



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 14, 2017 – 11:31 am GMT

PDB ID : 4CJC  
Title : orthorhombic crystal form of Bogt6a E192Q in complex with UDP-GalNAc, UDP, GalNAc  
Authors : Pham, T.; Stinson, B.; Thiyagarajan, N.; Lizotte-Waniewski, M.; Brew, K.; Acharya, K.R.  
Deposited on : 2013-12-19  
Resolution : 3.42 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](mailto: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.

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

MolProbity	:	4.02b-467
Mogul	:	1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix)	:	1.9-1692
EDS	:	trunk28620
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	recalc28949

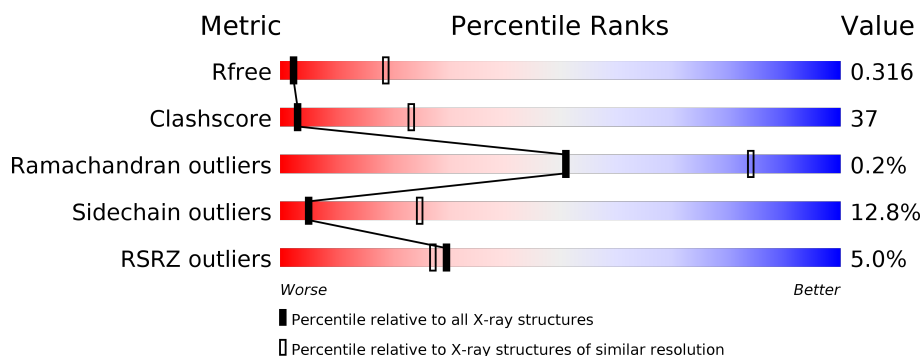
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.42 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))
$R_{free}$	100719	1074 (3.50-3.34)
Clashscore	112137	1179 (3.50-3.34)
Ramachandran outliers	110173	1147 (3.50-3.34)
Sidechain outliers	110143	1148 (3.50-3.34)
RSRZ outliers	101464	1100 (3.50-3.34)

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  $\geq 3$ , 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	246	
1	B	246	
1	C	246	
1	D	246	

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 8120 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.

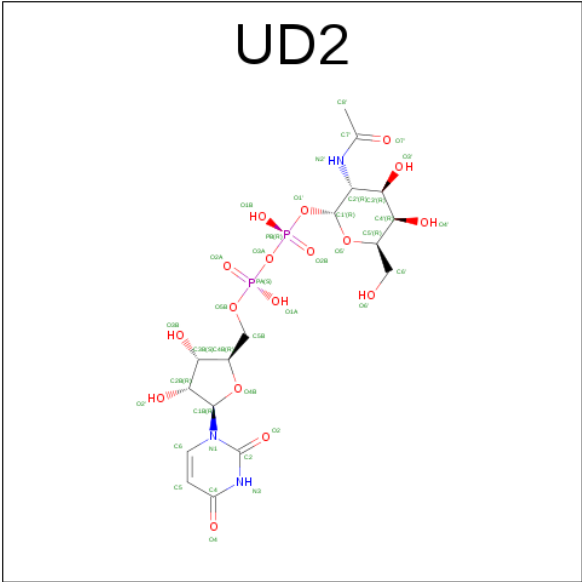
- Molecule 1 is a protein called GLYCOSYLTRANSFERASE FAMILY 6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	7	0	0
			2008	1312	327	362	7			
1	B	238	Total	C	N	O	S	10	0	0
			1981	1295	322	357	7			
1	C	240	Total	C	N	O	S	10	0	0
			2000	1306	326	361	7			
1	D	236	Total	C	N	O	S	10	0	0
			1973	1291	320	355	7			

There are 4 discrepancies between the modelled and reference sequences:

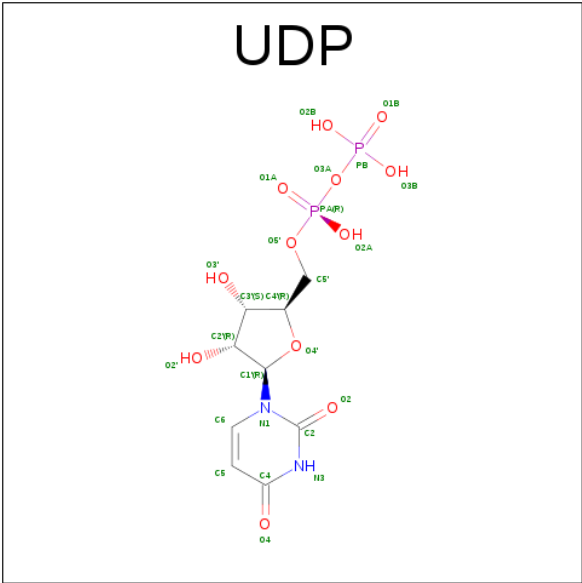
Chain	Residue	Modelled	Actual	Comment	Reference
A	192	GLN	GLU	ENGINEERED MUTATION	UNP A7LVT2
B	192	GLN	GLU	ENGINEERED MUTATION	UNP A7LVT2
C	192	GLN	GLU	ENGINEERED MUTATION	UNP A7LVT2
D	192	GLN	GLU	ENGINEERED MUTATION	UNP A7LVT2

- Molecule 2 is URIDINE-DIPHOSPHATE-N-ACETYLGALACTOSAMINE (three-letter code: UD2) (formula: C<sub>17</sub>H<sub>27</sub>N<sub>3</sub>O<sub>17</sub>P<sub>2</sub>).



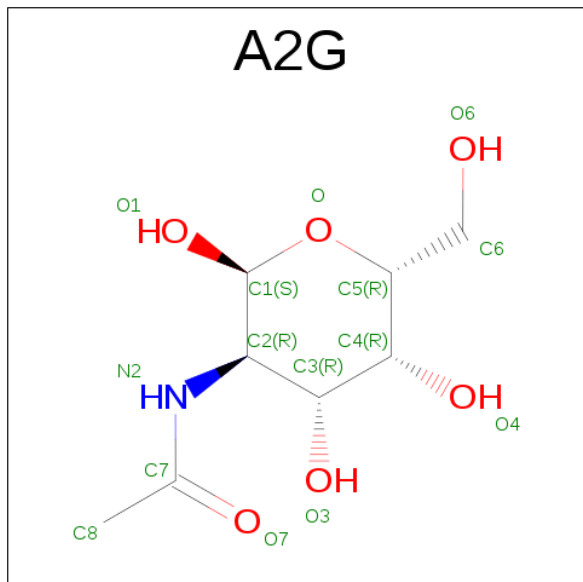
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			39	17	3	17	2		
2	C	1	Total	C	N	O	P	0	0
			39	17	3	17	2		

- Molecule 3 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C<sub>9</sub>H<sub>14</sub>N<sub>2</sub>O<sub>12</sub>P<sub>2</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		
3	D	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 4 is SUGAR (N-ACETYL-2-DEOXY-2-AMINO-GALACTOSE) (three-letter code: A2G) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			15	8	1	6		
4	D	1	Total	C	N	O	0	0
			15	8	1	6		



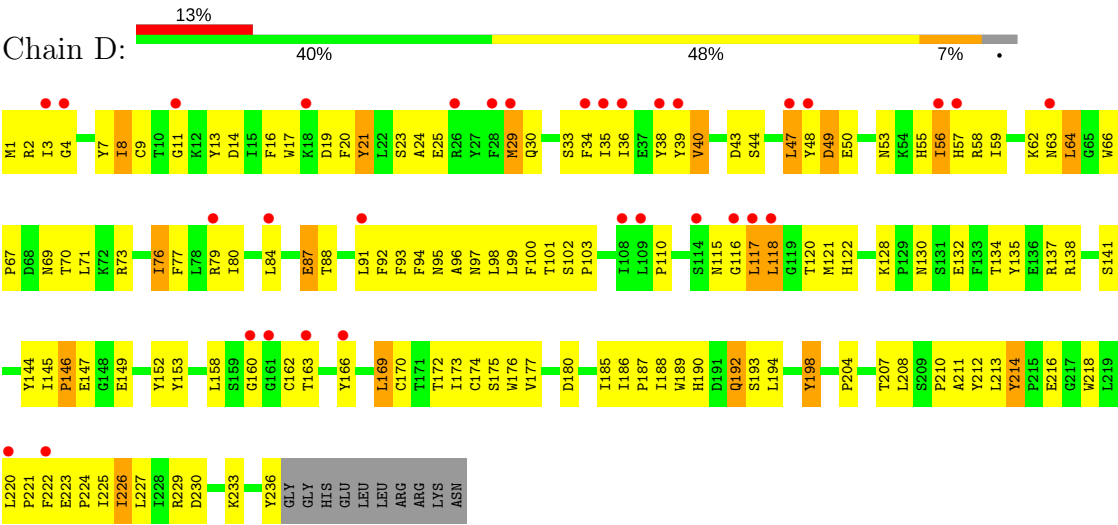
ARG

ARG

LYS

ASN

● Molecule 1: GLYCOSYLTRANSFERASE FAMILY 6



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.12Å 120.15Å 131.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	88.80 – 3.42 88.80 – 3.42	Depositor EDS
% Data completeness (in resolution range)	97.0 (88.80-3.42) 90.4 (88.80-3.42)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.12 (at 3.41Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, $R_{free}$	0.283 , 0.314 0.286 , 0.316	Depositor DCC
$R_{free}$ test set	875 reflections (5.07%)	DCC
Wilson B-factor (Å <sup>2</sup> )	89.6	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 53.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	8120	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: UD2, UDP, A2G

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	0.50	0/2074	0.65	2/2816 (0.1%)
1	B	0.47	0/2046	0.65	4/2778 (0.1%)
1	C	0.38	0/2066	0.62	0/2805
1	D	0.36	0/2038	0.67	2/2768 (0.1%)
All	All	0.43	0/8224	0.65	8/11167 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	49	ASP	N-CA-C	-8.23	88.78	111.00
1	B	47	LEU	CA-CB-CG	-7.24	98.66	115.30
1	D	169	LEU	CA-CB-CG	6.82	130.98	115.30
1	A	237	GLY	N-CA-C	-6.36	97.20	113.10
1	B	33	SER	CB-CA-C	-6.03	98.64	110.10
1	B	34	PHE	N-CA-CB	6.00	121.39	110.60
1	D	118	LEU	CA-CB-CG	5.76	128.54	115.30
1	B	30	GLN	CB-CA-C	5.07	120.54	110.40

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	2008	0	1944	201	0
1	B	1981	0	1920	100	0
1	C	2000	0	1933	130	0
1	D	1973	0	1914	157	0
2	A	39	0	25	9	0
2	C	39	0	25	5	0
3	B	25	0	11	2	0
3	D	25	0	11	2	0
4	B	15	0	15	0	0
4	D	15	0	15	1	0
All	All	8120	0	7813	586	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 37.

All (586) 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:D:29:MET:HG3	1:D:34:PHE:CZ	1.33	1.63
1:C:48:TYR:CD1	1:C:49:ASP:HB3	1.41	1.52
1:A:3:ILE:HD12	1:A:29:MET:CE	1.41	1.46
1:A:188:ILE:HD13	1:A:189:TRP:CD1	1.49	1.44
1:A:3:ILE:CD1	1:A:29:MET:HE3	1.42	1.44
1:A:3:ILE:HD11	1:A:29:MET:SD	1.61	1.40
1:A:3:ILE:CD1	1:A:29:MET:CE	1.95	1.39
1:D:29:MET:HG3	1:D:34:PHE:CE2	1.55	1.38
1:B:28:PHE:CE1	1:B:29:MET:HG3	1.61	1.35
1:C:48:TYR:CE1	1:C:49:ASP:HB3	1.62	1.32
1:A:188:ILE:HD12	1:A:189:TRP:N	1.48	1.26
1:C:29:MET:O	1:C:34:PHE:HZ	1.14	1.24
1:D:29:MET:CG	1:D:34:PHE:CE2	2.18	1.24
1:A:50:GLU:O	1:A:51:GLU:HG2	1.34	1.22
1:C:29:MET:O	1:C:34:PHE:CZ	1.92	1.22
1:A:188:ILE:HD12	1:A:189:TRP:CB	1.69	1.20
1:D:29:MET:HB3	1:D:34:PHE:CE2	1.76	1.19
1:D:29:MET:CG	1:D:34:PHE:CZ	2.26	1.18
1:A:29:MET:HB2	1:A:36:ILE:HD11	1.26	1.16
1:A:42:THR:HG23	1:A:44:SER:H	1.10	1.15
1:A:188:ILE:CD1	1:A:189:TRP:CD1	2.30	1.15
1:C:48:TYR:CE1	1:C:49:ASP:CB	2.30	1.15
1:D:50:GLU:OE1	1:D:58:ARG:NH2	1.78	1.14
1:C:28:PHE:O	1:C:29:MET:HG2	1.47	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:49:ASP:O	1:A:49:ASP:OD1	1.66	1.14
1:B:28:PHE:CE1	1:B:29:MET:CG	2.30	1.14
1:D:29:MET:CB	1:D:34:PHE:CE2	2.32	1.13
1:A:54:LYS:O	1:A:54:LYS:HD2	1.50	1.12
1:A:188:ILE:CD1	1:A:189:TRP:HB2	1.78	1.12
1:A:3:ILE:CD1	1:A:29:MET:SD	2.32	1.11
1:A:26:ARG:HD3	1:A:27:TYR:HE1	1.14	1.10
1:B:46:LYS:O	1:B:47:LEU:HD23	1.48	1.10
1:D:29:MET:HB3	1:D:34:PHE:CD2	1.86	1.09
1:A:188:ILE:CD1	1:A:189:TRP:CB	2.30	1.08
1:A:26:ARG:HD3	1:A:27:TYR:CE1	1.88	1.08
1:C:47:LEU:HD22	1:C:56:ILE:HG21	1.31	1.08
1:C:48:TYR:CD1	1:C:49:ASP:CB	2.37	1.07
1:A:188:ILE:HD12	1:A:189:TRP:CA	1.84	1.06
1:D:40:VAL:HG11	1:D:47:LEU:HD21	1.31	1.06
1:A:40:VAL:HG11	1:A:47:LEU:HD11	1.09	1.06
1:C:48:TYR:C	1:C:48:TYR:CD1	2.30	1.04
1:D:40:VAL:HG11	1:D:47:LEU:CD2	1.86	1.04
1:C:48:TYR:O	1:C:48:TYR:HD1	1.41	1.02
1:A:17:TRP:NE1	1:A:48:TYR:O	1.93	1.00
1:B:26:ARG:NH1	1:B:27:TYR:CZ	2.30	1.00
1:D:47:LEU:N	1:D:58:ARG:HH21	1.58	1.00
1:A:29:MET:HG2	1:A:36:ILE:HG12	1.41	1.00
1:C:45:PRO:HG2	1:C:46:LYS:N	1.76	0.99
1:A:50:GLU:CD	1:A:51:GLU:H	1.68	0.97
1:A:48:TYR:CE1	1:A:49:ASP:HB3	1.99	0.97
1:A:40:VAL:CG1	1:A:47:LEU:HD11	1.94	0.96
1:A:188:ILE:CD1	1:A:189:TRP:CG	2.46	0.96
1:D:47:LEU:H	1:D:58:ARG:NH2	1.62	0.96
1:D:120:THR:HG22	1:D:208:LEU:HB2	1.43	0.96
1:C:45:PRO:CD	1:C:46:LYS:H	1.79	0.96
1:A:42:THR:HG23	1:A:44:SER:N	1.81	0.94
1:A:188:ILE:CD1	1:A:189:TRP:N	2.30	0.94
1:C:45:PRO:CG	1:C:46:LYS:N	2.30	0.94
1:B:28:PHE:CD1	1:B:29:MET:CG	2.51	0.94
1:A:188:ILE:HD11	1:A:189:TRP:HB2	1.51	0.93
1:B:28:PHE:HE1	1:B:29:MET:HG3	1.01	0.92
1:C:45:PRO:CG	1:C:46:LYS:H	1.82	0.92
1:D:13:TYR:HD2	3:D:1237:UDP:H2'	1.35	0.92
1:A:42:THR:CG2	1:A:44:SER:N	2.32	0.91
1:A:42:THR:CG2	1:A:44:SER:H	1.83	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:MET:CB	1:A:36:ILE:HD11	2.01	0.90
1:C:48:TYR:C	1:C:48:TYR:HD1	1.71	0.90
1:A:25:GLU:OE2	1:A:38:TYR:OH	1.88	0.89
1:C:47:LEU:CD2	1:C:56:ILE:HG21	2.03	0.89
1:B:28:PHE:HD1	1:B:29:MET:HB2	1.37	0.88
1:A:53:ASN:OD1	1:A:56:ILE:HG22	1.74	0.88
1:D:47:LEU:N	1:D:58:ARG:NH2	2.22	0.88
1:A:10:THR:H	2:A:1242:UD2:H5	1.35	0.87
1:A:29:MET:HB2	1:A:36:ILE:CD1	2.02	0.87
1:C:20:PHE:HE1	1:C:100:PHE:HE1	1.23	0.87
1:A:3:ILE:HD11	1:A:29:MET:CE	1.80	0.86
1:C:48:TYR:HD1	1:C:49:ASP:HB3	1.14	0.86
1:A:188:ILE:HD12	1:A:189:TRP:CG	2.08	0.86
1:A:50:GLU:CD	1:A:51:GLU:N	2.28	0.86
1:A:40:VAL:HG11	1:A:47:LEU:CD1	2.03	0.85
1:A:29:MET:CG	1:A:36:ILE:CG1	2.55	0.84
1:A:28:PHE:CE2	1:A:29:MET:HE1	2.13	0.84
1:A:50:GLU:OE1	1:A:50:GLU:HA	1.74	0.84
1:C:47:LEU:HB3	1:C:50:GLU:OE2	1.78	0.84
1:C:48:TYR:HE1	1:C:49:ASP:CB	1.88	0.83
1:A:37:GLU:OE2	1:A:55:HIS:ND1	2.10	0.83
1:A:188:ILE:HD13	1:A:189:TRP:HD1	0.98	0.82
1:D:1:MET:N	1:D:33:SER:O	2.11	0.82
1:A:192:GLN:HE21	2:A:1242:UD2:H3'	1.44	0.81
1:A:26:ARG:HB3	1:A:27:TYR:CD1	2.16	0.81
1:A:50:GLU:CA	1:A:50:GLU:OE1	2.29	0.81
1:D:47:LEU:HB3	1:D:56:ILE:HD11	1.63	0.81
1:A:3:ILE:HD11	1:A:29:MET:CG	2.11	0.81
1:D:19:ASP:HB2	1:D:229:ARG:HH21	1.46	0.81
1:A:231:LYS:NZ	2:A:1242:UD2:O3A	2.15	0.80
1:D:84:LEU:O	1:D:88:THR:OG1	2.00	0.80
1:A:179:ARG:O	1:A:183:ASN:ND2	2.15	0.80
1:C:47:LEU:CB	1:C:50:GLU:OE2	2.29	0.80
1:A:29:MET:CG	1:A:36:ILE:HG12	2.12	0.79
1:D:13:TYR:CD2	3:D:1237:UDP:H2'	2.17	0.79
1:A:54:LYS:CD	1:A:54:LYS:O	2.30	0.79
1:B:46:LYS:O	1:B:47:LEU:CD2	2.30	0.79
1:A:17:TRP:CD1	1:A:47:LEU:HD23	2.16	0.79
1:C:45:PRO:HD2	1:C:46:LYS:H	1.45	0.79
1:A:29:MET:HG2	1:A:36:ILE:CG1	2.13	0.78
1:B:84:LEU:HD23	1:B:91:LEU:HD11	1.65	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:17:TRP:HE1	1:D:48:TYR:HD1	1.30	0.78
1:A:50:GLU:C	1:A:51:GLU:HG2	2.02	0.78
1:C:29:MET:C	1:C:34:PHE:CZ	2.56	0.78
1:B:121:MET:HB2	1:B:210:PRO:HD3	1.66	0.77
1:B:28:PHE:CD1	1:B:29:MET:HB2	2.19	0.77
1:A:53:ASN:OD1	1:A:56:ILE:CG2	2.32	0.77
1:C:45:PRO:HG2	1:C:46:LYS:H	1.39	0.77
1:A:48:TYR:CD1	1:A:49:ASP:HB3	2.19	0.77
1:D:50:GLU:OE2	1:D:58:ARG:NH1	2.18	0.76
1:A:192:GLN:NE2	2:A:1242:UD2:O7'	2.18	0.76
1:D:95:ASN:HB2	1:D:98:LEU:HD13	1.68	0.76
1:C:130:ASN:ND2	1:C:149:GLU:O	2.18	0.76
1:A:120:THR:HG22	1:A:208:LEU:HB2	1.66	0.76
1:A:17:TRP:CD1	1:A:47:LEU:CD2	2.68	0.75
1:D:216:GLU:HB3	1:D:227:LEU:HD21	1.69	0.75
1:D:50:GLU:OE1	1:D:58:ARG:CZ	2.33	0.75
1:C:135:TYR:CD2	1:C:145:ILE:HG12	2.20	0.75
1:A:29:MET:CG	1:A:36:ILE:HG13	2.18	0.74
1:A:53:ASN:O	1:A:56:ILE:HG23	1.87	0.74
1:C:37:GLU:OE2	1:C:57:HIS:NE2	2.20	0.74
1:A:30:GLN:OE1	1:A:30:GLN:HA	1.87	0.74
1:C:48:TYR:CE1	1:C:49:ASP:HB2	2.19	0.74
1:C:29:MET:C	1:C:34:PHE:HZ	1.90	0.74
1:B:118:LEU:HD11	1:B:208:LEU:HG	1.68	0.74
1:C:48:TYR:O	1:C:48:TYR:CD1	2.30	0.74
1:C:133:PHE:HB3	1:C:135:TYR:CE1	2.23	0.74
1:D:158:LEU:HD23	1:D:213:LEU:HD13	1.69	0.74
1:A:28:PHE:CE2	1:A:29:MET:CE	2.72	0.73
1:C:47:LEU:HB3	1:C:50:GLU:CD	2.09	0.73
1:D:128:LYS:NZ	1:D:132:GLU:OE1	2.20	0.73
1:A:54:LYS:HD2	1:A:54:LYS:C	2.10	0.72
1:B:28:PHE:CD1	1:B:29:MET:CB	2.72	0.72
1:C:3:ILE:HG22	1:C:90:TYR:HB2	1.71	0.72
1:A:95:ASN:OD1	2:A:1242:UD2:O3B	2.06	0.72
1:C:216:GLU:HB3	1:C:227:LEU:HD21	1.72	0.71
1:A:49:ASP:OD1	1:A:49:ASP:C	2.28	0.71
1:B:26:ARG:NH1	1:B:27:TYR:CE1	2.52	0.71
1:C:28:PHE:C	1:C:29:MET:HG2	2.11	0.71
1:B:28:PHE:HD1	1:B:29:MET:CB	2.03	0.71
1:D:120:THR:HG23	1:D:158:LEU:HD11	1.71	0.71
1:D:36:ILE:O	1:D:55:HIS:ND1	2.24	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:PHE:CD1	1:B:29:MET:HG2	2.25	0.71
1:D:208:LEU:HB3	1:D:212:TYR:HD2	1.56	0.70
1:D:173:ILE:HG12	1:D:194:LEU:HD11	1.73	0.70
1:D:189:TRP:O	1:D:193:SER:N	2.22	0.70
1:D:92:PHE:HD1	1:D:160:GLY:HA3	1.54	0.70
1:A:139:ASP:OD1	1:A:139:ASP:N	2.24	0.69
1:C:5:ILE:HD11	1:C:28:PHE:CD2	2.27	0.69
1:D:218:TRP:HE3	1:D:220:LEU:HD11	1.57	0.69
1:A:53:ASN:C	1:A:53:ASN:OD1	2.29	0.69
1:C:49:ASP:CG	1:C:49:ASP:O	2.30	0.69
1:D:64:LEU:HD13	1:D:69:ASN:HA	1.75	0.69
1:C:145:ILE:HD13	1:C:200:LEU:HD22	1.74	0.69
1:D:40:VAL:O	1:D:59:ILE:HB	1.92	0.69
1:A:26:ARG:HB3	1:A:27:TYR:HD1	1.58	0.69
1:A:28:PHE:HE1	1:A:104:ILE:HG21	1.58	0.68
1:A:50:GLU:C	1:A:50:GLU:OE1	2.32	0.68
1:D:29:MET:HG3	1:D:34:PHE:CE1	2.18	0.68
1:D:47:LEU:O	1:D:50:GLU:HB2	1.94	0.68
1:C:49:ASP:C	1:C:49:ASP:OD1	2.30	0.68
1:A:188:ILE:CD1	1:A:189:TRP:HD1	1.88	0.68
1:A:73:ARG:NH2	2:A:1242:UD2:O6'	2.27	0.68
1:A:198:TYR:O	1:A:202:ASN:ND2	2.27	0.68
1:A:84:LEU:HD23	1:A:91:LEU:HD11	1.76	0.67
1:B:78:LEU:HG	1:B:81:LYS:HD2	1.75	0.67
1:A:29:MET:HG3	1:A:36:ILE:HG13	1.77	0.67
1:A:12:LYS:HB3	1:A:240:GLU:HG2	1.77	0.67
1:C:188:ILE:O	1:C:193:SER:OG	2.12	0.67
1:A:54:LYS:HE2	1:A:57:HIS:NE2	2.10	0.67
1:D:172:THR:O	1:D:175:SER:OG	2.11	0.67
1:D:98:LEU:HD23	1:D:226:ILE:HD11	1.77	0.66
1:B:192:GLN:O	1:B:196:ASN:ND2	2.29	0.66
1:C:133:PHE:HB3	1:C:135:TYR:HE1	1.59	0.66
1:C:168:LYS:O	1:C:172:THR:OG1	2.13	0.66
1:A:45:PRO:HG2	1:A:46:LYS:N	2.10	0.66
1:D:70:THR:O	1:D:73:ARG:NE	2.29	0.66
1:A:84:LEU:O	1:A:88:THR:OG1	2.13	0.66
1:B:21:TYR:HE2	1:B:49:ASP:OD2	1.78	0.66
1:C:91:LEU:HG	1:C:163:THR:HG22	1.76	0.66
1:A:50:GLU:OE1	1:A:51:GLU:N	2.29	0.65
1:A:43:ASP:OD1	1:A:44:SER:N	2.29	0.65
1:B:25:GLU:O	1:B:30:GLN:NE2	2.30	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:169:LEU:HA	1:C:198:TYR:HE2	1.62	0.65
1:D:50:GLU:OE1	1:D:58:ARG:NH1	2.29	0.65
1:C:47:LEU:N	1:C:50:GLU:OE2	2.30	0.65
1:A:55:HIS:O	1:A:57:HIS:CD2	2.49	0.65
1:C:192:GLN:OE1	2:C:1241:UD2:O3'	2.12	0.65
1:D:110:PRO:HB2	1:D:116:GLY:HA2	1.78	0.65
1:D:137:ARG:NH1	1:D:147:GLU:OE2	2.30	0.65
1:A:26:ARG:NH1	1:A:27:TYR:OH	2.30	0.64
1:A:54:LYS:CD	1:A:54:LYS:C	2.64	0.64
1:C:70:THR:OG1	1:C:73:ARG:NH2	2.30	0.64
1:B:45:PRO:O	1:B:58:ARG:NH1	2.30	0.64
1:A:53:ASN:OD1	1:A:55:HIS:N	2.29	0.64
1:B:137:ARG:NH1	1:B:146:PRO:O	2.30	0.64
1:C:45:PRO:CD	1:C:46:LYS:N	2.46	0.64
1:C:212:TYR:HA	1:C:226:ILE:HG23	1.80	0.64
1:C:6:LEU:HD11	1:C:91:LEU:HD13	1.79	0.63
1:D:50:GLU:CD	1:D:58:ARG:HH12	2.02	0.63
1:D:50:GLU:CD	1:D:58:ARG:NH1	2.52	0.63
1:B:134:THR:OG1	1:B:189:TRP:NE1	2.29	0.63
1:A:42:THR:HG23	1:A:43:ASP:N	2.13	0.63
1:B:9:CYS:SG	1:B:14:ASP:HA	2.39	0.63
1:A:214:TYR:HE1	1:A:220:LEU:HB2	1.64	0.63
1:B:84:LEU:O	1:B:88:THR:OG1	2.15	0.63
1:C:213:LEU:HD22	1:C:228:ILE:HD11	1.80	0.63
1:D:122:HIS:NE2	4:D:1238:A2G:O1	2.32	0.63
1:C:31:ASP:OD1	1:C:33:SER:OG	2.15	0.62
1:A:188:ILE:HD11	1:A:193:SER:OG	1.98	0.62
1:A:104:ILE:HG22	1:A:105:GLY:H	1.64	0.62
1:A:144:TYR:O	1:A:197:LYS:NZ	2.24	0.62
1:A:29:MET:CB	1:A:36:ILE:CG1	2.77	0.62
1:D:2:ARG:HG3	1:D:88:THR:HA	1.82	0.62
1:B:28:PHE:CE1	1:B:29:MET:HG2	2.28	0.62
1:B:46:LYS:C	1:B:47:LEU:HD23	2.20	0.62
1:A:188:ILE:HD12	1:A:189:TRP:H	1.59	0.62
1:A:69:ASN:HD22	2:A:1242:UD2:C4	2.13	0.62
1:A:70:THR:OG1	1:A:73:ARG:NH2	2.33	0.62
1:D:40:VAL:CG1	1:D:47:LEU:HD21	2.20	0.62
1:A:188:ILE:CD1	1:A:189:TRP:H	2.13	0.61
1:A:188:ILE:CG1	1:A:189:TRP:N	2.62	0.61
1:A:53:ASN:CG	1:A:56:ILE:HG22	2.21	0.61
1:A:45:PRO:CG	1:A:46:LYS:N	2.63	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:22:LEU:HD21	1:A:48:TYR:OH	2.00	0.61
1:C:168:LYS:NZ	1:C:198:TYR:OH	2.34	0.60
1:C:5:ILE:HD11	1:C:28:PHE:CE2	2.36	0.60
1:D:70:THR:O	1:D:73:ARG:CZ	2.49	0.60
1:D:87:GLU:OE1	1:D:87:GLU:N	2.30	0.60
1:A:45:PRO:HG2	1:A:46:LYS:H	1.66	0.60
1:D:17:TRP:HA	1:D:20:PHE:CE1	2.37	0.60
1:A:3:ILE:HG22	1:A:90:TYR:HB2	1.84	0.60
1:D:173:ILE:HD12	1:D:176:TRP:HB2	1.83	0.60
1:D:77:PHE:CZ	1:D:170:CYS:HB2	2.37	0.60
1:A:37:GLU:OE2	1:A:55:HIS:CE1	2.55	0.59
1:A:73:ARG:NH1	1:A:191:ASP:OD2	2.35	0.59
1:A:50:GLU:O	1:A:52:ASN:N	2.30	0.59
1:D:67:PRO:O	1:D:71:LEU:N	2.29	0.59
1:D:7:TYR:HD2	1:D:40:VAL:HG23	1.65	0.59
1:D:115:ASN:OD1	1:D:115:ASN:N	2.35	0.59
1:D:138:ARG:O	1:D:141:SER:OG	2.20	0.59
1:D:7:TYR:CD2	1:D:40:VAL:HG23	2.38	0.59
1:A:73:ARG:HA	1:A:76:ILE:HD12	1.83	0.59
1:B:24:ALA:O	1:B:28:PHE:HB3	2.03	0.59
1:B:177:VAL:O	1:B:180:ASP:HB3	2.01	0.59
1:C:106:LYS:HG2	1:C:109:LEU:HD21	1.86	0.58
1:A:192:GLN:NE2	2:A:1242:UD2:H3'	2.16	0.58
1:C:19:ASP:HA	1:C:22:LEU:HD22	1.85	0.58
1:D:211:ALA:HB2	1:D:222:PHE:HB3	1.84	0.58
1:C:216:GLU:OE2	1:C:233:LYS:HE2	2.04	0.58
1:D:77:PHE:HZ	1:D:170:CYS:HB2	1.69	0.58
1:A:135:TYR:OH	1:A:152:TYR:O	2.22	0.58
1:B:147:GLU:N	1:B:147:GLU:OE1	2.36	0.58
1:C:89:ASP:OD1	1:C:89:ASP:N	2.36	0.58
1:D:92:PHE:CD1	1:D:160:GLY:HA3	2.37	0.58
1:D:99:LEU:HG	1:D:229:ARG:HG3	1.86	0.58
1:B:136:GLU:OE2	1:B:138:ARG:NH2	2.32	0.58
1:C:232:ASN:HA	1:C:238:GLY:HA2	1.86	0.58
1:D:189:TRP:HB2	1:D:193:SER:HB3	1.84	0.58
1:B:28:PHE:CD1	1:B:28:PHE:C	2.77	0.57
1:C:48:TYR:HE1	1:C:49:ASP:HB2	1.60	0.57
1:C:8:ILE:O	2:C:1241:UD2:O2'	2.10	0.57
1:D:120:THR:HG22	1:D:208:LEU:CB	2.26	0.57
1:C:20:PHE:HE1	1:C:100:PHE:CE1	2.14	0.57
1:B:65:GLY:N	1:B:69:ASN:OD1	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:81:LYS:HE3	1:C:167:LEU:HD21	1.85	0.57
1:D:186:ILE:HD12	1:D:187:PRO:HD2	1.87	0.57
1:D:19:ASP:HB2	1:D:229:ARG:NH2	2.18	0.57
1:A:37:GLU:CD	1:A:55:HIS:ND1	2.57	0.56
1:B:145:ILE:HD12	1:B:146:PRO:HD2	1.86	0.56
1:A:11:GLY:N	1:A:43:ASP:OD2	2.34	0.56
1:A:55:HIS:O	1:A:57:HIS:NE2	2.38	0.56
1:C:218:TRP:HE3	1:C:220:LEU:HD11	1.69	0.56
1:A:97:ASN:ND2	1:A:231:LYS:HE3	2.21	0.56
1:D:34:PHE:HE2	1:D:36:ILE:HG12	1.70	0.56
1:D:47:LEU:H	1:D:58:ARG:HH22	1.51	0.56
1:A:137:ARG:NH1	1:A:145:ILE:O	2.33	0.56
1:B:195:ILE:HG23	1:B:199:PHE:CE2	2.40	0.56
1:B:215:PRO:HA	1:B:228:ILE:HB	1.89	0.55
1:A:18:LYS:HG3	1:A:48:TYR:CD2	2.42	0.55
1:B:45:PRO:O	1:B:58:ARG:CZ	2.54	0.55
1:D:29:MET:CB	1:D:34:PHE:CD2	2.69	0.55
1:D:210:PRO:HG2	1:D:222:PHE:CE2	2.42	0.55
1:A:45:PRO:CG	1:A:46:LYS:H	2.20	0.54
1:A:51:GLU:HG3	1:A:52:ASN:OD1	2.07	0.54
1:A:27:TYR:N	1:A:27:TYR:CD1	2.72	0.54
1:A:26:ARG:HB3	1:A:27:TYR:CE1	2.43	0.54
1:A:50:GLU:C	1:A:51:GLU:CG	2.75	0.54
1:D:121:MET:HB2	1:D:210:PRO:HD3	1.90	0.54
1:C:235:GLN:O	1:C:235:GLN:NE2	2.36	0.54
1:A:42:THR:CG2	1:A:43:ASP:N	2.69	0.54
1:C:48:TYR:O	1:C:49:ASP:CB	2.54	0.54
1:D:57:HIS:O	1:D:57:HIS:ND1	2.41	0.54
1:D:166:TYR:O	1:D:169:LEU:HG	2.07	0.53
1:A:29:MET:HB2	1:A:36:ILE:CG1	2.38	0.53
1:A:10:THR:OG1	1:A:69:ASN:ND2	2.41	0.53
1:C:135:TYR:HD2	1:C:145:ILE:HG21	1.73	0.53
1:C:110:PRO:HG2	1:C:161:GLY:HA2	1.90	0.53
1:A:104:ILE:HG22	1:A:105:GLY:N	2.23	0.53
1:B:21:TYR:CE2	1:B:49:ASP:OD2	2.58	0.53
1:B:83:GLN:O	1:B:87:GLU:HG2	2.09	0.53
1:D:49:ASP:CG	1:D:53:ASN:HD22	2.12	0.53
1:D:47:LEU:HB2	1:D:58:ARG:NH2	2.24	0.53
1:A:137:ARG:NH1	1:A:146:PRO:O	2.41	0.53
1:C:147:GLU:OE1	1:C:147:GLU:N	2.42	0.53
1:C:48:TYR:HD1	1:C:49:ASP:CB	2.01	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:SER:CB	1:A:45:PRO:HD2	2.39	0.53
1:D:9:CYS:SG	1:D:14:ASP:HA	2.48	0.53
1:D:29:MET:CB	1:D:34:PHE:HE2	2.12	0.53
1:D:120:THR:CG2	1:D:158:LEU:HD11	2.38	0.53
1:B:214:TYR:HE2	1:B:224:PRO:HD3	1.74	0.52
1:C:29:MET:SD	1:C:105:GLY:O	2.67	0.52
1:A:6:LEU:HD21	1:A:91:LEU:HD13	1.91	0.52
1:B:135:TYR:OH	1:B:152:TYR:O	2.27	0.52
1:B:37:GLU:OE1	1:B:57:HIS:NE2	2.42	0.52
1:A:17:TRP:NE1	1:A:47:LEU:CD2	2.71	0.52
1:C:199:PHE:HD1	1:C:204:PRO:HD3	1.75	0.52
1:D:43:ASP:OD1	1:D:44:SER:N	2.43	0.52
1:D:188:ILE:HG23	1:D:189:TRP:H	1.74	0.52
1:A:138:ARG:O	1:A:144:TYR:HB2	2.09	0.52
1:A:50:GLU:O	1:A:51:GLU:CG	2.30	0.52
1:B:210:PRO:HG2	1:B:222:PHE:CZ	2.46	0.51
1:C:133:PHE:HB3	1:C:135:TYR:CD1	2.45	0.51
1:D:172:THR:OG1	1:D:173:ILE:N	2.43	0.51
1:B:210:PRO:HG2	1:B:222:PHE:CE2	2.45	0.51
1:C:48:TYR:O	1:C:49:ASP:HB3	2.09	0.51
1:B:68:ASP:O	1:B:72:LYS:HG2	2.10	0.51
1:A:191:ASP:OD2	2:A:1242:UD2:O6'	2.21	0.51
1:A:18:LYS:HG3	1:A:48:TYR:CE2	2.45	0.51
1:B:10:THR:OG1	3:B:1239:UDP:O4	2.15	0.51
1:B:125:PHE:HD2	1:B:153:TYR:CD2	2.28	0.51
1:C:30:GLN:CD	1:C:30:GLN:H	2.14	0.51
1:C:47:LEU:CB	1:C:50:GLU:CD	2.76	0.51
1:A:169:LEU:HD13	1:A:198:TYR:CD2	2.46	0.51
1:C:7:TYR:CE2	1:C:17:TRP:HE3	2.28	0.51
1:A:29:MET:CB	1:A:36:ILE:CD1	2.74	0.51
1:A:45:PRO:CD	1:A:46:LYS:H	2.24	0.51
1:A:147:GLU:N	1:A:147:GLU:OE1	2.44	0.50
1:B:25:GLU:O	1:B:30:GLN:OE1	2.29	0.50
1:C:118:LEU:N	1:C:160:GLY:O	2.43	0.50
1:C:48:TYR:O	1:C:49:ASP:OD1	2.30	0.50
1:B:126:TYR:OH	1:D:223:GLU:OE2	2.24	0.50
1:B:230:ASP:HB3	1:B:233:LYS:HG3	1.93	0.50
1:D:84:LEU:HD23	1:D:91:LEU:HD21	1.93	0.50
1:A:31:ASP:OD2	1:A:33:SER:OG	2.29	0.50
1:C:195:ILE:HG23	1:C:199:PHE:CE2	2.46	0.50
1:C:84:LEU:O	1:C:88:THR:OG1	2.14	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:214:TYR:HE2	1:D:224:PRO:HD3	1.75	0.50
1:D:1:MET:HG3	1:D:2:ARG:N	2.27	0.50
1:D:135:TYR:OH	1:D:152:TYR:O	2.29	0.50
1:A:2:ARG:HB3	1:A:35:ILE:HD12	1.94	0.50
1:D:146:PRO:HD2	1:D:149:GLU:OE2	2.12	0.50
1:A:51:GLU:HG2	1:A:52:ASN:H	1.76	0.49
1:C:43:ASP:OD1	1:C:43:ASP:N	2.45	0.49
1:A:133:PHE:CD1	1:A:153:TYR:HB2	2.47	0.49
1:B:188:ILE:HD12	1:B:188:ILE:O	2.12	0.49
1:D:214:TYR:HE1	1:D:218:TRP:HB2	1.77	0.49
1:D:40:VAL:HG11	1:D:47:LEU:HD23	1.86	0.49
1:C:48:TYR:CD1	1:C:49:ASP:N	2.80	0.49
1:D:180:ASP:HB3	1:D:185:ILE:O	2.12	0.49
1:A:42:THR:HG22	1:A:44:SER:N	2.25	0.49
1:A:28:PHE:CE1	1:A:104:ILE:HG21	2.44	0.49
1:A:188:ILE:CG1	1:A:189:TRP:H	2.26	0.49
1:C:65:GLY:N	1:C:69:ASN:OD1	2.46	0.49
1:C:157:GLY:N	2:C:1241:UD2:O6'	2.46	0.49
1:C:138:ARG:HH12	1:C:140:ALA:HB3	1.76	0.49
1:C:215:PRO:HG2	1:C:218:TRP:CD2	2.48	0.49
1:D:97:ASN:O	1:D:229:ARG:N	2.39	0.49
1:D:71:LEU:HA	1:D:73:ARG:NH2	2.28	0.49
1:D:70:THR:O	1:D:73:ARG:HB3	2.13	0.49
1:A:7:TYR:CE1	1:A:96:ALA:HA	2.47	0.49
1:C:95:ASN:H	1:C:98:LEU:HD12	1.78	0.49
1:A:48:TYR:CD1	1:A:49:ASP:CB	2.92	0.48
1:A:54:LYS:HE2	1:A:57:HIS:CD2	2.48	0.48
1:D:130:ASN:HD21	1:D:149:GLU:C	2.16	0.48
1:A:95:ASN:H	1:A:98:LEU:HD12	1.78	0.48
1:B:195:ILE:HG23	1:B:199:PHE:HE2	1.77	0.48
1:D:214:TYR:CE2	1:D:224:PRO:HD3	2.48	0.48
1:D:35:ILE:HG13	1:D:55:HIS:HE1	1.78	0.48
1:D:99:LEU:O	1:D:226:ILE:HD12	2.13	0.48
1:D:4:GLY:CA	1:D:39:TYR:HE2	2.26	0.48
1:D:66:TRP:CZ3	1:D:70:THR:HG21	2.49	0.48
1:A:28:PHE:CD2	1:A:29:MET:CE	2.97	0.48
1:D:79:ARG:HG3	1:D:80:ILE:HG23	1.94	0.48
1:A:27:TYR:HD2	1:A:102:SER:C	2.17	0.47
1:D:99:LEU:HG	1:D:229:ARG:CG	2.44	0.47
1:D:230:ASP:O	1:D:233:LYS:HG2	2.14	0.47
1:B:23:SER:HB2	1:B:100:PHE:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:2:ARG:HA	1:D:35:ILE:HG22	1.97	0.47
1:D:34:PHE:CE2	1:D:36:ILE:HG12	2.48	0.47
1:C:104:ILE:HG13	1:C:105:GLY:H	1.80	0.47
1:C:47:LEU:CA	1:C:50:GLU:OE2	2.62	0.47
1:D:23:SER:HB2	1:D:100:PHE:HB2	1.96	0.47
1:A:213:LEU:O	1:A:215:PRO:HD3	2.14	0.47
1:D:169:LEU:HB2	1:D:198:TYR:HE2	1.80	0.47
1:D:212:TYR:HA	1:D:226:ILE:HG23	1.97	0.47
1:B:78:LEU:O	1:B:81:LYS:HD3	2.14	0.47
1:D:11:GLY:H	1:D:63:ASN:HD21	1.63	0.47
1:D:8:ILE:HG23	1:D:93:PHE:HE2	1.80	0.47
1:A:53:ASN:O	1:A:53:ASN:OD1	2.32	0.47
1:B:28:PHE:HD1	1:B:28:PHE:C	2.18	0.47
2:C:1241:UD2:O4'	2:C:1241:UD2:O6'	2.21	0.47
1:C:18:LYS:HG3	1:C:48:TYR:CD2	2.49	0.47
1:A:151:ARG:NH2	1:A:152:TYR:OH	2.48	0.47
1:A:145:ILE:HG12	1:A:197:LYS:HE2	1.97	0.47
1:B:191:ASP:N	1:B:191:ASP:OD1	2.47	0.47
1:C:138:ARG:NH1	1:C:185:ILE:HD12	2.30	0.47
1:D:101:THR:OG1	1:D:225:ILE:O	2.29	0.47
1:D:7:TYR:CE1	1:D:96:ALA:HA	2.50	0.47
1:A:28:PHE:CZ	1:A:29:MET:HE1	2.47	0.47
1:B:231:LYS:NZ	3:B:1239:UDP:O1B	2.48	0.47
1:B:47:LEU:O	1:B:48:TYR:C	2.53	0.47
1:B:74:PHE:O	1:B:78:LEU:HD13	2.15	0.47
1:B:90:TYR:HE2	1:B:109:LEU:HD13	1.80	0.46
1:C:208:LEU:HD23	1:C:212:TYR:CD2	2.50	0.46
1:A:59:ILE:HD13	1:A:80:ILE:HD13	1.98	0.46
1:D:117:LEU:HD13	1:D:204:PRO:HG3	1.98	0.46
1:B:73:ARG:HA	1:B:76:ILE:HD12	1.98	0.46
1:D:208:LEU:HB3	1:D:212:TYR:CD2	2.42	0.46
1:A:3:ILE:HD12	1:A:29:MET:HE3	0.56	0.46
1:D:3:ILE:HD12	1:D:34:PHE:HE1	1.80	0.46
1:B:187:PRO:HG2	1:B:194:LEU:HD11	1.97	0.46
1:B:1:MET:HB3	1:B:89:ASP:OD2	2.15	0.46
1:D:134:THR:OG1	1:D:153:TYR:OH	2.25	0.46
1:A:173:ILE:O	1:A:177:VAL:HG12	2.16	0.46
1:A:34:PHE:CZ	1:A:106:LYS:HG2	2.50	0.46
1:A:47:LEU:O	1:A:50:GLU:HB2	2.15	0.46
1:C:138:ARG:CZ	1:C:141:SER:HB2	2.45	0.46
1:C:28:PHE:CD1	1:C:28:PHE:O	2.68	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:2:ARG:NH2	1:C:86:ARG:O	2.41	0.46
1:A:28:PHE:CD2	1:A:29:MET:HE1	2.51	0.46
1:C:145:ILE:HD12	1:C:146:PRO:HD2	1.97	0.46
1:D:169:LEU:HB2	1:D:198:TYR:CE2	2.51	0.46
1:B:199:PHE:CD1	1:B:204:PRO:HG3	2.50	0.46
1:C:7:TYR:HD1	1:C:8:ILE:N	2.14	0.46
1:C:91:LEU:HA	1:C:91:LEU:HD23	1.81	0.46
1:A:30:GLN:CA	1:A:30:GLN:OE1	2.59	0.45
1:A:98:LEU:HD22	1:A:226:ILE:HG22	1.96	0.45
1:B:176:TRP:O	1:B:180:ASP:HB2	2.16	0.45
1:D:173:ILE:HD13	1:D:176:TRP:CE3	2.51	0.45
1:D:220:LEU:HB3	1:D:222:PHE:CD2	2.52	0.45
1:A:235:GLN:H	1:A:235:GLN:HG2	1.53	0.45
1:C:8:ILE:HG22	1:C:93:PHE:HE1	1.82	0.45
1:D:64:LEU:H	1:D:64:LEU:HD12	1.81	0.45
1:B:136:GLU:HB3	1:B:143:ALA:O	2.17	0.45
1:A:54:LYS:HG3	1:A:55:HIS:N	2.29	0.45
1:C:20:PHE:CE1	1:C:100:PHE:HE1	2.15	0.45
1:C:40:VAL:HG21	1:C:47:LEU:HD11	1.99	0.45
1:B:8:ILE:HD11	1:B:77:PHE:CE1	2.52	0.45
1:D:169:LEU:O	1:D:172:THR:OG1	2.28	0.45
1:A:2:ARG:HB3	1:A:35:ILE:CD1	2.47	0.45
1:C:27:TYR:CE1	1:C:103:PRO:HD3	2.52	0.45
1:D:134:THR:HG1	1:D:153:TYR:HH	1.57	0.45
1:B:7:TYR:CE2	1:B:96:ALA:HA	2.52	0.45
1:B:222:PHE:O	1:D:221:PRO:HB3	2.16	0.45
1:C:73:ARG:HB2	1:C:77:PHE:CZ	2.51	0.45
1:D:76:ILE:HA	1:D:76:ILE:HD12	1.75	0.45
1:D:20:PHE:HB3	1:D:99:LEU:HD23	1.99	0.45
1:A:17:TRP:NE1	1:A:47:LEU:HD22	2.32	0.44
1:A:3:ILE:CD1	1:A:29:MET:HE2	2.26	0.44
1:B:18:LYS:HE3	1:B:48:TYR:CE1	2.52	0.44
1:B:203:PRO:HA	1:B:204:PRO:HD3	1.93	0.44
1:B:43:ASP:OD1	1:B:44:SER:N	2.51	0.44
1:D:4:GLY:HA3	1:D:39:TYR:HE2	1.82	0.44
1:B:90:TYR:HD2	1:B:109:LEU:HD22	1.83	0.44
1:C:28:PHE:HD1	1:C:104:ILE:HD11	1.82	0.44
1:C:49:ASP:OD1	1:C:56:ILE:CD1	2.66	0.44
1:A:55:HIS:O	1:A:57:HIS:CE1	2.70	0.44
1:B:135:TYR:CD2	1:B:145:ILE:HG12	2.53	0.44
1:D:152:TYR:HE2	1:D:207:THR:HG21	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:17:TRP:CG	1:A:47:LEU:CD2	3.00	0.44
1:C:130:ASN:HA	1:C:133:PHE:CD2	2.53	0.44
1:D:16:PHE:HE1	1:D:236:TYR:CD2	2.36	0.44
1:A:179:ARG:O	1:A:182:THR:HG22	2.17	0.44
1:A:3:ILE:HD11	1:A:29:MET:HG3	1.98	0.44
1:C:138:ARG:CZ	1:C:185:ILE:HD12	2.48	0.44
1:C:84:LEU:HD23	1:C:91:LEU:HD11	2.00	0.44
1:C:9:CYS:SG	1:C:14:ASP:HA	2.57	0.44
1:A:214:TYR:CE1	1:A:220:LEU:HB2	2.50	0.44
1:B:214:TYR:O	1:B:228:ILE:N	2.43	0.43
1:B:26:ARG:NH1	1:B:27:TYR:OH	2.50	0.43
1:D:94:PHE:HD2	1:D:98:LEU:HD23	1.82	0.43
1:D:173:ILE:CG1	1:D:194:LEU:HD11	2.45	0.43
1:A:208:LEU:HB3	1:A:212:TYR:CD2	2.54	0.43
1:A:62:LYS:HA	1:A:62:LYS:HD2	1.68	0.43
1:D:24:ALA:HA	1:D:100:PHE:CE2	2.53	0.43
1:D:7:TYR:CE1	1:D:20:PHE:HZ	2.36	0.43
1:A:34:PHE:HZ	1:A:106:LYS:HG2	1.82	0.43
1:A:38:TYR:C	1:A:39:TYR:HD1	2.21	0.43
1:B:30:GLN:O	1:B:31:ASP:C	2.56	0.43
1:D:50:GLU:CD	1:D:58:ARG:CZ	2.86	0.43
1:D:91:LEU:HD13	1:D:163:THR:OG1	2.18	0.43
1:B:180:ASP:OD1	1:B:185:ILE:HG13	2.19	0.43
1:C:173:ILE:HD12	1:C:194:LEU:HD23	2.01	0.43
1:D:76:ILE:O	1:D:79:ARG:HG2	2.19	0.43
1:A:168:LYS:HA	1:A:168:LYS:HD2	1.67	0.43
1:B:214:TYR:CE2	1:B:224:PRO:HD3	2.53	0.43
1:A:17:TRP:CG	1:A:47:LEU:HD21	2.53	0.43
1:A:91:LEU:HD23	1:A:91:LEU:HA	1.84	0.43
1:A:48:TYR:CD1	1:A:49:ASP:CA	3.02	0.43
1:A:59:ILE:CD1	1:A:80:ILE:HD13	2.48	0.43
1:C:142:THR:HG21	1:C:176:TRP:O	2.19	0.43
1:C:17:TRP:CD1	1:C:48:TYR:HB3	2.54	0.43
1:A:17:TRP:CE2	1:A:47:LEU:HD22	2.53	0.42
1:A:53:ASN:CG	1:A:56:ILE:CG2	2.83	0.42
1:C:133:PHE:CB	1:C:135:TYR:HE1	2.28	0.42
1:D:169:LEU:O	1:D:173:ILE:HG22	2.19	0.42
1:D:194:LEU:HD13	1:D:194:LEU:C	2.39	0.42
1:D:25:GLU:OE2	1:D:38:TYR:OH	2.25	0.42
1:A:115:ASN:ND2	1:A:203:PRO:O	2.52	0.42
1:A:236:TYR:C	1:A:237:GLY:O	2.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:16:PHE:HB3	1:C:96:ALA:O	2.19	0.42
1:D:20:PHE:O	1:D:24:ALA:N	2.43	0.42
1:D:92:PHE:CE1	1:D:118:LEU:HD21	2.54	0.42
1:A:48:TYR:HA	1:A:49:ASP:HA	1.73	0.42
1:B:28:PHE:HD2	1:B:100:PHE:CZ	2.37	0.42
1:D:17:TRP:HB2	1:D:21:TYR:CE2	2.54	0.42
1:A:40:VAL:CG1	1:A:47:LEU:CD1	2.82	0.42
1:D:173:ILE:O	1:D:173:ILE:HD12	2.19	0.42
1:D:7:TYR:HE1	1:D:96:ALA:HA	1.84	0.42
1:B:180:ASP:OD2	1:B:185:ILE:O	2.38	0.42
1:C:7:TYR:HE2	1:C:20:PHE:CD2	2.37	0.42
1:B:21:TYR:CZ	1:B:25:GLU:OE1	2.73	0.42
1:C:173:ILE:O	1:C:176:TRP:HB2	2.20	0.42
1:D:153:TYR:CZ	1:D:192:GLN:NE2	2.88	0.42
1:D:208:LEU:HD22	1:D:212:TYR:CE2	2.54	0.42
1:C:45:PRO:HD2	1:C:46:LYS:N	2.22	0.42
1:B:107:GLU:HG2	1:B:108:ILE:HG23	2.02	0.42
1:B:135:TYR:O	1:B:188:ILE:HD11	2.20	0.42
1:B:152:TYR:CD2	1:B:207:THR:HG21	2.54	0.42
1:C:225:ILE:HG23	1:C:226:ILE:H	1.85	0.42
1:C:2:ARG:HA	1:C:35:ILE:O	2.19	0.42
1:C:95:ASN:N	1:C:98:LEU:HD12	2.34	0.42
1:D:4:GLY:O	1:D:91:LEU:HA	2.20	0.42
1:A:104:ILE:CG2	1:A:105:GLY:H	2.33	0.42
1:A:212:TYR:O	1:A:226:ILE:HB	2.19	0.42
1:A:9:CYS:O	1:A:42:THR:OG1	2.23	0.42
1:C:27:TYR:HE1	1:C:103:PRO:HD3	1.84	0.42
1:D:48:TYR:O	1:D:49:ASP:CB	2.67	0.42
1:C:206:ILE:HG13	1:C:208:LEU:HD12	2.02	0.41
1:A:143:ALA:HA	1:A:197:LYS:HE3	2.02	0.41
1:C:195:ILE:HG23	1:C:199:PHE:CD2	2.55	0.41
1:B:18:LYS:HE3	1:B:48:TYR:CZ	2.56	0.41
1:D:71:LEU:CD2	1:D:186:ILE:HD11	2.50	0.41
1:D:39:TYR:HD1	1:D:57:HIS:CE1	2.38	0.41
1:A:107:GLU:HG2	1:A:108:ILE:HG23	2.02	0.41
1:A:126:TYR:CE2	1:B:219:LEU:HD21	2.56	0.41
1:A:202:ASN:HA	1:A:203:PRO:HD2	1.93	0.41
1:B:90:TYR:CD2	1:B:109:LEU:HD22	2.56	0.41
1:B:170:CYS:O	1:B:174:CYS:HB3	2.21	0.41
1:A:222:PHE:HA	1:B:216:GLU:HG3	2.02	0.41
1:C:27:TYR:O	1:C:28:PHE:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:235:GLN:HG2	1:B:235:GLN:H	1.73	0.41
2:C:1241:UD2:H6	2:C:1241:UD2:H2B	1.50	0.41
1:B:110:PRO:HG2	1:B:161:GLY:HA2	2.03	0.41
1:C:194:LEU:HD22	1:C:194:LEU:H	1.85	0.41
1:B:72:LYS:HE2	1:B:72:LYS:HB3	1.85	0.41
1:C:135:TYR:HB3	1:C:145:ILE:HG23	2.03	0.41
1:D:190:HIS:O	1:D:194:LEU:HB3	2.21	0.41
1:A:136:GLU:HB3	1:A:143:ALA:O	2.21	0.41
1:B:142:THR:HG21	1:B:176:TRP:HB3	2.01	0.41
1:B:90:TYR:CE2	1:B:109:LEU:HD13	2.55	0.41
1:D:173:ILE:CD1	1:D:194:LEU:HD21	2.51	0.41
1:D:7:TYR:CE1	1:D:20:PHE:CZ	3.08	0.41
1:A:28:PHE:CE2	1:A:29:MET:HE2	2.52	0.41
1:B:94:PHE:HD2	1:B:98:LEU:HD12	1.86	0.41
1:B:120:THR:HG21	1:B:213:LEU:HD13	2.03	0.40
1:B:25:GLU:O	1:B:30:GLN:CD	2.60	0.40
1:A:64:LEU:HB2	1:A:69:ASN:OD1	2.21	0.40
1:B:158:LEU:CB	1:B:213:LEU:HD11	2.51	0.40
1:C:50:GLU:H	1:C:50:GLU:HG2	1.40	0.40
1:D:198:TYR:HD1	1:D:198:TYR:O	2.04	0.40
1:D:29:MET:O	1:D:34:PHE:CD2	2.74	0.40
1:A:188:ILE:C	1:A:188:ILE:HD12	2.30	0.40
1:D:66:TRP:CG	1:D:67:PRO:HA	2.57	0.40
1:B:168:LYS:HA	1:B:171:THR:HG22	2.04	0.40
1:C:115:ASN:OD1	1:C:116:GLY:N	2.54	0.40
1:C:47:LEU:CD2	1:C:56:ILE:CG2	2.87	0.40
1:A:95:ASN:N	1:A:98:LEU:HD12	2.35	0.40
1:D:102:SER:HA	1:D:103:PRO:HD3	1.92	0.40
1:D:144:TYR:CE2	1:D:146:PRO:HG3	2.56	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	239/246 (97%)	222 (93%)	17 (7%)	0	100	100
1	B	236/246 (96%)	219 (93%)	16 (7%)	1 (0%)	38	75
1	C	238/246 (97%)	219 (92%)	19 (8%)	0	100	100
1	D	234/246 (95%)	218 (93%)	15 (6%)	1 (0%)	38	75
All	All	947/984 (96%)	878 (93%)	67 (7%)	2 (0%)	51	84

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	146	PRO
1	B	146	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	216/221 (98%)	184 (85%)	32 (15%)	3	19
1	B	213/221 (96%)	194 (91%)	19 (9%)	11	43
1	C	215/221 (97%)	177 (82%)	38 (18%)	2	11
1	D	213/221 (96%)	192 (90%)	21 (10%)	9	37
All	All	857/884 (97%)	747 (87%)	110 (13%)	5	25

All (110) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MET
1	A	5	ILE
1	A	6	LEU
1	A	26	ARG
1	A	28	PHE
1	A	29	MET
1	A	30	GLN
1	A	32	GLN
1	A	33	SER

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Mol	Chain	Res	Type
1	A	35	ILE
1	A	42	THR
1	A	44	SER
1	A	47	LEU
1	A	50	GLU
1	A	51	GLU
1	A	53	ASN
1	A	54	LYS
1	A	56	ILE
1	A	66	TRP
1	A	102	SER
1	A	121	MET
1	A	139	ASP
1	A	158	LEU
1	A	175	SER
1	A	177	VAL
1	A	187	PRO
1	A	190	HIS
1	A	202	ASN
1	A	209	SER
1	A	235	GLN
1	A	239	HIS
1	A	241	LEU
1	B	10	THR
1	B	15	ILE
1	B	25	GLU
1	B	28	PHE
1	B	40	VAL
1	B	51	GLU
1	B	81	LYS
1	B	89	ASP
1	B	98	LEU
1	B	134	THR
1	B	142	THR
1	B	145	ILE
1	B	163	THR
1	B	174	CYS
1	B	177	VAL
1	B	182	THR
1	B	189	TRP
1	B	206	ILE
1	B	214	TYR

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Mol	Chain	Res	Type
1	C	1	MET
1	C	7	TYR
1	C	8	ILE
1	C	14	ASP
1	C	22	LEU
1	C	31	ASP
1	C	35	ILE
1	C	40	VAL
1	C	43	ASP
1	C	44	SER
1	C	45	PRO
1	C	46	LYS
1	C	47	LEU
1	C	48	TYR
1	C	49	ASP
1	C	50	GLU
1	C	64	LEU
1	C	89	ASP
1	C	109	LEU
1	C	138	ARG
1	C	142	THR
1	C	145	ILE
1	C	149	GLU
1	C	158	LEU
1	C	163	THR
1	C	171	THR
1	C	172	THR
1	C	173	ILE
1	C	174	CYS
1	C	183	ASN
1	C	185	ILE
1	C	190	HIS
1	C	194	LEU
1	C	198	TYR
1	C	202	ASN
1	C	225	ILE
1	C	226	ILE
1	C	235	GLN
1	D	8	ILE
1	D	21	TYR
1	D	29	MET
1	D	30	GLN

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Mol	Chain	Res	Type
1	D	40	VAL
1	D	47	LEU
1	D	49	ASP
1	D	56	ILE
1	D	62	LYS
1	D	64	LEU
1	D	76	ILE
1	D	87	GLU
1	D	117	LEU
1	D	145	ILE
1	D	162	CYS
1	D	174	CYS
1	D	177	VAL
1	D	192	GLN
1	D	198	TYR
1	D	214	TYR
1	D	226	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	192	GLN
1	A	202	ASN
1	B	61	GLN
1	D	53	ASN
1	D	69	ASN
1	D	130	ASN
1	D	196	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

### 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry

6 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	UD2	A	1242	-	34,41,41	0.64	0	43,62,62	1.66	4 (9%)
3	UDP	B	1239	-	21,26,26	0.87	1 (4%)	22,40,40	1.96	1 (4%)
4	A2G	B	1240	-	15,15,15	0.40	0	21,21,21	0.66	0
2	UD2	C	1241	-	34,41,41	0.63	0	43,62,62	1.80	6 (13%)
3	UDP	D	1237	-	21,26,26	0.81	1 (4%)	22,40,40	1.78	1 (4%)
4	A2G	D	1238	-	15,15,15	0.41	0	21,21,21	0.40	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	UD2	A	1242	-	-	0/22/63/63	0/3/3/3
3	UDP	B	1239	-	-	0/12/32/32	0/2/2/2
4	A2G	B	1240	-	-	0/6/26/26	0/1/1/1
2	UD2	C	1241	-	-	0/22/63/63	0/3/3/3
3	UDP	D	1237	-	-	0/12/32/32	0/2/2/2
4	A2G	D	1238	-	-	2/6/26/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1239	UDP	C2-N3	-2.37	1.33	1.38
3	D	1237	UDP	C2-N3	-2.17	1.33	1.38

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1241	UD2	C2'-N2'-C7'	-2.75	116.24	123.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1242	UD2	C4'-C3'-C2'	2.17	113.54	110.33
2	C	1241	UD2	C3'-C2'-N2'	2.31	115.04	110.61
2	C	1241	UD2	C1'-O5'-C5'	2.47	118.37	113.72
2	A	1242	UD2	O4B-C1B-N1	2.54	113.17	108.08
2	A	1242	UD2	C3'-C2'-N2'	2.55	115.50	110.61
2	C	1241	UD2	C3'-C4'-C5'	3.18	115.82	110.22
2	C	1241	UD2	O5'-C5'-C4'	3.98	117.00	109.66
3	D	1237	UDP	C4-N3-C2	7.15	120.27	114.13
3	B	1239	UDP	C4-N3-C2	7.89	120.91	114.13
2	C	1241	UD2	C4-N3-C2	8.08	121.07	114.13
2	A	1242	UD2	C4-N3-C2	8.17	121.15	114.13

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1238	A2G	C8-C7-N2-C2
4	D	1238	A2G	O7-C7-N2-C2

There are no ring outliers.

5 monomers are involved in 19 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1242	UD2	9	0
3	B	1239	UDP	2	0
2	C	1241	UD2	5	0
3	D	1237	UDP	2	0
4	D	1238	A2G	1	0

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	241/246 (97%)	-0.12	2 (0%) 86 82	23, 51, 79, 94	2 (0%)
1	B	238/246 (96%)	-0.04	2 (0%) 86 82	33, 64, 84, 95	3 (1%)
1	C	240/246 (97%)	0.25	12 (5%) 30 27	25, 97, 148, 184	3 (1%)
1	D	236/246 (95%)	0.69	32 (13%) 3 5	46, 119, 199, 358	3 (1%)
All	All	955/984 (97%)	0.19	48 (5%) 30 27	23, 74, 160, 358	11 (1%)

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	116	GLY	7.6
1	D	166	TYR	4.9
1	D	108	ILE	4.6
1	D	161	GLY	4.3
1	D	84	LEU	3.9
1	D	3	ILE	3.8
1	D	91	LEU	3.8
1	D	56	ILE	3.7
1	D	63	ASN	3.6
1	C	75	HIS	3.5
1	D	35	ILE	3.5
1	D	117	LEU	3.3
1	D	34	PHE	3.3
1	D	29	MET	3.3
1	C	4	GLY	3.2
1	A	29	MET	3.2
1	C	5	ILE	3.1
1	D	48	TYR	3.1
1	D	4	GLY	3.0
1	D	36	ILE	3.0
1	D	79	ARG	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	56	ILE	2.8
1	D	118	LEU	2.8
1	D	38	TYR	2.7
1	D	39	TYR	2.7
1	D	11	GLY	2.6
1	D	47	LEU	2.6
1	A	5	ILE	2.6
1	D	18	LYS	2.5
1	D	160	GLY	2.5
1	D	57	HIS	2.5
1	D	109	LEU	2.5
1	B	200	LEU	2.4
1	D	28	PHE	2.4
1	C	39	TYR	2.4
1	D	26	ARG	2.4
1	C	159	SER	2.3
1	C	71	LEU	2.3
1	D	163	THR	2.3
1	D	222	PHE	2.2
1	C	140	ALA	2.1
1	C	100	PHE	2.1
1	C	93	PHE	2.1
1	D	114	SER	2.1
1	C	139	ASP	2.1
1	C	35	ILE	2.0
1	D	220	LEU	2.0
1	B	77	PHE	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains.



The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
4	A2G	B	1240	15/15	0.83	0.23	0.50	62,79,86,89	0
3	UDP	B	1239	25/25	0.84	0.24	0.09	65,78,105,116	0
2	UD2	C	1241	39/39	0.84	0.21	-0.46	69,86,97,98	0
3	UDP	D	1237	25/25	0.80	0.20	-0.55	97,127,136,141	0
2	UD2	A	1242	39/39	0.91	0.19	-0.70	33,49,62,65	0
4	A2G	D	1238	15/15	0.88	0.19	-2.82	50,59,71,72	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.