



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 22, 2020 – 03:59 AM BST

PDB ID : 4XP6
Title : X-ray structure of Drosophila dopamine transporter bound to psychostimulant methamphetamine
Authors : Aravind, P.; Wang, K.; Gouaux, E.
Deposited on : 2015-01-16
Resolution : 3.10 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

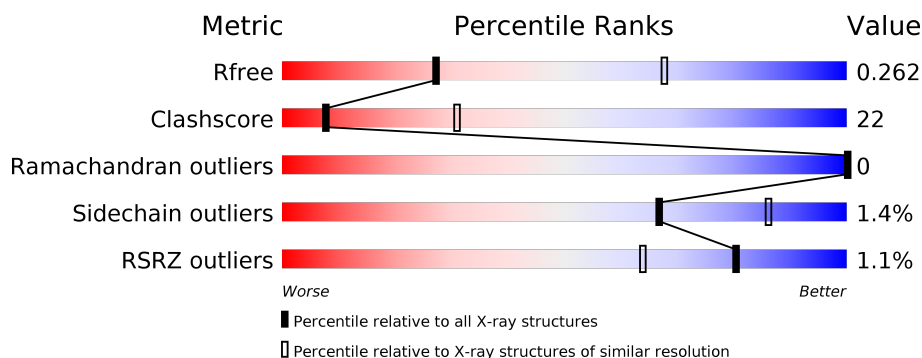
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

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 respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	534	<div> <div>57%</div> <div>42%</div> <div>.</div> </div>
2	L	213	<div> <div>%</div> <div>68%</div> <div>30%</div> <div>.</div> </div>
3	H	219	<div> <div>3%</div> <div>68%</div> <div>32%</div> </div>
4	B	2	<div> <div>100%</div> </div>

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	B40	A	601	-	-	-	X

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 7596 atoms, of which 14 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 Transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	534	Total	C	N	O	S	0	1	0
			4195	2815	646	716	18			

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	74	ALA	VAL	engineered mutation	UNP A0A0B4KEX2
A	?	-	SER	deletion	UNP A0A0B4KEX2
A	?	-	GLN	deletion	UNP A0A0B4KEX2
A	?	-	ASN	deletion	UNP A0A0B4KEX2
A	?	-	ALA	deletion	UNP A0A0B4KEX2
A	?	-	SER	deletion	UNP A0A0B4KEX2
A	?	-	ARG	deletion	UNP A0A0B4KEX2
A	?	-	VAL	deletion	UNP A0A0B4KEX2
A	?	-	PRO	deletion	UNP A0A0B4KEX2
A	?	-	VAL	deletion	UNP A0A0B4KEX2
A	?	-	ILE	deletion	UNP A0A0B4KEX2
A	?	-	GLY	deletion	UNP A0A0B4KEX2
A	?	-	ASN	deletion	UNP A0A0B4KEX2
A	?	-	TYR	deletion	UNP A0A0B4KEX2
A	?	-	SER	deletion	UNP A0A0B4KEX2
A	?	-	ASP	deletion	UNP A0A0B4KEX2
A	?	-	LEU	deletion	UNP A0A0B4KEX2
A	?	-	TYR	deletion	UNP A0A0B4KEX2
A	?	-	ALA	deletion	UNP A0A0B4KEX2
A	?	-	MET	deletion	UNP A0A0B4KEX2
A	?	-	GLY	deletion	UNP A0A0B4KEX2
A	?	-	ASN	deletion	UNP A0A0B4KEX2
A	?	-	GLN	deletion	UNP A0A0B4KEX2
A	?	-	SER	deletion	UNP A0A0B4KEX2
A	?	-	LEU	deletion	UNP A0A0B4KEX2
A	?	-	LEU	deletion	UNP A0A0B4KEX2
A	?	-	TYR	deletion	UNP A0A0B4KEX2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	ASN	deletion	UNP A0A0B4KEX2
A	?	-	GLU	deletion	UNP A0A0B4KEX2
A	?	-	THR	deletion	UNP A0A0B4KEX2
A	?	-	TYR	deletion	UNP A0A0B4KEX2
A	?	-	MET	deletion	UNP A0A0B4KEX2
A	?	-	ASN	deletion	UNP A0A0B4KEX2
A	?	-	GLY	deletion	UNP A0A0B4KEX2
A	?	-	SER	deletion	UNP A0A0B4KEX2
A	?	-	SER	deletion	UNP A0A0B4KEX2
A	?	-	LEU	deletion	UNP A0A0B4KEX2
A	?	-	ASP	deletion	UNP A0A0B4KEX2
A	?	-	THR	deletion	UNP A0A0B4KEX2
A	?	-	SER	deletion	UNP A0A0B4KEX2
A	?	-	ALA	deletion	UNP A0A0B4KEX2
A	?	-	VAL	deletion	UNP A0A0B4KEX2
A	415	ALA	LEU	engineered mutation	UNP A0A0B4KEX2

- Molecule 2 is a protein called Antibody fragment heavy chain-protein, 9D5-heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	L	213	Total	C	N	O	S	0	0	0
			1615	1006	267	334	8			

- Molecule 3 is a protein called Antibody fragment light chain-protein, 9D5-light chain.

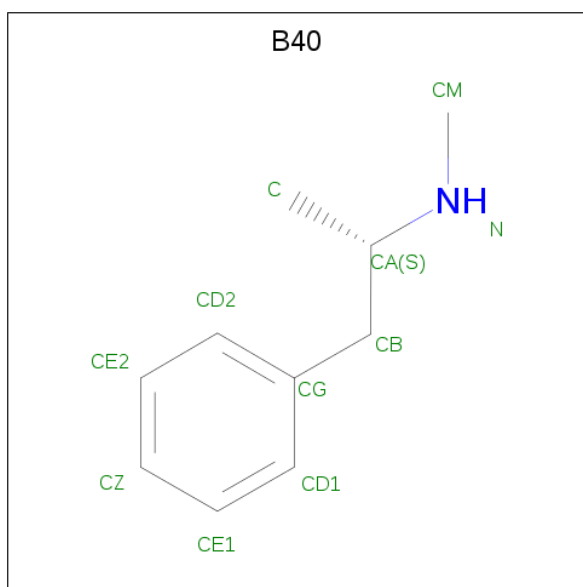
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	219	Total	C	N	O	S	0	0	0
			1636	1028	277	323	8			

- Molecule 4 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
4	B	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 5 is (2S)-N-methyl-1-phenylpropan-2-amine (three-letter code: B40) (formula: C₁₀H₁₅N).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	N	0	0
			11	10	1		

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Na	0	0
			2	2		

- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

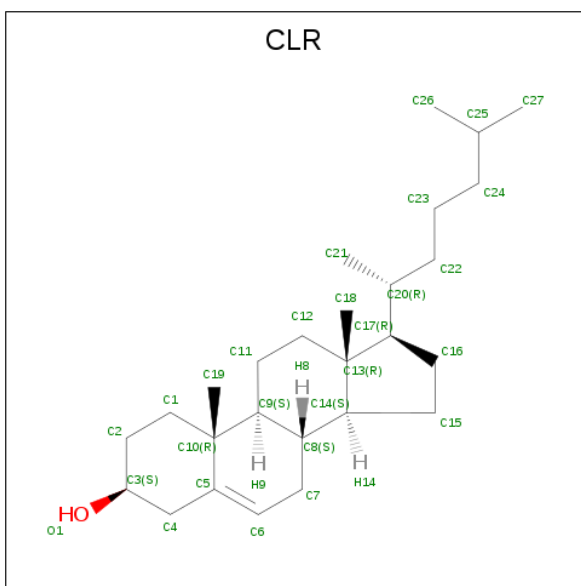
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	Cl	0	0
			1	1		

- Molecule 8 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



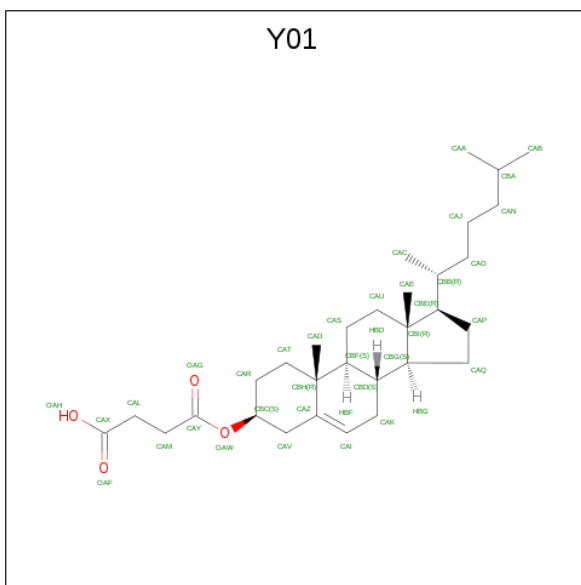
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
8	A	1	Total	C	H	N	O	0	0
			28	8	14	1	5		

- Molecule 9 is CHOLESTEROL (three-letter code: CLR) (formula: $C_{27}H_{46}O$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	1	Total	C O	0	0
			28	27 1		

- Molecule 10 is CHOLESTEROL HEMISUCCINATE (three-letter code: Y01) (formula: $C_{31}H_{50}O_4$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			35	31	4		

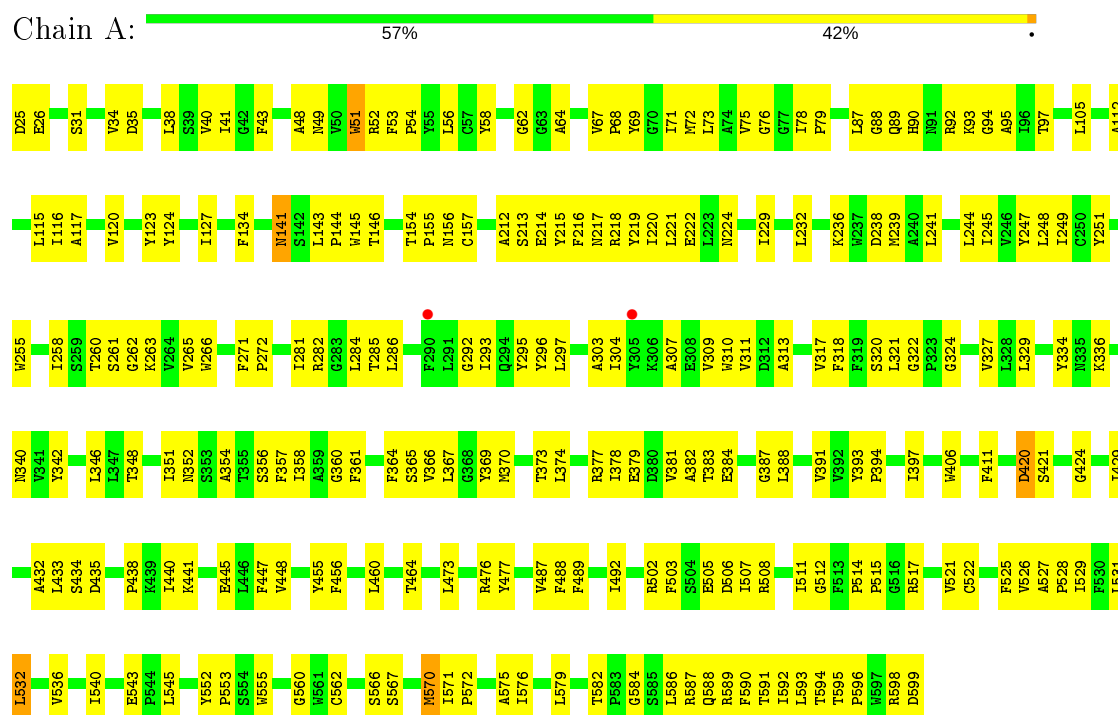
- Molecule 11 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	12	Total O 12 12	0	0
11	L	5	Total O 5 5	0	0
11	H	5	Total O 5 5	0	0

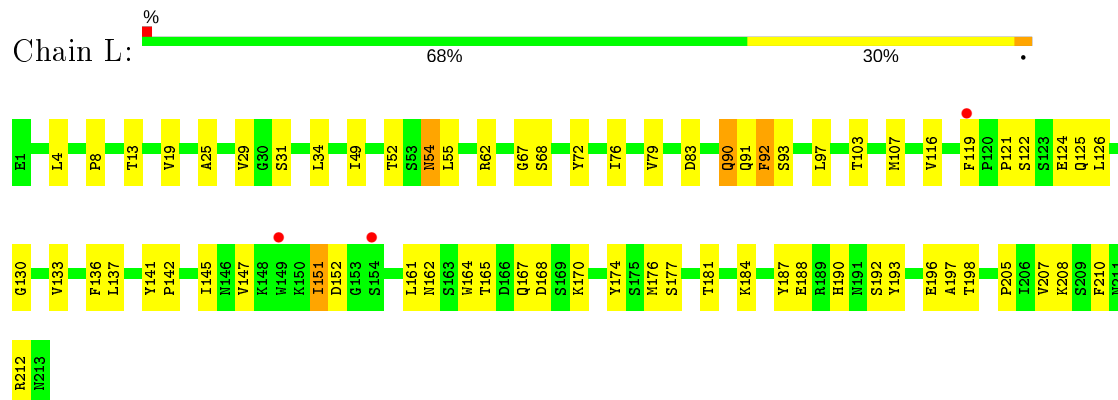
3 Residue-property plots

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

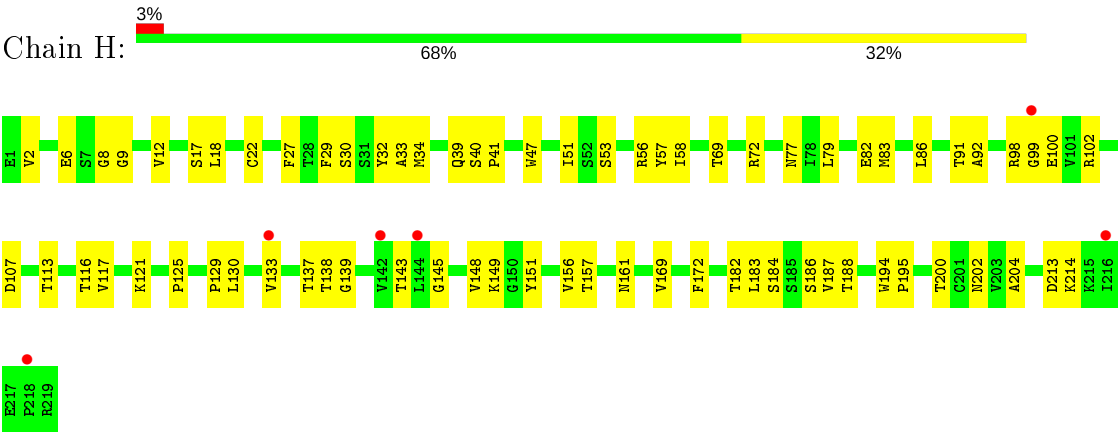
- Molecule 1: Transporter



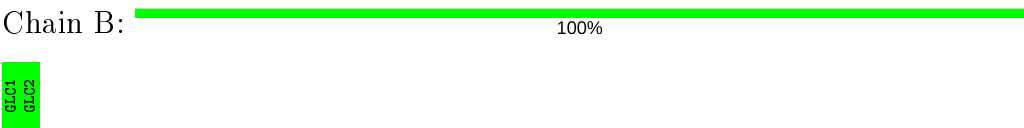
- Molecule 2: Antibody fragment heavy chain-protein, 9D5-heavy chain



- Molecule 3: Antibody fragment light chain-protein, 9D5-light chain



- Molecule 4: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	97.04Å 141.37Å 165.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.45 – 3.10 48.52 – 3.10	Depositor EDS
% Data completeness (in resolution range)	97.7 (45.45-3.10) 97.8 (48.52-3.10)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.24 (at 3.12Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.236 , 0.259 0.239 , 0.262	Depositor DCC
R_{free} test set	2067 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	98.8	Xtriage
Anisotropy	0.007	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 72.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	7596	wwPDB-VP
Average B, all atoms (Å ²)	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.68% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: Y01, NAG, CL, NA, GLC, CLR, B40

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	0.22	0/4340	0.38	0/5938
2	L	0.22	0/1653	0.39	0/2247
3	H	0.21	0/1675	0.38	0/2285
All	All	0.21	0/7668	0.38	0/10470

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	4195	0	4082	198	0
2	L	1615	0	1528	65	0
3	H	1636	0	1576	75	0
4	B	23	0	21	0	0
5	A	11	0	15	2	0
6	A	2	0	0	0	0
7	A	1	0	0	0	0
8	A	14	14	13	0	0
9	A	28	0	46	3	0
10	A	35	0	49	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
11	A	12	0	0	1	0
11	H	5	0	0	1	0
11	L	5	0	0	0	0
All	All	7582	14	7330	325	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 22.

All (325) 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)
2:L:151:ILE:O	2:L:151:ILE:HG12	1.70	0.90
3:H:51:ILE:HD13	3:H:72:ARG:HB2	1.55	0.88
1:A:258:ILE:HA	1:A:261:SER:HB3	1.53	0.87
3:H:83:MET:HB3	3:H:86:LEU:HD21	1.57	0.84
3:H:157:THR:HB	3:H:204:ALA:HB3	1.59	0.83
2:L:92:PHE:HD2	3:H:102:ARG:HA	1.43	0.82
1:A:141:ASN:ND2	1:A:141:ASN:H	1.76	0.80
2:L:137:LEU:HD23	2:L:145:ILE:HD13	1.62	0.79
2:L:198:THR:HG22	2:L:205:PRO:HB3	1.65	0.79
1:A:40:VAL:HG12	1:A:348:THR:HG21	1.63	0.78
1:A:75:VAL:HB	1:A:526:VAL:HG11	1.66	0.78
3:H:130:LEU:HD12	3:H:145:GLY:HA3	1.66	0.77
10:A:608:Y01:OAG	10:A:608:Y01:CAX	2.30	0.77
9:A:607:CLR:H212	9:A:607:CLR:H183	1.67	0.77
1:A:336:LYS:H	1:A:336:LYS:HD2	1.48	0.76
1:A:489:PHE:HD2	1:A:571:ILE:HD13	1.50	0.76
1:A:527:ALA:HB3	1:A:528:PRO:HD3	1.68	0.75
1:A:53:PHE:HB3	1:A:54:PRO:HD3	1.69	0.75
2:L:34:LEU:HD22	2:L:72:TYR:CG	2.23	0.74
2:L:92:PHE:CE1	2:L:97:LEU:HD13	2.23	0.74
1:A:73:LEU:HA	1:A:317:VAL:HG11	1.69	0.74
3:H:125:PRO:HB3	3:H:151:TYR:HB3	1.70	0.73
2:L:151:ILE:O	2:L:151:ILE:CG1	2.36	0.73
2:L:92:PHE:CD2	3:H:102:ARG:HA	2.24	0.72
1:A:143:LEU:HD12	1:A:143:LEU:H	1.54	0.72
1:A:220:ILE:O	1:A:236:LYS:NZ	2.20	0.71
1:A:502:ARG:HD2	1:A:598:ARG:NH2	2.05	0.71
1:A:95:ALA:HA	1:A:329:LEU:HD23	1.73	0.71
1:A:43:PHE:HE2	1:A:322:GLY:HA3	1.55	0.69
2:L:145:ILE:HG22	2:L:164:TRP:CH2	2.28	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:TYR:CE2	1:A:448:VAL:HG23	2.28	0.69
3:H:51:ILE:HG13	3:H:58:ILE:CD1	2.23	0.69
1:A:236:LYS:HG2	1:A:238:ASP:OD1	1.94	0.68
1:A:512:GLY:HA2	3:H:102:ARG:HH21	1.59	0.67
1:A:222:GLU:HG3	1:A:236:LYS:HZ3	1.59	0.67
3:H:91:THR:HG23	3:H:116:THR:HA	1.77	0.66
1:A:364:PHE:HA	1:A:367:LEU:HB2	1.77	0.66
1:A:370:MET:HG2	1:A:374:LEU:HD12	1.77	0.65
1:A:87:LEU:HB3	1:A:503:PHE:HE1	1.61	0.65
3:H:77:ASN:ND2	11:H:301:HOH:O	2.29	0.65
3:H:22:CYS:HB3	3:H:79:LEU:HB3	1.79	0.65
3:H:40:SER:HB2	3:H:41:PRO:HD2	1.77	0.65
1:A:303:ALA:HB1	1:A:309:VAL:HG21	1.79	0.65
1:A:40:VAL:CG1	1:A:348:THR:HG21	2.28	0.64
1:A:397:ILE:HG23	1:A:406:TRP:HB2	1.80	0.64
2:L:34:LEU:HD22	2:L:72:TYR:CD2	2.33	0.64
1:A:324:GLY:HA3	1:A:487:VAL:HG22	1.78	0.64
2:L:116:VAL:C	2:L:208:LYS:HE3	2.19	0.63
3:H:98:ARG:O	3:H:107:ASP:N	2.31	0.63
1:A:94:GLY:HA3	1:A:432:ALA:HA	1.80	0.63
1:A:43:PHE:CE2	1:A:322:GLY:HA3	2.34	0.63
1:A:115:LEU:HD11	1:A:567:SER:HA	1.81	0.63
2:L:190:HIS:O	2:L:212:ARG:NH1	2.32	0.63
2:L:137:LEU:HD21	2:L:197:ALA:HB2	1.80	0.63
1:A:369:TYR:O	1:A:373:THR:HG22	1.99	0.62
2:L:193:TYR:HB2	2:L:210:PHE:CE1	2.34	0.62
1:A:41:ILE:HD11	1:A:348:THR:HA	1.80	0.62
2:L:145:ILE:HG22	2:L:164:TRP:CZ3	2.34	0.62
1:A:587:ARG:O	1:A:591:THR:HG22	2.00	0.62
2:L:152:ASP:OD1	2:L:192:SER:HB3	2.00	0.62
1:A:239:MET:CE	1:A:239:MET:HA	2.30	0.61
3:H:29:PHE:O	3:H:72:ARG:NH2	2.34	0.61
1:A:370:MET:HE1	1:A:381:VAL:HB	1.83	0.61
1:A:154:THR:OG1	1:A:218:ARG:NH1	2.34	0.60
1:A:477:TYR:CD2	1:A:560:GLY:HA3	2.36	0.60
1:A:71:ILE:O	1:A:75:VAL:HG22	2.02	0.60
1:A:43:PHE:HA	1:A:421:SER:HA	1.84	0.60
1:A:38:LEU:HD13	1:A:266:TRP:HA	1.82	0.59
1:A:282:ARG:CZ	1:A:286:LEU:HD11	2.33	0.59
2:L:121:PRO:HG2	2:L:187:TYR:CE1	2.38	0.59
1:A:75:VAL:O	1:A:79:PRO:HG2	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:LEU:HB2	1:A:593:LEU:HB3	1.85	0.59
1:A:115:LEU:HD11	1:A:567:SER:CA	2.33	0.59
1:A:78:ILE:HB	1:A:79:PRO:HD3	1.85	0.59
1:A:545:LEU:HG	1:A:552:TYR:CD1	2.38	0.59
1:A:134:PHE:HB3	1:A:411:PHE:CE2	2.38	0.58
1:A:282:ARG:O	1:A:286:LEU:HD13	2.03	0.58
1:A:271:PHE:HB3	1:A:272:PRO:HD3	1.86	0.58
1:A:590:PHE:CZ	1:A:594:THR:HG21	2.38	0.58
1:A:71:ILE:HD12	1:A:310:TRP:HH2	1.68	0.58
1:A:393:TYR:HB3	1:A:394:PRO:HD3	1.85	0.58
1:A:218:ARG:HH21	1:A:224:ASN:HD22	1.50	0.58
1:A:369:TYR:CE1	1:A:373:THR:HG21	2.39	0.57
3:H:9:GLY:HA2	3:H:18:LEU:HD21	1.85	0.57
2:L:167:GLN:HB2	2:L:174:TYR:CE2	2.40	0.57
1:A:393:TYR:CE2	1:A:397:ILE:HD11	2.40	0.57
1:A:476:ARG:HD2	1:A:545:LEU:HD13	1.87	0.57
3:H:51:ILE:CD1	3:H:72:ARG:HB2	2.31	0.57
1:A:154:THR:CG2	1:A:155:PRO:HD2	2.35	0.56
3:H:30:SER:O	3:H:53:SER:HB2	2.06	0.56
1:A:62:GLY:HA2	1:A:296:TYR:O	2.06	0.56
1:A:586:LEU:HA	1:A:587:ARG:C	2.26	0.56
1:A:420:ASP:OD1	1:A:420:ASP:N	2.37	0.56
1:A:89:GLN:O	1:A:92:ARG:HG2	2.06	0.56
1:A:143:LEU:O	1:A:146:THR:HG22	2.06	0.56
1:A:553:PRO:HB2	1:A:555:TRP:CD1	2.41	0.56
3:H:32:TYR:O	3:H:72:ARG:NH2	2.39	0.56
2:L:19:VAL:HG13	2:L:79:VAL:HG21	1.88	0.56
1:A:154:THR:HG23	1:A:155:PRO:HD2	1.88	0.55
1:A:141:ASN:ND2	1:A:141:ASN:N	2.50	0.55
2:L:161:LEU:CD1	3:H:182:THR:HB	2.37	0.55
1:A:51:TRP:HH2	1:A:127:ILE:HD13	1.72	0.55
2:L:161:LEU:HD13	3:H:182:THR:HB	1.89	0.55
1:A:570:MET:CE	1:A:570:MET:HA	2.37	0.55
2:L:187:TYR:O	2:L:193:TYR:OH	2.25	0.55
1:A:575:ALA:O	1:A:579:LEU:HB2	2.06	0.55
1:A:433:LEU:C	1:A:440:ILE:HD11	2.27	0.55
2:L:141:TYR:CG	2:L:142:PRO:HA	2.42	0.55
3:H:161:ASN:HA	3:H:200:THR:CG2	2.36	0.54
1:A:48:ALA:O	1:A:52:ARG:HB3	2.08	0.54
1:A:75:VAL:HG23	1:A:76:GLY:N	2.22	0.54
1:A:51:TRP:HA	1:A:388:LEU:HD23	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:505:GLU:HB3	3:H:56:ARG:HH21	1.73	0.54
3:H:129:PRO:HB3	3:H:214:LYS:HE3	1.90	0.54
3:H:51:ILE:HG13	3:H:58:ILE:HD11	1.89	0.54
1:A:438:PRO:HA	1:A:441:LYS:HB3	1.90	0.54
1:A:588:GLN:O	1:A:592:ILE:HG13	2.08	0.54
2:L:92:PHE:HD2	3:H:102:ARG:CA	2.17	0.54
3:H:33:ALA:N	3:H:100:GLU:OE1	2.41	0.54
3:H:202:ASN:HA	3:H:213:ASP:HA	1.88	0.54
2:L:29:VAL:HG13	2:L:93:SER:HB3	1.89	0.54
1:A:340:ASN:HA	1:A:511:ILE:HG22	1.90	0.53
1:A:584:GLY:O	1:A:589:ARG:NH1	2.41	0.53
2:L:90:GLN:HG2	2:L:91:GLN:N	2.23	0.53
2:L:137:LEU:HD21	2:L:197:ALA:CB	2.39	0.53
2:L:13:THR:HG21	2:L:19:VAL:CG1	2.38	0.53
1:A:572:PRO:O	1:A:576:ILE:HG12	2.09	0.52
1:A:590:PHE:CE1	1:A:594:THR:HG21	2.43	0.52
1:A:41:ILE:HD13	1:A:348:THR:HG23	1.91	0.52
1:A:522:CYS:HA	1:A:526:VAL:HB	1.90	0.52
1:A:58:TYR:HB2	1:A:364:PHE:CZ	2.45	0.52
1:A:72:MET:CE	1:A:72:MET:HA	2.40	0.52
1:A:52:ARG:CZ	1:A:56:LEU:HD21	2.40	0.52
1:A:354:ALA:O	1:A:358:ILE:HG12	2.10	0.52
1:A:488:PHE:HA	1:A:531:LEU:HD12	1.91	0.52
3:H:129:PRO:HD3	3:H:214:LYS:HE2	1.91	0.52
1:A:292:GLY:HA3	1:A:364:PHE:O	2.10	0.52
1:A:94:GLY:N	1:A:435:ASP:OD2	2.40	0.52
3:H:129:PRO:HD3	3:H:214:LYS:CE	2.39	0.52
2:L:62:ARG:NH1	2:L:83:ASP:OD1	2.43	0.52
1:A:112:ALA:O	1:A:116:ILE:HG13	2.10	0.52
1:A:239:MET:HA	1:A:239:MET:HE3	1.92	0.52
2:L:168:ASP:OD2	2:L:170:LYS:NZ	2.42	0.51
1:A:154:THR:HG22	1:A:156:ASN:H	1.75	0.51
3:H:143:THR:HG22	3:H:188:THR:OG1	2.11	0.51
3:H:83:MET:CB	3:H:86:LEU:HD21	2.33	0.51
3:H:2:VAL:HG13	3:H:27:PHE:CD1	2.46	0.51
3:H:125:PRO:HB3	3:H:151:TYR:CB	2.41	0.50
3:H:137:THR:HG22	3:H:138:THR:H	1.75	0.50
1:A:336:LYS:N	1:A:336:LYS:HD2	2.22	0.50
3:H:34:MET:HG2	3:H:72:ARG:HH12	1.76	0.50
2:L:121:PRO:HB2	2:L:126:LEU:HD11	1.93	0.50
2:L:19:VAL:HG22	2:L:76:ILE:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:571:ILE:HB	1:A:572:PRO:HD3	1.93	0.50
3:H:69:THR:HB	3:H:82:GLU:HB2	1.93	0.50
1:A:75:VAL:HG23	1:A:76:GLY:H	1.76	0.50
3:H:98:ARG:O	3:H:98:ARG:HG3	2.12	0.50
2:L:210:PHE:HB2	3:H:133:VAL:HG21	1.94	0.50
1:A:241:LEU:O	1:A:245:ILE:HG13	2.11	0.50
1:A:247:TYR:CZ	1:A:455:TYR:HB3	2.47	0.50
1:A:387:GLY:O	1:A:391:VAL:HB	2.12	0.50
1:A:488:PHE:O	1:A:492:ILE:HG12	2.12	0.50
3:H:183:LEU:HD23	3:H:184:SER:N	2.26	0.50
2:L:196:GLU:HB2	2:L:207:VAL:HG22	1.93	0.50
1:A:213:SER:O	1:A:217:ASN:ND2	2.37	0.50
1:A:215:TYR:O	1:A:219:TYR:HB3	2.11	0.49
1:A:52:ARG:NH1	1:A:384:GLU:OE2	2.46	0.49
1:A:598:ARG:HH12	3:H:56:ARG:HH11	1.60	0.49
2:L:116:VAL:HB	2:L:208:LYS:HZ2	1.77	0.49
3:H:6:GLU:HB3	3:H:113:THR:HG22	1.95	0.49
1:A:222:GLU:CG	1:A:236:LYS:HZ3	2.23	0.49
2:L:151:ILE:O	2:L:152:ASP:HB2	2.12	0.49
10:A:608:Y01:OAG	10:A:608:Y01:OAH	2.30	0.49
1:A:115:LEU:HD11	1:A:567:SER:HB3	1.94	0.49
1:A:377:ARG:HB3	1:A:379:GLU:OE1	2.13	0.49
1:A:434:SER:HA	1:A:440:ILE:CD1	2.42	0.48
1:A:88:GLY:CA	1:A:329:LEU:HD12	2.44	0.48
3:H:125:PRO:CB	3:H:151:TYR:HB3	2.41	0.48
1:A:434:SER:HA	1:A:440:ILE:HD12	1.96	0.48
1:A:145:TRP:HB2	1:A:212:ALA:HA	1.95	0.48
1:A:297:LEU:HD11	1:A:361:PHE:CZ	2.49	0.48
1:A:512:GLY:HA2	3:H:102:ARG:NH2	2.27	0.48
9:A:607:CLR:C21	9:A:607:CLR:H121	2.43	0.48
3:H:130:LEU:HB2	3:H:145:GLY:CA	2.43	0.48
3:H:17:SER:HB2	3:H:83:MET:O	2.14	0.48
2:L:107:MET:HA	2:L:107:MET:CE	2.44	0.48
2:L:67:GLY:HA3	2:L:72:TYR:HA	1.96	0.48
1:A:488:PHE:CE1	1:A:532[B]:LEU:HG	2.49	0.48
1:A:582:THR:O	1:A:589:ARG:HD2	2.13	0.48
1:A:281:ILE:O	1:A:285:THR:HG23	2.13	0.47
1:A:318:PHE:HZ	1:A:487:VAL:HG21	1.78	0.47
1:A:502:ARG:O	3:H:56:ARG:NH2	2.46	0.47
1:A:383:THR:OG1	1:A:384:GLU:N	2.46	0.47
2:L:31:SER:O	2:L:52:THR:OG1	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:147:VAL:HG11	2:L:176:MET:HE1	1.96	0.47
1:A:324:GLY:HA3	1:A:487:VAL:CG2	2.43	0.47
1:A:502:ARG:HD2	1:A:598:ARG:HH21	1.75	0.47
2:L:19:VAL:CG1	2:L:79:VAL:HG21	2.45	0.47
1:A:67:VAL:HB	1:A:68:PRO:HD3	1.96	0.47
1:A:95:ALA:HA	1:A:329:LEU:CD2	2.42	0.47
3:H:8:GLY:O	3:H:113:THR:OG1	2.32	0.47
2:L:126:LEU:O	2:L:184:LYS:HD3	2.15	0.47
1:A:508:ARG:HD3	1:A:508:ARG:C	2.34	0.47
1:A:54:PRO:HG3	1:A:360:GLY:HA2	1.96	0.47
1:A:245:ILE:O	1:A:249:ILE:HG13	2.14	0.47
1:A:67:VAL:HB	1:A:68:PRO:CD	2.45	0.47
1:A:43:PHE:CD1	1:A:327:VAL:HG11	2.50	0.47
1:A:571:ILE:HB	1:A:572:PRO:CD	2.45	0.47
1:A:258:ILE:HD13	1:A:334:TYR:CG	2.50	0.46
1:A:570:MET:HE2	1:A:570:MET:HA	1.96	0.46
2:L:116:VAL:HB	2:L:208:LYS:NZ	2.30	0.46
1:A:117:ALA:HB3	1:A:429:ILE:HD11	1.97	0.46
2:L:196:GLU:CB	2:L:207:VAL:HG22	2.45	0.46
1:A:373:THR:HG23	1:A:374:LEU:HG	1.96	0.46
1:A:87:LEU:HD12	1:A:329:LEU:HD11	1.98	0.46
1:A:525:PHE:O	1:A:529:ILE:HD13	2.16	0.46
1:A:293:ILE:HD12	1:A:361:PHE:HD1	1.80	0.46
1:A:598:ARG:NH1	3:H:56:ARG:HD2	2.30	0.46
3:H:169:VAL:HG22	3:H:187:VAL:HG23	1.97	0.46
3:H:194:TRP:CG	3:H:195:PRO:HA	2.51	0.46
1:A:321:LEU:HD23	1:A:352:ASN:HD22	1.81	0.46
1:A:456:PHE:O	1:A:460:LEU:HG	2.16	0.46
10:A:608:Y01:HAJ1	10:A:608:Y01:HAC3	1.61	0.46
1:A:25:ASP:HA	1:A:26:GLU:HA	1.55	0.46
1:A:393:TYR:HE2	1:A:397:ILE:HD11	1.80	0.45
1:A:72:MET:HE2	1:A:72:MET:HA	1.98	0.45
1:A:244:LEU:O	1:A:248:LEU:HG	2.15	0.45
1:A:506:ASP:OD1	3:H:57:TYR:OH	2.26	0.45
3:H:12:VAL:HG11	3:H:86:LEU:HD12	1.96	0.45
1:A:49:ASN:ND2	1:A:356:SER:OG	2.50	0.45
1:A:295:TYR:CE1	1:A:378:ILE:HG21	2.52	0.45
2:L:116:VAL:O	2:L:208:LYS:HE3	2.16	0.45
1:A:120:VAL:HA	1:A:123:TYR:CE2	2.51	0.45
1:A:487:VAL:HG12	1:A:531:LEU:HD11	1.98	0.45
1:A:351:ILE:HD11	9:A:607:CLR:H72	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:122:SER:HB2	2:L:124:GLU:OE1	2.17	0.45
1:A:251:TYR:O	1:A:255:TRP:HB2	2.16	0.45
1:A:342:TYR:CZ	1:A:346:LEU:HD11	2.52	0.45
2:L:181:THR:HG21	3:H:149:LYS:NZ	2.31	0.45
1:A:263:LYS:O	1:A:266:TRP:HB2	2.17	0.45
1:A:71:ILE:HD12	1:A:310:TRP:CH2	2.49	0.45
1:A:397:ILE:CG2	1:A:406:TRP:HB2	2.46	0.45
2:L:136:PHE:CD2	3:H:186:SER:HB3	2.51	0.45
1:A:255:TRP:CD1	1:A:445:GLU:HG3	2.52	0.45
3:H:161:ASN:OD1	3:H:200:THR:HG22	2.16	0.45
1:A:591:THR:HA	1:A:594:THR:OG1	2.17	0.45
3:H:98:ARG:HA	3:H:99:GLY:HA3	1.55	0.44
2:L:121:PRO:HG2	2:L:187:TYR:CZ	2.52	0.44
1:A:244:LEU:HB2	1:A:456:PHE:CE1	2.53	0.44
1:A:232:LEU:O	1:A:464:THR:HB	2.16	0.44
1:A:229:ILE:CD1	1:A:473:LEU:HD22	2.47	0.44
5:A:601:B40:HBA	5:A:601:B40:HMA	1.75	0.44
1:A:517:ARG:O	1:A:521:VAL:HG23	2.17	0.44
1:A:598:ARG:O	1:A:599:ASP:HB2	2.17	0.44
2:L:54:ASN:OD1	2:L:54:ASN:N	2.51	0.44
1:A:115:LEU:HD21	1:A:570:MET:HG3	2.00	0.44
1:A:598:ARG:HH22	3:H:56:ARG:HH11	1.66	0.44
1:A:505:GLU:CG	3:H:56:ARG:HH21	2.31	0.43
1:A:115:LEU:HD11	1:A:567:SER:CB	2.48	0.43
1:A:433:LEU:HD12	1:A:447:PHE:HZ	1.83	0.43
1:A:87:LEU:HA	1:A:90:HIS:HB3	2.00	0.43
2:L:68:SER:HA	2:L:72:TYR:CZ	2.54	0.43
1:A:579:LEU:HD13	1:A:593:LEU:HD12	2.00	0.43
3:H:6:GLU:HB3	3:H:113:THR:CG2	2.49	0.43
2:L:107:MET:HA	2:L:107:MET:HE2	2.01	0.43
1:A:361:PHE:O	1:A:365:SER:HB2	2.19	0.43
1:A:525:PHE:O	1:A:528:PRO:HD2	2.18	0.43
2:L:97:LEU:HD12	3:H:47:TRP:CD1	2.54	0.43
1:A:64:ALA:O	1:A:304:ILE:HD11	2.18	0.43
1:A:514:PRO:HA	1:A:515:PRO:HD3	1.95	0.43
1:A:93:LYS:HB3	1:A:97:THR:OG1	2.19	0.43
2:L:119:PHE:O	2:L:133:VAL:HG13	2.19	0.43
1:A:307:ALA:O	1:A:311:VAL:HG23	2.18	0.42
1:A:357:PHE:CE2	1:A:361:PHE:HE2	2.37	0.42
3:H:156:VAL:CG2	3:H:183:LEU:HD13	2.49	0.42
1:A:293:ILE:HD12	1:A:361:PHE:CD1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:123:TYR:CG	1:A:124:TYR:N	2.87	0.42
1:A:262:GLY:O	1:A:265:VAL:HG22	2.19	0.42
1:A:69:TYR:HA	1:A:313:ALA:HB1	2.01	0.42
1:A:95:ALA:CA	1:A:329:LEU:HD23	2.47	0.42
1:A:236:LYS:HB2	1:A:236:LYS:HE3	1.82	0.42
1:A:536:VAL:O	1:A:540:ILE:HG12	2.19	0.42
1:A:595:THR:HA	1:A:596:PRO:HD3	1.82	0.42
1:A:73:LEU:CD1	1:A:317:VAL:HG13	2.49	0.42
3:H:12:VAL:O	3:H:117:VAL:HA	2.20	0.42
2:L:8:PRO:O	2:L:103:THR:HG23	2.19	0.42
2:L:125:GLN:HG2	2:L:130:GLY:O	2.18	0.42
2:L:165:THR:HG23	3:H:172:PHE:CD2	2.54	0.42
3:H:83:MET:HB3	3:H:86:LEU:CD2	2.39	0.42
1:A:284:LEU:HD23	1:A:365:SER:OG	2.20	0.42
1:A:216:PHE:CE1	1:A:221:LEU:HD13	2.55	0.42
1:A:562:CYS:O	1:A:566:SER:N	2.47	0.42
1:A:320:SER:HA	11:A:703:HOH:O	2.18	0.41
5:A:601:B40:HD2	5:A:601:B40:HA	1.71	0.41
3:H:137:THR:HG22	3:H:138:THR:N	2.35	0.41
2:L:4:LEU:CD2	2:L:25:ALA:HB2	2.50	0.41
3:H:34:MET:HB3	3:H:79:LEU:HD22	2.02	0.41
2:L:162:ASN:HB3	2:L:176:MET:HE2	2.00	0.41
1:A:476:ARG:NH2	1:A:543:GLU:O	2.54	0.41
2:L:68:SER:HA	2:L:72:TYR:CE2	2.54	0.41
10:A:608:Y01:HBB	10:A:608:Y01:HAE2	1.49	0.41
3:H:143:THR:HG22	3:H:188:THR:HG23	2.02	0.41
3:H:138:THR:HA	3:H:139:GLY:HA3	1.83	0.41
3:H:148:VAL:N	3:H:183:LEU:O	2.47	0.41
1:A:327:VAL:HG22	1:A:424:GLY:O	2.21	0.41
3:H:129:PRO:CB	3:H:214:LYS:HE3	2.49	0.41
3:H:39:GLN:O	3:H:92:ALA:HB1	2.21	0.41
2:L:147:VAL:CG1	2:L:176:MET:HE1	2.50	0.41
1:A:31:SER:HB3	1:A:35:ASP:OD2	2.21	0.40
3:H:183:LEU:HD23	3:H:183:LEU:C	2.41	0.40
1:A:366:VAL:HG21	1:A:393:TYR:CE1	2.56	0.40
1:A:144:PRO:HB2	1:A:215:TYR:CE1	2.56	0.40
1:A:366:VAL:HG21	1:A:393:TYR:CZ	2.57	0.40
1:A:34:VAL:O	1:A:38:LEU:HG	2.21	0.40
1:A:508:ARG:HD3	1:A:508:ARG:O	2.21	0.40
2:L:188:GLU:HA	2:L:212:ARG:NH1	2.36	0.40
1:A:157:CYS:HB2	1:A:214:GLU:OE1	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:367:LEU:HD21	1:A:382:ALA:HA	2.03	0.40
2:L:49:ILE:HG12	2:L:55:LEU:HD23	2.03	0.40
1:A:134:PHE:HB3	1:A:411:PHE:CD2	2.56	0.40
1:A:34:VAL:HG11	1:A:266:TRP:CH2	2.57	0.40
1:A:507:ILE:HD12	1:A:515:PRO:CG	2.52	0.40
2:L:177:SER:HB2	3:H:172:PHE:CE1	2.56	0.40
1:A:598:ARG:HH22	3:H:56:ARG:NH1	2.19	0.40
2:L:188:GLU:HA	2:L:212:ARG:CZ	2.51	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	533/534 (100%)	510 (96%)	23 (4%)	0	100	100
2	L	211/213 (99%)	204 (97%)	7 (3%)	0	100	100
3	H	217/219 (99%)	210 (97%)	7 (3%)	0	100	100
All	All	961/966 (100%)	924 (96%)	37 (4%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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	427/439 (97%)	420 (98%)	7 (2%)	62	84
2	L	182/186 (98%)	178 (98%)	4 (2%)	52	78
3	H	180/187 (96%)	179 (99%)	1 (1%)	86	94
All	All	789/812 (97%)	777 (98%)	12 (2%)	67	85

All (12) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	TRP
1	A	141	ASN
1	A	260	THR
1	A	420	ASP
1	A	532[A]	LEU
1	A	532[B]	LEU
1	A	570	MET
2	L	54	ASN
2	L	90	GLN
2	L	92	PHE
2	L	151	ILE
3	H	121	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

2 monosaccharides 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	$\# Z > 2$
4	GLC	B	1	4	12,12,12	0.54	0	17,17,17	0.41	0
4	GLC	B	2	4	11,11,12	0.62	0	15,15,17	0.68	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
4	GLC	B	1	4	-	1/2/22/22	0/1/1/1
4	GLC	B	2	4	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1	GLC	O5-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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
5	B40	A	601	-	11,11,11	0.34	0	12,13,13	0.79	0
9	CLR	A	607	-	31,31,31	0.71	0	48,48,48	1.16	5 (10%)
8	NAG	A	606	1	14,14,15	0.73	1 (7%)	17,19,21	0.65	0
10	Y01	A	608	-	35,38,38	4.41	17 (48%)	54,57,57	2.19	17 (31%)

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
5	B40	A	601	-	-	4/6/6/6	0/1/1/1
9	CLR	A	607	-	-	5/10/68/68	0/4/4/4
8	NAG	A	606	1	-	3/6/23/26	0/1/1/1
10	Y01	A	608	-	-	10/17/77/77	0/4/4/4

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
10	A	608	Y01	CAI-CAZ	16.46	1.69	1.33
10	A	608	Y01	CBB-CBE	-11.31	1.34	1.54
10	A	608	Y01	CAU-CBI	-7.74	1.40	1.54
10	A	608	Y01	CBH-CBF	6.82	1.67	1.56
10	A	608	Y01	CBH-CAZ	-5.32	1.42	1.52
10	A	608	Y01	CAP-CBE	5.10	1.65	1.54
10	A	608	Y01	CAU-CAS	4.81	1.63	1.53
10	A	608	Y01	CAK-CBD	4.70	1.61	1.53
10	A	608	Y01	CBI-CBE	3.80	1.62	1.55
10	A	608	Y01	CBD-CBF	-3.10	1.47	1.53
10	A	608	Y01	CAE-CBI	-3.01	1.49	1.54
10	A	608	Y01	OAW-CAY	2.75	1.42	1.34
8	A	606	NAG	O5-C1	-2.63	1.39	1.43
10	A	608	Y01	OAW-CBC	-2.27	1.40	1.46
10	A	608	Y01	CAO-CBB	2.25	1.60	1.54
10	A	608	Y01	CAS-CBF	-2.21	1.50	1.53
10	A	608	Y01	CAQ-CBG	2.10	1.58	1.54
10	A	608	Y01	CBI-CBG	-2.01	1.51	1.55

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
10	A	608	Y01	CBI-CBE-CBB	-5.91	110.23	119.49
10	A	608	Y01	CAU-CBI-CBG	4.90	114.87	107.27
10	A	608	Y01	CBH-CAZ-CAI	-4.54	115.96	122.90
10	A	608	Y01	CAK-CAI-CAZ	-4.32	117.10	125.06
10	A	608	Y01	CAE-CBI-CBG	-4.01	104.24	111.71
10	A	608	Y01	CAU-CBI-CBE	3.96	122.50	116.57
10	A	608	Y01	OAW-CAY-CAM	3.89	119.89	111.50
10	A	608	Y01	CAE-CBI-CBE	-3.82	104.59	111.71
9	A	607	CLR	C4-C5-C10	3.29	120.79	116.42
10	A	608	Y01	CAD-CBH-CBF	-3.24	107.82	111.68
10	A	608	Y01	CAV-CAZ-CAI	-2.77	116.61	120.61
10	A	608	Y01	CAK-CBD-CBG	-2.72	106.96	110.91
9	A	607	CLR	C11-C12-C13	-2.63	108.27	112.78
10	A	608	Y01	CAC-CBB-CBE	-2.54	109.03	112.92
10	A	608	Y01	CAU-CAS-CBF	-2.53	108.73	113.11
10	A	608	Y01	CAE-CBI-CAU	-2.52	106.61	110.59
9	A	607	CLR	C13-C17-C20	-2.50	115.57	119.49
9	A	607	CLR	C8-C7-C6	-2.44	109.23	112.73
10	A	608	Y01	CAP-CBE-CBB	-2.38	108.47	112.15
10	A	608	Y01	CAK-CBD-CBF	2.32	112.52	109.71
10	A	608	Y01	CAS-CBF-CBH	-2.31	110.04	113.08
9	A	607	CLR	C13-C14-C8	-2.04	111.35	114.38

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
10	A	608	Y01	CAC-CBB-CBE-CBI
8	A	606	NAG	C8-C7-N2-C2
8	A	606	NAG	O7-C7-N2-C2
10	A	608	Y01	CAN-CAJ-CAO-CBB
10	A	608	Y01	CAX-CAL-CAM-CAY
10	A	608	Y01	CAJ-CAO-CBB-CAC
9	A	607	CLR	C17-C20-C22-C23
9	A	607	CLR	C21-C20-C22-C23
10	A	608	Y01	CAO-CBB-CBE-CBI
9	A	607	CLR	C16-C17-C20-C22
10	A	608	Y01	CAM-CAY-OAW-CBC
10	A	608	Y01	OAG-CAY-OAW-CBC
8	A	606	NAG	O5-C5-C6-O6
5	A	601	B40	CA-CB-CG-CD2
5	A	601	B40	CA-CB-CG-CD1
10	A	608	Y01	CAC-CBB-CBE-CAP

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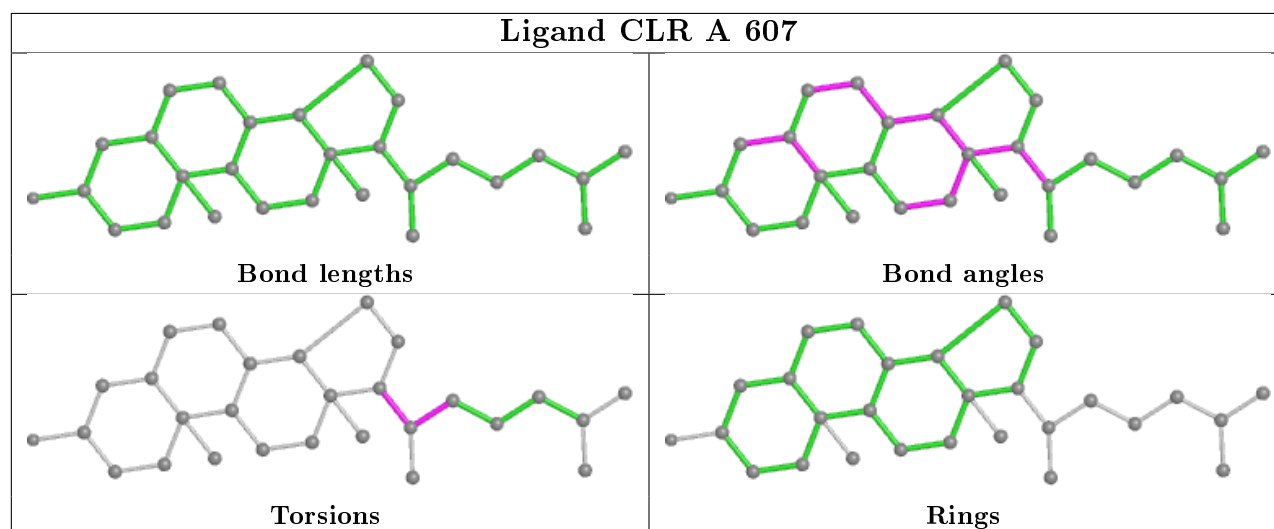
Mol	Chain	Res	Type	Atoms
9	A	607	CLR	C13-C17-C20-C21
5	A	601	B40	CB-CA-N-CM
9	A	607	CLR	C16-C17-C20-C21
10	A	608	Y01	CAO-CAJ-CAN-CBA
5	A	601	B40	C-CA-N-CM
10	A	608	Y01	CAO-CBB-CBE-CAP

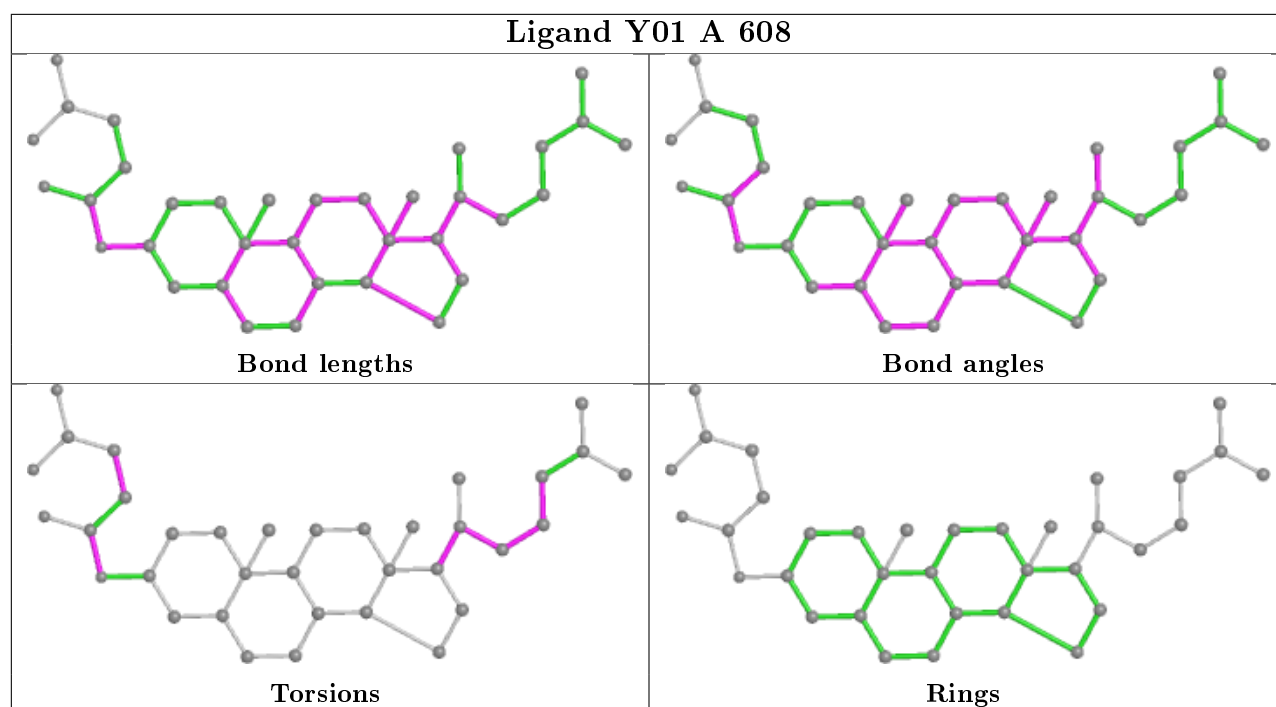
There are no ring outliers.

3 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	601	B40	2	0
9	A	607	CLR	3	0
10	A	608	Y01	4	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





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	534/534 (100%)	-0.07	2 (0%) 92 84	67, 90, 117, 159	0
2	L	213/213 (100%)	0.13	3 (1%) 75 56	66, 86, 117, 131	0
3	H	219/219 (100%)	0.09	6 (2%) 54 31	70, 89, 135, 166	0
All	All	966/966 (100%)	0.01	11 (1%) 80 64	66, 89, 122, 166	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	L	154	SER	3.2
3	H	216	ILE	2.9
3	H	99	GLY	2.8
1	A	305	TYR	2.7
3	H	142	VAL	2.7
3	H	144	LEU	2.5
1	A	290	PHE	2.5
3	H	133	VAL	2.3
3	H	218	PRO	2.3
2	L	149	TRP	2.3
2	L	119	PHE	2.2

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

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

6.3 Carbohydrates ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	GLC	B	2	11/12	0.86	0.16	88,108,122,126	0
4	GLC	B	1	12/12	0.89	0.15	94,102,116,123	0

6.4 Ligands ⓘ

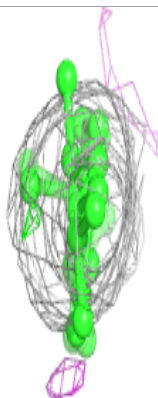
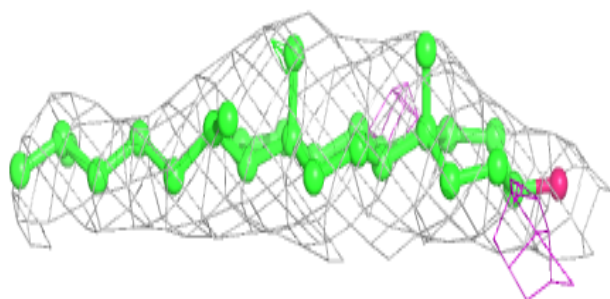
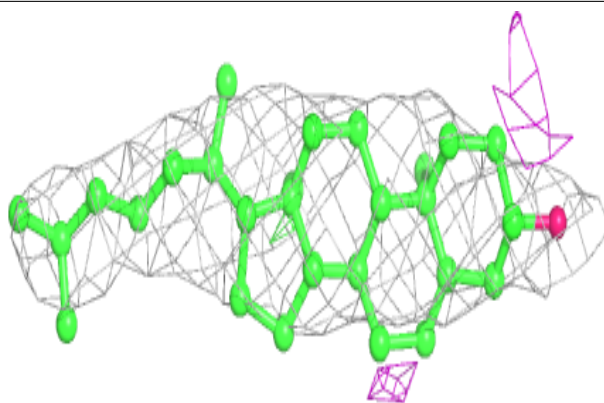
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	B40	A	601	11/11	0.76	0.48	86,95,106,107	0
6	NA	A	604	1/1	0.85	0.17	80,80,80,80	0
8	NAG	A	606	14/15	0.87	0.19	119,135,151,156	0
7	CL	A	605	1/1	0.90	0.16	83,83,83,83	0
9	CLR	A	607	28/28	0.90	0.33	77,100,108,113	0
10	Y01	A	608	35/35	0.93	0.25	87,100,122,128	0
6	NA	A	603	1/1	0.97	0.26	76,76,76,76	0

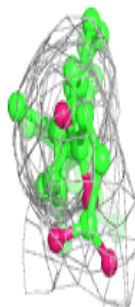
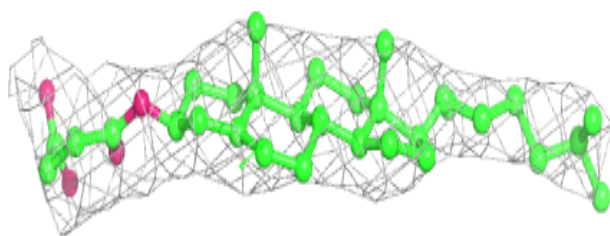
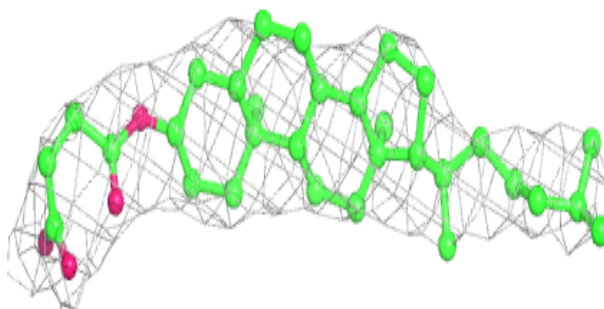
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around CLR A 607:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around Y01 A 608:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers

There are no such residues in this entry.