.42
7:E:308:MAN:H61	7:E:309:MAN:H2	1.61	0.42
2:N:23:TYR:HB3	2:N:67:ILE:HD11	2.01	0.42
2:D:81:THR:CG2	2:D:85:ARG:NH1	2.82	0.42
1:M:38:GLU:HG3	2:N:76:ARG:NH1	2.34	0.42
2:L:77:LYS:HA	2:L:78:PRO:HD3	1.90	0.42
2:N:77:LYS:HA	2:N:78:PRO:HD3	1.83	0.42
1:A:195:TRP:HE1	3:A:301:MAN:H2	0.96	0.42
1:O:109:VAL:HG22	1:O:117:ILE:HG13	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:H:92:THR:HG22	2:H:92:THR:O	2.18	0.42
2:D:81:THR:CG2	2:D:85:ARG:HH12	2.33	0.42
1:K:37:GLU:OE2	1:K:40:LYS:HE3	2.19	0.42
1:M:109:VAL:HG11	1:M:204:PHE:CZ	2.53	0.42
1:G:66:VAL:HA	1:G:69:PHE:HD2	1.84	0.42
1:A:140:GLN:HB2	1:A:198:TRP:CH2	2.54	0.42
2:H:78:PRO:HA	2:H:79:PRO:HD3	1.92	0.42
1:K:27:THR:OG1	1:K:80:THR:HB	2.20	0.42
1:C:12:GLN:HA	1:C:64:MET:O	2.19	0.42
9:I:308:NAG:C4	7:I:309:BMA:C2	2.95	0.42
2:L:102:LYS:HD2	2:L:103:PRO:HD2	2.00	0.42
11:M:302:NAG:H61	11:M:303:NAG:HN2	1.84	0.42
1:A:11:LEU:HD22	1:A:128:PHE:CD2	2.54	0.42
2:H:117:LYS:CE	2:H:121:GLN:HE22	2.30	0.42
1:E:83:SER:OG	1:E:85:GLN:CG	2.67	0.42
2:H:6:HIS:O	2:H:10:MET:HG2	2.19	0.42
1:M:70:MET:O	1:M:95:LEU:HD23	2.20	0.42
1:E:117:ILE:O	1:E:164:VAL:N	2.44	0.42
13:O:302:NAG:H61	13:O:303:NAG:HN2	1.83	0.42
1:G:121:SER:HB3	1:G:162:ARG:NE	2.35	0.42
1:C:10:TYR:CE2	1:C:67:PHE:HA	2.54	0.42
1:A:94:LEU:HD23	1:A:97:GLU:CD	2.39	0.42
2:J:77:LYS:HA	2:J:78:PRO:HD3	1.91	0.42
2:D:80:SER:O	2:D:82:ASN:N	2.51	0.42
1:G:121:SER:O	1:G:124:GLU:HB2	2.20	0.42
7:I:311:MAN:H61	7:I:312:MAN:H2	1.61	0.42
1:O:83:SER:OG	1:O:85:GLN:HG2	2.20	0.42
1:M:154:ARG:NH2	12:M:311:MAN:H61	2.23	0.42
1:A:70:MET:O	1:A:95:LEU:HD23	2.20	0.42
2:D:91:LEU:HA	2:D:91:LEU:HD12	1.94	0.42
1:I:173:LYS:H	1:I:173:LYS:HG3	1.59	0.42
2:J:23:TYR:HB3	2:J:67:ILE:HD11	2.02	0.42
1:E:25:PRO:HD3	1:E:50:ARG:HH21	1.85	0.42
1:O:165:SER:C	1:O:166:LEU:HD23	2.40	0.42
2:L:60:THR:CG2	2:L:61:GLY:H	2.26	0.42
2:H:11:ARG:HD2	2:H:11:ARG:HA	1.91	0.42
1:I:99:ILE:O	1:I:193:GLY:HA3	2.20	0.42
1:A:99:ILE:O	1:A:193:GLY:HA3	2.20	0.42
1:O:175:SER:OG	1:O:177:TYR:HE2	2.03	0.41
1:E:147:PRO:HB3	1:M:145:GLY:O	2.20	0.41
9:C:309:NAG:H61	9:C:310:NAG:HN2	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:8:THR:HG21	1:M:95:LEU:HD13	2.02	0.41
1:G:174:ASP:CG	1:G:174:ASP:O	2.59	0.41
1:C:83:SER:OG	1:C:85:GLN:HB2	2.21	0.41
1:E:8:THR:HG21	1:E:95:LEU:HD13	2.02	0.41
1:E:70:MET:O	1:E:95:LEU:HD23	2.20	0.41
2:H:39:GLU:HB2	2:H:42:CYS:SG	2.60	0.41
2:F:95:SER:OG	2:F:97:ASP:OD1	2.37	0.41
9:G:308:NAG:H61	9:G:309:NAG:HN2	1.85	0.41
9:C:310:NAG:C3	7:C:311:BMA:O2	2.69	0.41
6:E:304:NAG:O3	7:E:306:BMA:O2	2.27	0.41
2:P:62:ASN:ND2	2:P:65:ARG:HH12	2.18	0.41
1:E:141:TYR:OH	1:E:153:ARG:HD2	2.20	0.41
1:A:18:LEU:HD21	1:A:28:LEU:HD11	2.00	0.41
1:C:142:ARG:CG	1:C:152:PRO:HB3	2.49	0.41
1:C:1:CYS:N	5:C:305:SO4:O1	2.52	0.41
6:A:308:NAG:H61	6:A:309:NAG:HN2	1.86	0.41
2:D:84:GLY:O	2:D:85:ARG:CB	2.68	0.41
2:D:91:LEU:HB3	2:D:92:THR:H	1.45	0.41
2:P:92:THR:CG2	2:P:93:CYS:H	2.21	0.41
1:G:15:ILE:HD13	1:G:15:ILE:HG21	1.74	0.41
1:K:71:ALA:HB1	1:K:191:TYR:CE1	2.55	0.41
2:H:54:GLN:HE21	2:H:56:LYS:HZ2	1.67	0.41
1:G:134:LYS:HD3	1:G:191:TYR:CE2	2.55	0.41
9:I:307:NAG:H61	9:I:308:NAG:HN2	1.86	0.41
1:O:159:VAL:CG1	1:O:160:ASP:CB	2.95	0.41
1:M:48:LEU:HD23	1:M:62:CYS:HB3	2.01	0.41
1:A:28:LEU:HB2	1:A:48:LEU:HB2	2.03	0.41
2:H:54:GLN:NE2	2:H:56:LYS:NZ	2.68	0.41
1:O:195:TRP:HE1	3:O:307:MAN:H2	1.68	0.41
2:H:93:CYS:HA	2:H:94:PRO:HD3	1.95	0.41
1:M:117:ILE:HB	1:M:164:VAL:HG23	2.03	0.41
1:E:53:HIS:CD2	1:E:54:ASN:O	2.71	0.41
1:M:15:ILE:HG22	1:M:61:THR:HG22	2.02	0.41
2:F:23:TYR:HB3	2:F:67:ILE:HD11	2.02	0.41
1:E:172:ARG:HD3	1:E:173:LYS:CG	2.51	0.41
9:G:309:NAG:C3	7:G:310:BMA:O2	2.69	0.41
6:E:304:NAG:C3	7:E:306:BMA:O2	2.69	0.41
1:C:38:GLU:HG2	1:C:38:GLU:H	1.62	0.41
1:C:54:ASN:HB2	1:C:55:ALA:H	1.73	0.41
1:G:155:LYS:NZ	1:G:170:GLU:OE1	2.29	0.41
1:K:1:CYS:SG	1:K:90:CYS:HA	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:174:ASP:O	1:O:206:THR:HG22	2.21	0.41
1:E:9:ASP:O	1:E:123:TYR:OH	2.38	0.41
1:K:9:ASP:OD2	1:K:11:LEU:HB2	2.20	0.41
1:O:11:LEU:CD2	1:O:128:PHE:CB	2.99	0.41
2:P:20:LEU:HD12	2:P:20:LEU:HA	1.74	0.41
1:I:142:ARG:CG	1:I:152:PRO:HB3	2.51	0.41
1:C:10:TYR:HD2	1:C:10:TYR:O	1.99	0.41
2:L:24:VAL:HA	2:L:27:LEU:HD12	2.02	0.41
2:L:10:MET:HE3	2:L:115:LEU:HD22	2.02	0.41
1:A:195:TRP:NE1	3:A:301:MAN:C3	2.57	0.41
2:H:6:HIS:HE2	2:H:44:TRP:HZ2	1.69	0.41
1:G:121:SER:CB	1:G:162:ARG:NH2	2.84	0.41
1:E:140:GLN:HB2	1:E:198:TRP:CH2	2.56	0.41
1:A:153:ARG:HD2	1:A:153:ARG:HA	1.77	0.41
2:D:6:HIS:HE1	2:D:44:TRP:CZ2	2.39	0.41
1:C:206:THR:OG1	1:C:207:GLN:N	2.54	0.40
1:I:74:ILE:HD13	1:I:94:LEU:HA	2.02	0.40
1:I:30:LEU:CG	1:I:46:CYS:SG	3.10	0.40
2:H:27:LEU:HD13	2:H:55:LEU:HD11	2.03	0.40
1:E:39:LEU:HD23	1:E:39:LEU:HA	1.58	0.40
2:J:24:VAL:HA	2:J:27:LEU:HD12	2.02	0.40
9:G:309:NAG:H4	7:G:310:BMA:C1	2.47	0.40
1:M:169:LEU:CD1	1:M:170:GLU:CA	2.79	0.40
1:M:139:LEU:HD22	1:M:179:LEU:HD21	2.02	0.40
2:P:102:LYS:HD2	2:P:103:PRO:HD2	2.04	0.40
2:P:70:SER:O	2:P:74:LEU:HG	2.21	0.40
1:I:171:PHE:HB3	1:I:206:THR:HG21	2.03	0.40
2:N:110:ARG:O	2:N:113:SER:OG	2.29	0.40
11:M:303:NAG:C4	12:M:308:BMA:C2	2.99	0.40
9:I:308:NAG:C3	7:I:309:BMA:O2	2.69	0.40
1:A:18:LEU:HD23	1:A:28:LEU:HD11	2.02	0.40
3:G:301:MAN:HO4	7:G:312:MAN:HO3	1.65	0.40
2:J:10:MET:HE3	2:J:78:PRO:HB3	2.04	0.40
1:G:11:LEU:HD22	1:G:128:PHE:CD2	2.56	0.40
1:O:18:LEU:HD23	1:O:28:LEU:HD11	2.02	0.40
1:C:99:ILE:O	1:C:193:GLY:HA3	2.22	0.40
1:A:56:THR:OG1	1:A:57:HIS:HD2	2.04	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)
1:M:156:LEU:O	2:N:39:GLU:CG[4_455]	2.07	0.13

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	206/219 (94%)	202 (98%)	4 (2%)	0	100	100
1	C	207/219 (94%)	198 (96%)	9 (4%)	0	100	100
1	E	205/219 (94%)	200 (98%)	5 (2%)	0	100	100
1	G	207/219 (94%)	199 (96%)	8 (4%)	0	100	100
1	I	207/219 (94%)	199 (96%)	7 (3%)	1 (0%)	34	69
1	K	207/219 (94%)	197 (95%)	10 (5%)	0	100	100
1	M	206/219 (94%)	197 (96%)	8 (4%)	1 (0%)	34	69
1	O	206/219 (94%)	196 (95%)	10 (5%)	0	100	100
2	B	111/134 (83%)	107 (96%)	3 (3%)	1 (1%)	21	55
2	D	113/134 (84%)	109 (96%)	3 (3%)	1 (1%)	21	55
2	F	109/134 (81%)	102 (94%)	6 (6%)	1 (1%)	21	55
2	H	112/134 (84%)	107 (96%)	4 (4%)	1 (1%)	21	55
2	J	112/134 (84%)	108 (96%)	4 (4%)	0	100	100
2	L	106/134 (79%)	99 (93%)	6 (6%)	1 (1%)	21	55
2	N	103/134 (77%)	96 (93%)	5 (5%)	2 (2%)	10	32
2	P	106/134 (79%)	97 (92%)	9 (8%)	0	100	100
All	All	2523/2824 (89%)	2413 (96%)	101 (4%)	9 (0%)	39	74

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	84	GLY

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Mol	Chain	Res	Type
2	L	40	THR
1	M	170	GLU
2	H	62	ASN
1	I	159	VAL
2	B	62	ASN
2	N	42	CYS
2	N	93	CYS
2	F	35	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	190/201 (94%)	187 (98%)	3 (2%)	70	93
1	C	191/201 (95%)	188 (98%)	3 (2%)	70	93
1	E	189/201 (94%)	185 (98%)	4 (2%)	61	90
1	G	191/201 (95%)	184 (96%)	7 (4%)	41	76
1	I	191/201 (95%)	183 (96%)	8 (4%)	36	71
1	K	191/201 (95%)	188 (98%)	3 (2%)	70	93
1	M	190/201 (94%)	187 (98%)	3 (2%)	70	93
1	O	190/201 (94%)	186 (98%)	4 (2%)	61	90
2	B	109/125 (87%)	107 (98%)	2 (2%)	66	91
2	D	109/125 (87%)	106 (97%)	3 (3%)	51	84
2	F	107/125 (86%)	105 (98%)	2 (2%)	65	91
2	H	111/125 (89%)	107 (96%)	4 (4%)	42	76
2	J	109/125 (87%)	107 (98%)	2 (2%)	66	91
2	L	105/125 (84%)	102 (97%)	3 (3%)	50	83
2	N	102/125 (82%)	93 (91%)	9 (9%)	12	35
2	P	105/125 (84%)	102 (97%)	3 (3%)	50	83
All	All	2380/2608 (91%)	2317 (97%)	63 (3%)	54	86

All (63) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	10	TYR
1	A	81	ASP
1	A	92	SER
2	B	19	GLN
2	B	111	PHE
1	C	10	TYR
1	C	38	GLU
1	C	81	ASP
2	D	19	GLN
2	D	80	SER
2	D	111	PHE
1	E	10	TYR
1	E	46	CYS
1	E	81	ASP
1	E	175	SER
2	F	19	GLN
2	F	111	PHE
1	G	9	ASP
1	G	10	TYR
1	G	81	ASP
1	G	85	GLN
1	G	167	LEU
1	G	174	ASP
1	G	175	SER
2	H	19	GLN
2	H	38	VAL
2	H	91	LEU
2	H	111	PHE
1	I	10	TYR
1	I	81	ASP
1	I	157	ILE
1	I	164	VAL
1	I	172	ARG
1	I	173	LYS
1	I	175	SER
1	I	194	THR
2	J	19	GLN
2	J	111	PHE
1	K	10	TYR
1	K	89	GLU
1	K	159	VAL
2	L	38	VAL

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Mol	Chain	Res	Type
2	L	92	THR
2	L	111	PHE
1	M	10	TYR
1	M	81	ASP
1	M	82	GLN
2	N	19	GLN
2	N	25	ASN
2	N	36	GLU
2	N	37	ASP
2	N	39	GLU
2	N	40	THR
2	N	64	GLU
2	N	76	ARG
2	N	111	PHE
1	O	10	TYR
1	O	81	ASP
1	O	150	VAL
1	O	207	GLN
2	P	19	GLN
2	P	76	ARG
2	P	111	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (46) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	53	HIS
1	A	57	HIS
1	A	136	GLN
1	A	205	GLN
2	B	19	GLN
2	B	89	HIS
2	B	121	GLN
1	C	53	HIS
1	C	57	HIS
1	C	85	GLN
1	C	136	GLN
1	C	205	GLN
2	D	3	GLN
2	D	6	HIS
2	D	122	HIS
1	E	53	HIS
1	E	57	HIS

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Mol	Chain	Res	Type
1	E	205	GLN
2	F	120	HIS
1	G	53	HIS
1	G	57	HIS
1	G	136	GLN
1	G	192	GLN
2	H	19	GLN
2	H	54	GLN
2	H	62	ASN
2	H	89	HIS
2	H	120	HIS
2	H	122	HIS
1	I	53	HIS
1	I	57	HIS
1	I	136	GLN
2	J	19	GLN
1	K	53	HIS
1	K	57	HIS
1	K	136	GLN
1	K	205	GLN
1	M	53	HIS
1	M	57	HIS
1	M	63	HIS
1	M	136	GLN
1	M	205	GLN
2	N	19	GLN
1	O	53	HIS
1	O	143	ASN
1	O	207	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

49 carbohydrates 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	$\# Z > 2$
6	FUL	A	307	6	10,10,11	0.28	0	14,14,16	0.82	0
6	NAG	A	308	6	14,14,15	0.49	0	15,19,21	1.26	2 (13%)
6	NAG	A	309	7,6	14,14,15	0.52	0	15,19,21	1.20	2 (13%)
7	BMA	A	310	7,6	11,11,12	0.27	0	14,15,17	0.59	0
7	MAN	A	311	7	11,11,12	0.60	0	14,15,17	0.90	0
7	MAN	A	312	7	11,11,12	0.67	0	14,15,17	1.91	3 (21%)
7	MAN	A	313	7	11,11,12	0.55	0	14,15,17	0.74	0
9	NAG	C	309	9,8	14,14,15	0.48	0	15,19,21	1.26	2 (13%)
9	NAG	C	310	9,7	14,14,15	0.51	0	15,19,21	1.20	2 (13%)
7	BMA	C	311	9,7	11,11,12	0.27	0	14,15,17	0.59	0
7	MAN	C	312	7	11,11,12	0.61	0	14,15,17	0.91	0
7	MAN	C	313	7	11,11,12	0.66	0	14,15,17	1.91	3 (21%)
7	MAN	C	314	7	11,11,12	0.55	0	14,15,17	0.73	0
6	FUL	E	301	6	10,10,11	0.51	0	14,14,16	1.71	4 (28%)
6	NAG	E	303	1,6	14,14,15	0.48	0	15,19,21	1.26	2 (13%)
6	NAG	E	304	7,6	14,14,15	0.52	0	15,19,21	1.20	2 (13%)
7	BMA	E	306	7,6	11,11,12	0.28	0	14,15,17	0.59	0
7	MAN	E	307	7	11,11,12	0.62	0	14,15,17	0.91	0
7	MAN	E	308	7	11,11,12	0.67	0	14,15,17	1.90	3 (21%)
7	MAN	E	309	7	11,11,12	0.55	0	14,15,17	0.72	0
9	NAG	G	308	9,8	14,14,15	0.47	0	15,19,21	1.25	2 (13%)
9	NAG	G	309	9,7	14,14,15	0.52	0	15,19,21	1.20	2 (13%)
7	BMA	G	310	9,7	11,11,12	0.28	0	14,15,17	0.59	0
7	MAN	G	311	7	11,11,12	0.61	0	14,15,17	0.90	0
7	MAN	G	312	7	11,11,12	0.67	0	14,15,17	1.91	3 (21%)
7	MAN	G	313	7	11,11,12	0.56	0	14,15,17	0.73	0
9	NAG	I	307	9,8	14,14,15	0.47	0	15,19,21	1.25	2 (13%)
9	NAG	I	308	9,7	14,14,15	0.53	0	15,19,21	1.20	2 (13%)
7	BMA	I	309	9,7	11,11,12	0.28	0	14,15,17	0.59	0
7	MAN	I	310	7	11,11,12	0.61	0	14,15,17	0.91	0
7	MAN	I	311	7	11,11,12	0.68	0	14,15,17	1.90	3 (21%)
7	MAN	I	312	7	11,11,12	0.56	0	14,15,17	0.72	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
10	NAG	K	307	10,8	14,14,15	0.58	0	15,19,21	1.27	3 (20%)
10	NAG	K	308	10	14,14,15	0.48	0	15,19,21	1.35	2 (13%)
10	BMA	K	310	10	11,11,12	0.26	0	14,15,17	0.61	0
10	MAN	K	311	10	11,11,12	0.62	0	14,15,17	0.82	0
10	MAN	K	312	10	11,11,12	0.69	0	14,15,17	2.57	5 (35%)
11	FUC	M	301	11	10,10,11	0.89	0	14,14,16	3.27	7 (50%)
11	NAG	M	302	11	14,14,15	0.52	0	15,19,21	0.97	1 (6%)
11	NAG	M	303	11,12	14,14,15	0.58	0	15,19,21	1.40	3 (20%)
12	BMA	M	308	11,12	11,11,12	0.26	0	14,15,17	0.61	0
12	MAN	M	310	12	11,11,12	0.65	0	14,15,17	1.05	1 (7%)
12	MAN	M	311	12	11,11,12	0.58	0	14,15,17	2.79	4 (28%)
13	FUL	O	301	13	10,10,11	0.30	0	14,14,16	0.79	1 (7%)
13	NAG	O	302	13	14,14,15	0.51	0	15,19,21	1.13	2 (13%)
13	NAG	O	303	13	14,14,15	0.54	0	15,19,21	1.36	2 (13%)
13	BMA	O	304	13	11,11,12	0.25	0	14,15,17	0.60	0
13	MAN	O	305	13	11,11,12	0.65	0	14,15,17	1.04	1 (7%)
13	MAN	O	306	13	11,11,12	0.61	0	14,15,17	2.24	3 (21%)

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
6	FUL	A	307	6	-	0/0/17/20	0/1/1/1
6	NAG	A	308	6	-	0/6/23/26	0/1/1/1
6	NAG	A	309	7,6	-	0/6/23/26	0/1/1/1
7	BMA	A	310	7,6	-	0/2/19/22	0/1/1/1
7	MAN	A	311	7	-	0/2/19/22	1/1/1/1
7	MAN	A	312	7	-	0/2/19/22	0/1/1/1
7	MAN	A	313	7	-	0/2/19/22	0/1/1/1
9	NAG	C	309	9,8	-	0/6/23/26	0/1/1/1
9	NAG	C	310	9,7	-	0/6/23/26	0/1/1/1
7	BMA	C	311	9,7	-	0/2/19/22	0/1/1/1
7	MAN	C	312	7	-	0/2/19/22	1/1/1/1
7	MAN	C	313	7	-	0/2/19/22	0/1/1/1
7	MAN	C	314	7	-	0/2/19/22	0/1/1/1
6	FUL	E	301	6	-	0/0/17/20	0/1/1/1
6	NAG	E	303	1,6	-	0/6/23/26	0/1/1/1
6	NAG	E	304	7,6	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	BMA	E	306	7,6	-	0/2/19/22	0/1/1/1
7	MAN	E	307	7	-	0/2/19/22	1/1/1/1
7	MAN	E	308	7	-	0/2/19/22	0/1/1/1
7	MAN	E	309	7	-	0/2/19/22	0/1/1/1
9	NAG	G	308	9,8	-	0/6/23/26	0/1/1/1
9	NAG	G	309	9,7	-	0/6/23/26	0/1/1/1
7	BMA	G	310	9,7	-	0/2/19/22	0/1/1/1
7	MAN	G	311	7	-	0/2/19/22	1/1/1/1
7	MAN	G	312	7	-	0/2/19/22	0/1/1/1
7	MAN	G	313	7	-	0/2/19/22	0/1/1/1
9	NAG	I	307	9,8	-	0/6/23/26	0/1/1/1
9	NAG	I	308	9,7	-	0/6/23/26	0/1/1/1
7	BMA	I	309	9,7	-	0/2/19/22	0/1/1/1
7	MAN	I	310	7	-	0/2/19/22	1/1/1/1
7	MAN	I	311	7	-	0/2/19/22	0/1/1/1
7	MAN	I	312	7	-	0/2/19/22	0/1/1/1
10	NAG	K	307	10,8	-	0/6/23/26	0/1/1/1
10	NAG	K	308	10	-	0/6/23/26	0/1/1/1
10	BMA	K	310	10	-	0/2/19/22	0/1/1/1
10	MAN	K	311	10	-	0/2/19/22	0/1/1/1
10	MAN	K	312	10	-	0/2/19/22	0/1/1/1
11	FUC	M	301	11	-	0/0/17/20	0/1/1/1
11	NAG	M	302	11	-	0/6/23/26	0/1/1/1
11	NAG	M	303	11,12	-	0/6/23/26	0/1/1/1
12	BMA	M	308	11,12	-	0/2/19/22	0/1/1/1
12	MAN	M	310	12	-	0/2/19/22	1/1/1/1
12	MAN	M	311	12	-	0/2/19/22	0/1/1/1
13	FUL	O	301	13	-	0/0/17/20	0/1/1/1
13	NAG	O	302	13	-	0/6/23/26	0/1/1/1
13	NAG	O	303	13	-	0/6/23/26	0/1/1/1
13	BMA	O	304	13	-	0/2/19/22	0/1/1/1
13	MAN	O	305	13	-	0/2/19/22	0/1/1/1
13	MAN	O	306	13	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	M	301	FUC	O4-C4-C3	-5.04	99.00	110.34
11	M	301	FUC	C2-C3-C4	-3.63	104.87	111.04
6	A	308	NAG	C2-N2-C7	-3.12	119.04	123.04
9	C	309	NAG	C2-N2-C7	-3.11	119.04	123.04

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	G	308	NAG	C2-N2-C7	-3.10	119.06	123.04
6	E	303	NAG	C2-N2-C7	-3.10	119.06	123.04
9	I	307	NAG	C2-N2-C7	-3.07	119.10	123.04
11	M	303	NAG	C2-N2-C7	-2.78	119.47	123.04
13	O	302	NAG	C2-N2-C7	-2.61	119.69	123.04
10	K	307	NAG	O4-C4-C3	-2.39	104.95	110.34
11	M	301	FUC	O4-C4-C5	-2.37	104.27	109.84
6	E	301	FUL	O2-C2-C3	-2.35	105.40	110.12
9	I	308	NAG	C4-C3-C2	-2.26	107.72	111.23
11	M	301	FUC	O2-C2-C3	-2.26	105.58	110.12
9	C	310	NAG	C4-C3-C2	-2.24	107.74	111.23
6	E	304	NAG	C4-C3-C2	-2.24	107.75	111.23
9	G	309	NAG	C4-C3-C2	-2.21	107.80	111.23
6	A	309	NAG	C4-C3-C2	-2.20	107.81	111.23
10	K	308	NAG	C4-C3-C2	-2.13	107.92	111.23
10	K	307	NAG	C2-N2-C7	-2.13	120.31	123.04
13	O	303	NAG	C2-N2-C7	-2.10	120.34	123.04
11	M	303	NAG	C4-C3-C2	-2.09	107.97	111.23
13	O	301	FUL	O5-C5-C6	2.03	109.48	106.13
10	K	312	MAN	C2-C3-C4	2.07	114.56	111.04
13	O	302	NAG	C1-O5-C5	2.29	115.16	112.25
11	M	302	NAG	C1-O5-C5	2.39	115.28	112.25
12	M	311	MAN	O5-C5-C6	2.41	112.56	107.35
13	O	306	MAN	O5-C5-C6	2.49	112.73	107.35
13	O	305	MAN	O2-C2-C1	2.51	114.24	109.21
7	A	312	MAN	C2-C3-C4	2.57	115.40	111.04
7	G	312	MAN	C2-C3-C4	2.57	115.41	111.04
7	E	308	MAN	C2-C3-C4	2.58	115.42	111.04
6	E	301	FUL	C1-O5-C5	2.58	116.36	112.38
7	C	313	MAN	C2-C3-C4	2.58	115.42	111.04
7	I	311	MAN	C2-C3-C4	2.59	115.44	111.04
12	M	310	MAN	O2-C2-C1	2.68	114.58	109.21
6	E	301	FUL	O5-C5-C6	2.81	110.78	106.13
10	K	312	MAN	O5-C5-C6	2.88	113.58	107.35
9	I	307	NAG	C1-O5-C5	2.89	115.91	112.25
13	O	306	MAN	C1-C2-C3	2.90	112.97	109.54
9	G	308	NAG	C1-O5-C5	2.90	115.92	112.25
6	E	303	NAG	C1-O5-C5	2.91	115.94	112.25
6	A	308	NAG	C1-O5-C5	2.92	115.95	112.25
9	C	309	NAG	C1-O5-C5	2.94	115.97	112.25
11	M	303	NAG	C1-O5-C5	3.14	116.23	112.25
10	K	312	MAN	O5-C1-C2	3.18	116.01	110.86

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	C	310	NAG	C1-O5-C5	3.21	116.32	112.25
6	E	304	NAG	C1-O5-C5	3.22	116.33	112.25
9	I	308	NAG	C1-O5-C5	3.23	116.34	112.25
9	G	309	NAG	C1-O5-C5	3.23	116.35	112.25
6	A	309	NAG	C1-O5-C5	3.25	116.37	112.25
10	K	307	NAG	C1-O5-C5	3.31	116.44	112.25
6	E	301	FUL	C1-C2-C3	3.32	113.47	109.54
11	M	301	FUC	O5-C5-C6	3.40	111.76	106.13
10	K	308	NAG	C1-O5-C5	3.72	116.96	112.25
13	O	303	NAG	C1-O5-C5	3.80	117.07	112.25
7	I	311	MAN	C1-C2-C3	3.81	114.05	109.54
7	A	312	MAN	C1-C2-C3	3.81	114.05	109.54
7	E	308	MAN	C1-C2-C3	3.82	114.06	109.54
7	G	312	MAN	C1-C2-C3	3.82	114.06	109.54
7	C	313	MAN	C1-C2-C3	3.83	114.07	109.54
7	I	311	MAN	C1-O5-C5	3.86	117.15	112.25
7	E	308	MAN	C1-O5-C5	3.86	117.15	112.25
7	G	312	MAN	C1-O5-C5	3.87	117.17	112.25
7	C	313	MAN	C1-O5-C5	3.88	117.17	112.25
7	A	312	MAN	C1-O5-C5	3.88	117.18	112.25
12	M	311	MAN	O5-C1-C2	4.22	117.71	110.86
11	M	301	FUC	O5-C1-C2	4.28	117.79	110.86
10	K	312	MAN	C1-O5-C5	5.10	118.72	112.25
12	M	311	MAN	C1-O5-C5	6.30	120.25	112.25
10	K	312	MAN	C1-C2-C3	6.31	117.00	109.54
12	M	311	MAN	C1-C2-C3	6.51	117.24	109.54
13	O	306	MAN	C1-O5-C5	6.69	120.73	112.25
11	M	301	FUC	C1-C2-C3	7.89	118.88	109.54

There are no chirality outliers.

There are no torsion outliers.

All (6) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	M	310	MAN	C1-C2-C3-C4-C5-O5
7	I	310	MAN	C1-C2-C3-C4-C5-O5
7	G	311	MAN	C1-C2-C3-C4-C5-O5
7	E	307	MAN	C1-C2-C3-C4-C5-O5
7	A	311	MAN	C1-C2-C3-C4-C5-O5
7	C	312	MAN	C1-C2-C3-C4-C5-O5

41 monomers are involved in 132 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	308	NAG	6	0
6	A	309	NAG	8	0
7	A	310	BMA	6	0
7	A	312	MAN	8	0
7	A	313	MAN	1	0
9	C	309	NAG	8	0
9	C	310	NAG	9	0
7	C	311	BMA	7	0
7	C	313	MAN	4	0
7	C	314	MAN	1	0
6	E	303	NAG	1	0
6	E	304	NAG	10	0
7	E	306	BMA	9	0
7	E	308	MAN	4	0
7	E	309	MAN	1	0
9	G	308	NAG	8	0
9	G	309	NAG	11	0
7	G	310	BMA	9	0
7	G	312	MAN	3	0
7	G	313	MAN	1	0
9	I	307	NAG	9	0
9	I	308	NAG	11	0
7	I	309	BMA	8	0
7	I	311	MAN	1	0
7	I	312	MAN	3	0
10	K	307	NAG	4	0
10	K	308	NAG	5	0
10	K	310	BMA	5	0
10	K	311	MAN	1	0
10	K	312	MAN	2	0
11	M	301	FUC	1	0
11	M	302	NAG	6	0
11	M	303	NAG	8	0
12	M	308	BMA	8	0
12	M	310	MAN	3	0
12	M	311	MAN	4	0
13	O	302	NAG	5	0
13	O	303	NAG	4	0
13	O	304	BMA	2	0
13	O	305	MAN	1	0
13	O	306	MAN	1	0

5.6 Ligand geometry

Of 55 ligands modelled in this entry, 4 are monoatomic - leaving 51 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
3	MAN	A	301	-	11,11,12	0.95	1 (9%)	14,15,17	2.21	4 (28%)
5	SO4	A	303	-	4,4,4	0.23	0	6,6,6	0.07	0
5	SO4	A	304	-	4,4,4	0.24	0	6,6,6	0.09	0
5	SO4	A	305	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	A	306	-	4,4,4	0.22	0	6,6,6	0.07	0
5	SO4	C	301	-	4,4,4	0.22	0	6,6,6	0.08	0
5	SO4	C	302	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	C	303	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	C	304	-	4,4,4	0.22	0	6,6,6	0.09	0
5	SO4	C	305	-	4,4,4	0.23	0	6,6,6	0.09	0
5	SO4	C	306	-	4,4,4	0.22	0	6,6,6	0.08	0
3	MAN	C	307	-	11,11,12	0.72	0	14,15,17	1.97	4 (28%)
8	FUL	C	308	9	10,10,11	0.29	0	14,14,16	0.79	1 (7%)
3	MAN	E	302	-	11,11,12	0.72	0	14,15,17	1.97	4 (28%)
5	SO4	E	310	-	4,4,4	0.23	0	6,6,6	0.09	0
5	SO4	E	311	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	E	312	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	E	313	-	4,4,4	0.23	0	6,6,6	0.08	0
3	MAN	G	301	-	11,11,12	0.88	0	14,15,17	2.19	4 (28%)
5	SO4	G	303	-	4,4,4	0.22	0	6,6,6	0.08	0
5	SO4	G	304	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	G	305	-	4,4,4	0.22	0	6,6,6	0.10	0
5	SO4	G	306	-	4,4,4	0.23	0	6,6,6	0.07	0
8	FUL	G	307	9	10,10,11	0.29	0	14,14,16	0.78	1 (7%)
5	SO4	H	201	-	4,4,4	0.24	0	6,6,6	0.07	0
5	SO4	H	202	-	4,4,4	0.54	0	6,6,6	0.34	0
3	MAN	I	301	-	11,11,12	0.78	0	14,15,17	2.03	4 (28%)
5	SO4	I	302	-	4,4,4	0.24	0	6,6,6	0.09	0
5	SO4	I	303	-	4,4,4	0.24	0	6,6,6	0.09	0
5	SO4	I	304	-	4,4,4	0.23	0	6,6,6	0.08	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	SO4	I	305	-	4,4,4	0.22	0	6,6,6	0.07	0
8	FUL	I	306	9	10,10,11	0.30	0	14,14,16	0.79	1 (7%)
8	FUL	K	301	10	10,10,11	0.30	0	14,14,16	0.79	1 (7%)
3	MAN	K	302	-	11,11,12	0.97	1 (9%)	14,15,17	2.11	4 (28%)
5	SO4	K	303	-	4,4,4	0.11	0	6,6,6	0.15	0
5	SO4	K	304	-	4,4,4	0.25	0	6,6,6	0.08	0
5	SO4	K	305	-	4,4,4	0.23	0	6,6,6	0.10	0
5	SO4	K	306	-	4,4,4	0.24	0	6,6,6	0.09	0
5	SO4	K	309	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	L	201	-	4,4,4	0.23	0	6,6,6	0.08	0
3	MAN	M	304	-	11,11,12	0.82	1 (9%)	14,15,17	1.79	4 (28%)
5	SO4	M	305	-	4,4,4	0.24	0	6,6,6	0.09	0
5	SO4	M	306	-	4,4,4	0.24	0	6,6,6	0.08	0
5	SO4	M	307	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	M	309	-	4,4,4	0.23	0	6,6,6	0.09	0
3	MAN	O	307	-	11,11,12	0.79	0	14,15,17	2.00	4 (28%)
5	SO4	O	309	-	4,4,4	0.21	0	6,6,6	0.27	0
5	SO4	O	310	-	4,4,4	0.35	0	6,6,6	0.35	0
5	SO4	O	311	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	O	312	-	4,4,4	0.23	0	6,6,6	0.08	0
5	SO4	O	313	-	4,4,4	0.23	0	6,6,6	0.07	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	A	301	-	-	0/2/19/22	0/1/1/1
5	SO4	A	303	-	-	0/0/0/0	0/0/0/0
5	SO4	A	304	-	-	0/0/0/0	0/0/0/0
5	SO4	A	305	-	-	0/0/0/0	0/0/0/0
5	SO4	A	306	-	-	0/0/0/0	0/0/0/0
5	SO4	C	301	-	-	0/0/0/0	0/0/0/0
5	SO4	C	302	-	-	0/0/0/0	0/0/0/0
5	SO4	C	303	-	-	0/0/0/0	0/0/0/0
5	SO4	C	304	-	-	0/0/0/0	0/0/0/0
5	SO4	C	305	-	-	0/0/0/0	0/0/0/0
5	SO4	C	306	-	-	0/0/0/0	0/0/0/0
3	MAN	C	307	-	-	0/2/19/22	0/1/1/1
8	FUL	C	308	9	-	0/0/17/20	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	MAN	E	302	-	-	0/2/19/22	0/1/1/1
5	SO4	E	310	-	-	0/0/0/0	0/0/0/0
5	SO4	E	311	-	-	0/0/0/0	0/0/0/0
5	SO4	E	312	-	-	0/0/0/0	0/0/0/0
5	SO4	E	313	-	-	0/0/0/0	0/0/0/0
3	MAN	G	301	-	-	0/2/19/22	0/1/1/1
5	SO4	G	303	-	-	0/0/0/0	0/0/0/0
5	SO4	G	304	-	-	0/0/0/0	0/0/0/0
5	SO4	G	305	-	-	0/0/0/0	0/0/0/0
5	SO4	G	306	-	-	0/0/0/0	0/0/0/0
8	FUL	G	307	9	-	0/0/17/20	0/1/1/1
5	SO4	H	201	-	-	0/0/0/0	0/0/0/0
5	SO4	H	202	-	-	0/0/0/0	0/0/0/0
3	MAN	I	301	-	-	0/2/19/22	0/1/1/1
5	SO4	I	302	-	-	0/0/0/0	0/0/0/0
5	SO4	I	303	-	-	0/0/0/0	0/0/0/0
5	SO4	I	304	-	-	0/0/0/0	0/0/0/0
5	SO4	I	305	-	-	0/0/0/0	0/0/0/0
8	FUL	I	306	9	-	0/0/17/20	0/1/1/1
8	FUL	K	301	10	-	0/0/17/20	0/1/1/1
3	MAN	K	302	-	-	0/2/19/22	0/1/1/1
5	SO4	K	303	-	-	0/0/0/0	0/0/0/0
5	SO4	K	304	-	-	0/0/0/0	0/0/0/0
5	SO4	K	305	-	-	0/0/0/0	0/0/0/0
5	SO4	K	306	-	-	0/0/0/0	0/0/0/0
5	SO4	K	309	-	-	0/0/0/0	0/0/0/0
5	SO4	L	201	-	-	0/0/0/0	0/0/0/0
3	MAN	M	304	-	-	0/2/19/22	0/1/1/1
5	SO4	M	305	-	-	0/0/0/0	0/0/0/0
5	SO4	M	306	-	-	0/0/0/0	0/0/0/0
5	SO4	M	307	-	-	0/0/0/0	0/0/0/0
5	SO4	M	309	-	-	0/0/0/0	0/0/0/0
3	MAN	O	307	-	-	0/2/19/22	0/1/1/1
5	SO4	O	309	-	-	0/0/0/0	0/0/0/0
5	SO4	O	310	-	-	0/0/0/0	0/0/0/0
5	SO4	O	311	-	-	0/0/0/0	0/0/0/0
5	SO4	O	312	-	-	0/0/0/0	0/0/0/0
5	SO4	O	313	-	-	0/0/0/0	0/0/0/0

All (3) bond length outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	K	302	MAN	O5-C1	-2.15	1.40	1.43
3	A	301	MAN	O5-C1	-2.15	1.40	1.43
3	M	304	MAN	O5-C1	-2.10	1.40	1.43

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	G	301	MAN	C1-C2-C3	-4.80	103.86	109.54
3	I	301	MAN	O5-C1-C2	-4.74	103.17	110.86
3	A	301	MAN	O5-C1-C2	-4.48	103.59	110.86
3	K	302	MAN	O5-C1-C2	-4.46	103.62	110.86
3	E	302	MAN	O5-C1-C2	-4.27	103.93	110.86
3	C	307	MAN	O5-C1-C2	-4.25	103.96	110.86
3	O	307	MAN	C1-C2-C3	-4.14	104.64	109.54
3	G	301	MAN	O5-C1-C2	-4.06	104.28	110.86
3	A	301	MAN	C1-C2-C3	-3.89	104.94	109.54
3	K	302	MAN	C1-C2-C3	-3.84	105.00	109.54
3	I	301	MAN	C1-C2-C3	-3.45	105.46	109.54
3	O	307	MAN	O5-C1-C2	-3.39	105.36	110.86
3	C	307	MAN	C1-C2-C3	-3.28	105.66	109.54
3	E	302	MAN	C1-C2-C3	-3.27	105.67	109.54
3	M	304	MAN	O5-C1-C2	-3.13	105.78	110.86
3	M	304	MAN	C1-C2-C3	-2.95	106.05	109.54
3	K	302	MAN	O4-C4-C3	-2.69	104.28	110.34
3	A	301	MAN	O4-C4-C3	-2.61	104.47	110.34
3	G	301	MAN	O4-C4-C3	-2.57	104.54	110.34
3	E	302	MAN	O4-C4-C3	-2.50	104.70	110.34
3	C	307	MAN	O4-C4-C3	-2.50	104.71	110.34
3	I	301	MAN	O4-C4-C3	-2.39	104.95	110.34
3	M	304	MAN	O4-C4-C3	-2.36	105.03	110.34
3	O	307	MAN	O4-C4-C3	-2.35	105.04	110.34
8	G	307	FUL	O5-C5-C6	2.00	109.44	106.13
8	C	308	FUL	O5-C5-C6	2.02	109.47	106.13
8	I	306	FUL	O5-C5-C6	2.02	109.47	106.13
8	K	301	FUL	O5-C5-C6	2.02	109.47	106.13
3	I	301	MAN	C3-C4-C5	3.10	115.60	110.20
3	K	302	MAN	C3-C4-C5	3.27	115.90	110.20
3	G	301	MAN	C3-C4-C5	3.33	116.00	110.20
3	E	302	MAN	C3-C4-C5	3.45	116.21	110.20
3	C	307	MAN	C3-C4-C5	3.45	116.22	110.20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	M	304	MAN	C3-C4-C5	3.63	116.52	110.20
3	A	301	MAN	C3-C4-C5	3.74	116.72	110.20
3	O	307	MAN	C3-C4-C5	3.88	116.96	110.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 27 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	301	MAN	7	0
5	C	305	SO4	1	0
8	C	308	FUL	4	0
3	G	301	MAN	1	0
8	G	307	FUL	4	0
3	I	301	MAN	4	0
8	I	306	FUL	4	0
5	K	306	SO4	1	0
3	O	307	MAN	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	208/219 (94%)	0.34	0 100 100	23, 45, 83, 109	0
1	C	209/219 (95%)	0.36	1 (0%) 91 88	23, 47, 86, 179	0
1	E	207/219 (94%)	0.56	12 (5%) 26 16	41, 69, 128, 160	0
1	G	209/219 (95%)	0.52	7 (3%) 50 38	17, 45, 92, 146	0
1	I	209/219 (95%)	0.58	11 (5%) 30 20	33, 66, 134, 171	0
1	K	209/219 (95%)	0.48	5 (2%) 62 50	25, 46, 88, 189	0
1	M	208/219 (94%)	0.62	12 (5%) 26 16	36, 67, 135, 153	0
1	O	208/219 (94%)	0.89	28 (13%) 4 2	34, 69, 142, 194	0
2	B	115/134 (85%)	0.63	10 (8%) 13 6	35, 68, 135, 151	0
2	D	117/134 (87%)	0.53	4 (3%) 49 36	31, 63, 135, 169	0
2	F	113/134 (84%)	0.93	17 (15%) 3 2	43, 80, 138, 189	0
2	H	116/134 (86%)	0.39	3 (2%) 59 47	28, 50, 102, 125	0
2	J	116/134 (86%)	0.46	5 (4%) 39 27	34, 60, 112, 140	0
2	L	110/134 (82%)	0.70	3 (2%) 58 45	36, 79, 121, 143	0
2	N	107/134 (79%)	0.80	9 (8%) 14 6	26, 98, 148, 194	0
2	P	110/134 (82%)	1.38	29 (26%) 1 0	52, 97, 152, 172	0
All	All	2571/2824 (91%)	0.61	156 (6%) 25 15	17, 63, 132, 194	0

All (156) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	160	ASP	7.6
2	P	120	HIS	6.8
2	L	62	ASN	6.7
1	O	160	ASP	6.6
2	P	62	ASN	6.5

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Mol	Chain	Res	Type	RSRZ
2	F	123	LEU	6.3
2	F	117	LYS	5.9
1	E	159	VAL	5.7
1	K	160	ASP	5.6
2	B	2	GLY	5.6
2	D	62	ASN	5.4
1	I	160	ASP	5.1
2	J	2	GLY	5.0
2	N	59	ASN	4.8
2	F	121	GLN	4.7
2	D	3	GLN	4.6
2	F	62	ASN	4.5
2	P	37	ASP	4.5
1	O	141	TYR	4.3
1	K	158	SER	4.3
2	P	51	GLN	4.2
2	P	81	THR	4.2
2	N	62	ASN	4.2
1	O	166	LEU	4.1
1	M	148	TRP	4.1
1	G	160	ASP	4.1
1	O	169	LEU	4.0
2	P	59	ASN	4.0
2	J	124	SER	4.0
1	O	148	TRP	3.9
1	M	158	SER	3.9
2	P	117	LYS	3.9
2	B	54	GLN	3.8
1	I	166	LEU	3.8
1	E	172	ARG	3.7
1	G	158	SER	3.7
2	P	121	GLN	3.6
1	I	148	TRP	3.6
2	P	61	GLY	3.5
1	I	169	LEU	3.5
2	F	119	ILE	3.4
2	P	122	HIS	3.4
1	M	139	LEU	3.4
2	P	7	MET	3.4
2	J	61	GLY	3.4
1	K	21	TRP	3.4
2	J	62	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	O	114	GLN	3.3
2	B	3	GLN	3.3
2	B	81	THR	3.3
2	F	82	ASN	3.3
2	F	42	CYS	3.3
1	I	141	TYR	3.3
2	P	36	GLU	3.2
1	O	139	LEU	3.2
2	F	3	GLN	3.2
1	E	171	PHE	3.1
1	C	166	LEU	3.1
1	I	149	ALA	3.1
2	P	119	ILE	3.1
1	E	18	LEU	3.0
1	M	156	LEU	3.0
1	O	170	GLU	3.0
2	P	111	PHE	2.9
2	P	123	LEU	2.9
2	N	117	LYS	2.9
1	O	208	SER	2.9
1	M	166	LEU	2.9
2	P	10	MET	2.9
2	P	115	LEU	2.8
1	O	136	GLN	2.8
2	P	99	TYR	2.8
2	P	80	SER	2.7
2	N	40	THR	2.7
1	I	209	GLU	2.7
1	O	131	LEU	2.7
1	E	15	ILE	2.7
1	O	159	VAL	2.7
2	H	90	ARG	2.6
2	B	4	ASP	2.6
1	O	207	GLN	2.6
1	O	153	ARG	2.6
2	L	61	GLY	2.6
2	L	91	LEU	2.6
1	E	158	SER	2.6
1	O	152	PRO	2.6
2	P	67	ILE	2.5
2	F	44	TRP	2.5
1	M	161	SER	2.5

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Mol	Chain	Res	Type	RSRZ
2	P	40	THR	2.5
2	P	41	ASN	2.5
2	P	48	SER	2.5
2	D	59	ASN	2.5
2	P	50	PHE	2.5
2	F	81	THR	2.5
1	G	162	ARG	2.5
1	M	164	VAL	2.5
2	N	92	THR	2.4
1	E	148	TRP	2.4
1	E	161	SER	2.4
2	F	7	MET	2.4
1	O	143	ASN	2.4
1	M	109	VAL	2.4
2	B	117	LYS	2.4
2	F	61	GLY	2.4
1	G	30	LEU	2.4
2	F	5	ARG	2.4
2	P	38	VAL	2.4
2	F	96	CYS	2.4
1	E	173	LYS	2.4
2	F	80	SER	2.4
1	I	203	ILE	2.4
1	O	171	PHE	2.3
1	G	139	LEU	2.3
2	B	80	SER	2.3
2	N	32	LEU	2.3
2	N	18	ASP	2.3
2	N	81	THR	2.3
1	O	106	ASP	2.3
2	P	55	LEU	2.3
1	M	131	LEU	2.3
1	O	142	ARG	2.3
1	I	46	CYS	2.2
1	I	179	LEU	2.2
1	O	151	SER	2.2
2	J	3	GLN	2.2
1	O	155	LYS	2.2
2	D	82	ASN	2.2
1	O	158	SER	2.2
1	K	55	ALA	2.2
1	I	106	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
2	P	79	PRO	2.1
1	M	205	GLN	2.1
1	O	202	VAL	2.1
2	B	44	TRP	2.1
1	K	150	VAL	2.1
2	N	39	GLU	2.1
1	G	46	CYS	2.1
2	F	45	SER	2.1
1	O	146	ASP	2.1
2	P	96	CYS	2.1
1	O	30	LEU	2.1
2	H	61	GLY	2.1
1	M	160	ASP	2.1
1	G	156	LEU	2.1
2	P	31	PHE	2.0
2	B	122	HIS	2.0
1	M	190	SER	2.0
1	O	46	CYS	2.0
1	E	142	ARG	2.0
1	E	8	THR	2.0
1	O	4	LEU	2.0
2	B	59	ASN	2.0
2	H	88	LYS	2.0
2	F	37	ASP	2.0
1	O	173	LYS	2.0

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

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

6.3 Carbohydrates [i](#)

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
7	MAN	C	314	11/12	0.83	0.57	16.23	107,139,150,152	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	MAN	G	313	11/12	0.58	0.46	7.27	107,139,150,152	0
7	MAN	I	312	11/12	0.33	1.03	7.06	107,139,150,152	0
7	MAN	A	313	11/12	0.76	0.41	6.58	107,139,150,152	0
6	FUL	A	307	10/11	0.60	0.41	6.18	70,81,97,104	0
6	FUL	E	301	10/11	0.67	0.41	5.84	70,81,97,104	0
13	FUL	O	301	10/11	0.71	0.40	3.92	72,82,99,104	0
12	BMA	M	308	11/12	0.56	0.27	-	126,136,149,154	0
12	MAN	M	311	11/12	0.83	0.34	-	76,111,132,133	0
11	FUC	M	301	10/11	0.88	0.38	-	73,85,99,102	0
6	NAG	E	304	14/15	0.88	0.18	-	52,84,107,117	0
10	NAG	K	307	14/15	0.86	0.18	-	37,48,56,73	0
7	MAN	E	308	11/12	0.80	0.28	-	80,120,133,134	0
9	NAG	I	307	14/15	0.88	0.16	-	46,54,61,76	0
9	NAG	C	310	14/15	0.88	0.17	-	52,84,107,117	0
12	MAN	M	310	11/12	0.56	0.26	-	88,129,133,134	0
7	MAN	G	311	11/12	0.82	0.19	-	123,146,163,168	0
7	MAN	C	312	11/12	0.72	0.20	-	123,146,163,168	0
13	MAN	O	306	11/12	0.71	0.43	-	79,126,141,150	0
9	NAG	G	309	14/15	0.88	0.22	-	52,84,107,117	0
7	MAN	C	313	11/12	0.81	0.35	-	80,120,133,134	0
13	MAN	O	305	11/12	0.62	0.40	-	123,156,166,175	0
9	NAG	G	308	14/15	0.89	0.22	-	46,54,61,76	0
7	MAN	E	309	11/12	0.71	0.79	-	107,139,150,152	0
7	MAN	E	307	11/12	0.49	0.47	-	123,146,163,168	0
9	NAG	I	308	14/15	0.87	0.20	-	52,84,107,117	0
11	NAG	M	303	14/15	0.90	0.18	-	57,85,108,123	0
7	MAN	I	310	11/12	0.48	0.40	-	123,146,163,168	0
13	NAG	O	302	14/15	0.90	0.17	-	43,52,57,75	0
10	MAN	K	311	11/12	0.65	0.30	-	114,148,165,173	0
9	NAG	C	309	14/15	0.92	0.19	-	46,54,61,76	0
10	MAN	K	312	11/12	0.87	0.36	-	49,96,120,121	0
11	NAG	M	302	14/15	0.96	0.15	-	41,49,57,71	0
7	BMA	I	309	11/12	0.77	0.26	-	128,140,152,153	0
13	NAG	O	303	14/15	0.89	0.18	-	54,90,111,120	0
7	BMA	A	310	11/12	0.57	0.22	-	128,140,152,153	0
7	BMA	C	311	11/12	0.79	0.16	-	128,140,152,153	0
7	MAN	A	311	11/12	0.71	0.21	-	123,146,163,168	0
6	NAG	A	309	14/15	0.83	0.24	-	52,84,107,117	0
7	BMA	E	306	11/12	0.74	0.38	-	128,140,152,153	0
10	NAG	K	308	14/15	0.86	0.21	-	55,87,106,122	0
6	NAG	E	303	14/15	0.91	0.16	-	46,54,61,76	0
7	MAN	I	311	11/12	0.68	0.31	-	80,120,133,134	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	MAN	A	312	11/12	0.72	0.29	-	80,120,133,134	0
13	BMA	O	304	11/12	0.45	0.35	-	127,142,152,156	0
7	MAN	G	312	11/12	0.79	0.33	-	80,120,133,134	0
10	BMA	K	310	11/12	0.64	0.32	-	129,139,152,154	0
7	BMA	G	310	11/12	0.67	0.23	-	128,140,152,153	0
6	NAG	A	308	14/15	0.89	0.25	-	46,54,61,76	0

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(\AA^2)	Q<0.9
8	FUL	K	301	10/11	0.69	0.40	9.34	70,82,97,98	0
8	FUL	G	307	10/11	0.67	0.43	9.14	70,81,97,104	0
8	FUL	C	308	10/11	0.56	0.39	7.54	70,81,97,104	0
8	FUL	I	306	10/11	0.58	0.39	3.94	70,81,97,104	0
4	NI	O	308	1/1	0.41	0.30	2.72	76,76,76,76	0
5	SO4	K	304	5/5	0.75	0.33	1.18	112,121,124,133	0
5	SO4	C	302	5/5	0.97	0.22	0.44	54,63,89,93	0
5	SO4	I	303	5/5	0.95	0.23	0.41	92,105,105,114	0
5	SO4	A	304	5/5	0.97	0.21	0.17	68,77,82,88	0
5	SO4	G	304	5/5	0.96	0.21	-0.28	57,65,73,77	0
5	SO4	M	306	5/5	0.98	0.17	-0.69	76,77,80,90	0
5	SO4	E	311	5/5	0.92	0.18	-0.84	108,108,115,119	0
5	SO4	O	310	5/5	0.99	0.16	-2.20	51,53,63,69	0
5	SO4	O	312	5/5	0.66	0.46	-	154,155,160,166	0
5	SO4	E	310	5/5	0.82	0.28	-	124,131,134,137	0
5	SO4	K	306	5/5	0.78	0.21	-	112,116,118,118	0
5	SO4	M	305	5/5	0.94	0.21	-	89,105,109,114	0
5	SO4	G	306	5/5	0.86	0.32	-	114,118,118,122	0
5	SO4	I	302	5/5	0.93	0.18	-	107,115,118,122	0
5	SO4	K	309	5/5	0.89	0.40	-	128,129,133,139	0
5	SO4	O	313	5/5	0.66	0.65	-	163,164,166,169	0
5	SO4	G	305	5/5	0.58	0.29	-	110,122,137,140	0
5	SO4	O	311	5/5	0.68	0.31	-	166,166,169,173	0
3	MAN	A	301	11/12	0.74	0.30	-	54,76,89,97	0
5	SO4	C	301	5/5	0.94	0.24	-	81,94,110,123	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MAN	G	301	11/12	0.88	0.25	-	52,70,88,101	0
5	SO4	C	303	5/5	0.89	0.21	-	145,147,148,152	0
5	SO4	A	303	5/5	0.93	0.28	-	85,97,104,106	0
3	MAN	M	304	11/12	0.91	0.20	-	58,74,90,95	0
5	SO4	M	309	5/5	0.81	0.58	-	128,135,142,143	0
5	SO4	E	312	5/5	0.73	0.36	-	142,150,154,154	0
3	MAN	C	307	11/12	0.86	0.26	-	63,77,91,94	0
5	SO4	C	306	5/5	0.86	0.21	-	130,132,137,141	0
5	SO4	M	307	5/5	0.57	0.38	-	139,149,151,153	0
3	MAN	O	307	11/12	0.87	0.29	-	62,80,90,99	0
3	MAN	E	302	11/12	0.85	0.21	-	63,77,91,94	0
5	SO4	C	305	5/5	0.73	0.29	-	144,148,150,153	0
5	SO4	I	304	5/5	0.83	0.16	-	133,140,142,147	0
5	SO4	H	201	5/5	0.95	0.26	-	91,97,101,111	0
5	SO4	K	303	5/5	0.85	0.29	-	64,65,103,105	0
5	SO4	A	306	5/5	0.68	0.37	-	135,142,143,144	0
5	SO4	I	305	5/5	0.68	0.46	-	140,141,152,159	0
3	MAN	K	302	11/12	0.91	0.23	-	51,73,81,91	0
5	SO4	K	305	5/5	0.90	0.21	-	148,149,155,157	0
5	SO4	A	305	5/5	0.61	0.44	-	145,145,151,153	0
5	SO4	O	309	5/5	0.94	0.12	-	59,67,94,100	0
5	SO4	L	201	5/5	0.80	0.18	-	138,143,149,152	0
5	SO4	C	304	5/5	0.87	0.36	-	136,139,141,146	0
5	SO4	E	313	5/5	0.80	0.29	-	123,129,137,150	0
4	NI	G	302	1/1	0.90	0.51	-	103,103,103,103	0
5	SO4	H	202	5/5	0.87	0.40	-	30,30,30,30	0
3	MAN	I	301	11/12	0.85	0.24	-	62,78,89,98	0
4	NI	A	302	1/1	0.97	0.36	-	65,65,65,65	0
4	NI	E	305	1/1	0.96	0.30	-	64,64,64,64	0
5	SO4	G	303	5/5	0.95	0.26	-	64,79,96,106	0

6.5 Other polymers

There are no such residues in this entry.