



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 16, 2023 – 02:07 AM JST

PDB ID : 6KXW
Title : Crystal structure of human aquaporin AQP7 in bound to glycerol
Authors : Zhang, L.; Yao, D.; Zhou, F.; Zhang, Q.; Zhou, L.; Cao, Y.
Deposited on : 2019-09-13
Resolution : 3.70 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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 : 2.36
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) : 2.36

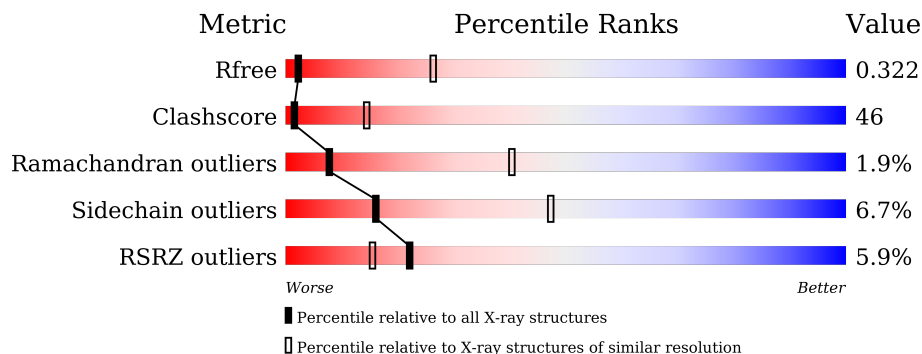
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.70 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	1049 (3.88-3.52)
Clashscore	141614	1027 (3.86-3.54)
Ramachandran outliers	138981	1069 (3.88-3.52)
Sidechain outliers	138945	1065 (3.88-3.52)
RSRZ outliers	127900	1578 (3.90-3.50)

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 of 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	342	
1	B	342	
1	C	342	
1	D	342	

2 Entry composition [i](#)

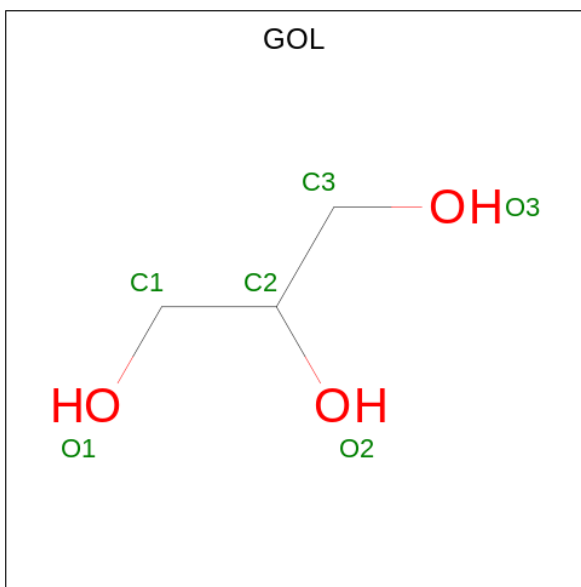
There are 2 unique types of molecules in this entry. The entry contains 7586 atoms, of which 0 are hydrogens and 0 are deuteriums.

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.

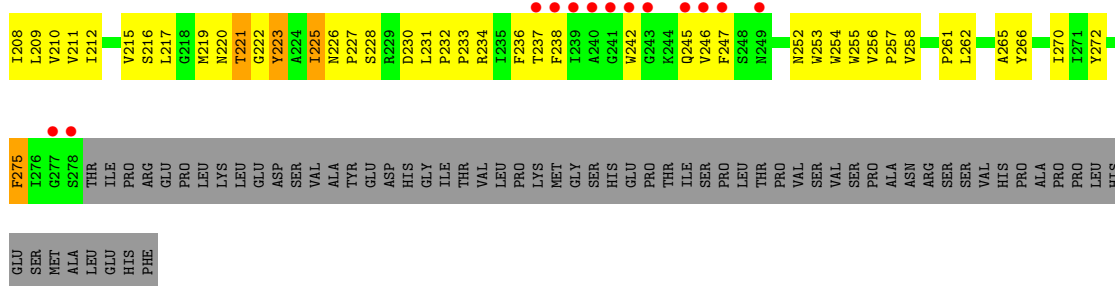
- Molecule 1 is a protein called Aquaporin-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	252	Total 1925	C 1278	N 312	O 322	S 13	0	0	0
1	B	249	Total 1890	C 1253	N 308	O 316	S 13	0	0	0
1	C	249	Total 1894	C 1258	N 306	O 317	S 13	0	0	0
1	D	249	Total 1865	C 1234	N 302	O 316	S 13	0	0	0

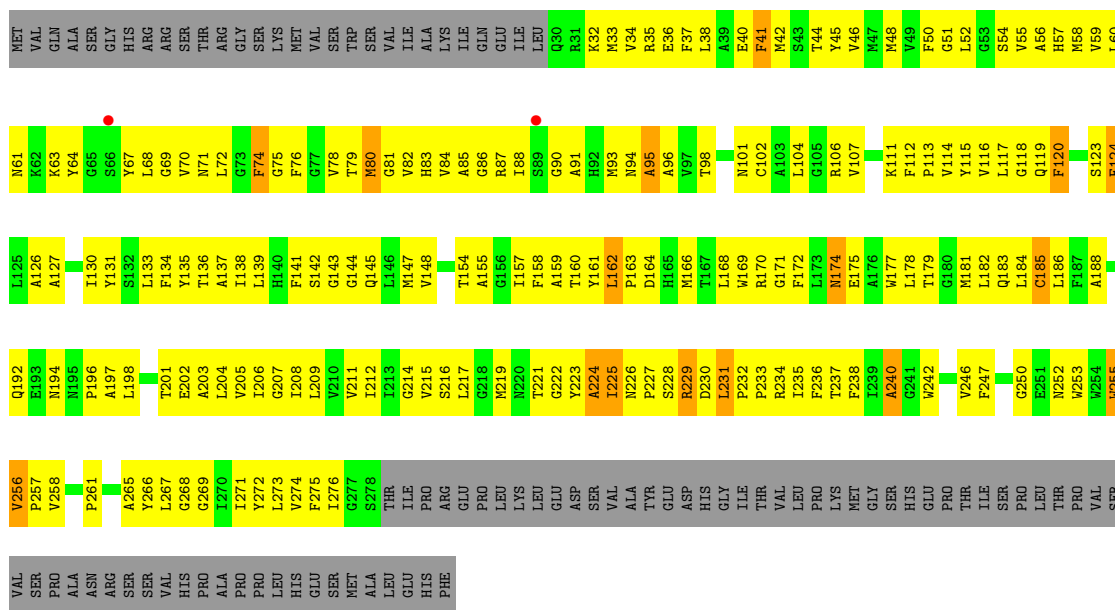
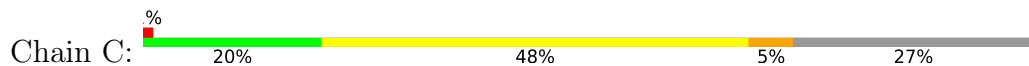
- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃) (labeled as "Ligand of Interest" by depositor).



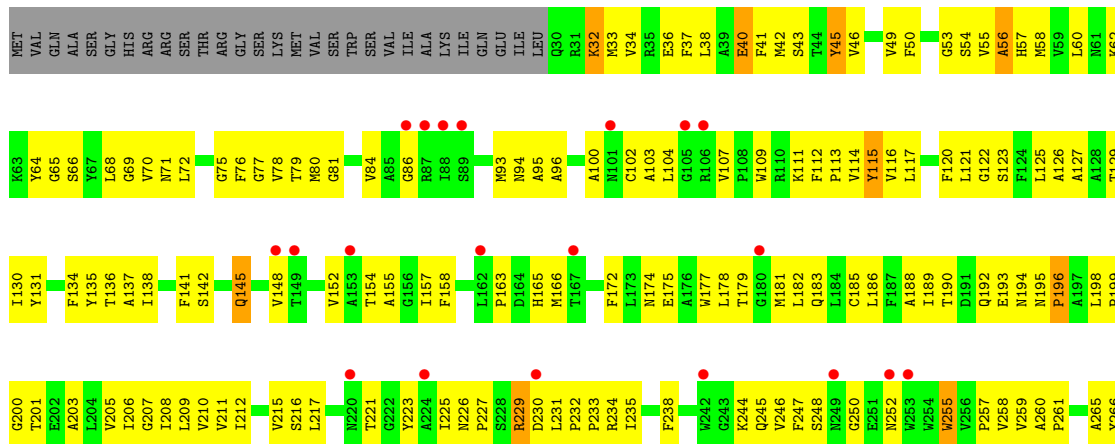
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
2	A	1	Total 6	C 3	O 3	0	0
2	C	1	Total 6	C 3	O 3	0	0



● Molecule 1: Aquaporin-7



● Molecule 1: Aquaporin-7



L267	G268	G269	I270	I271	Y272	L273	F274	F275	I276	G277	S278	THR	ILE	PRO	ARG	GLU	PRO	LEU	LYS	LEU	GLU	ASP	SER	VAL	ALA	ALA	TYR	GLU	ASP	HIS	HIS	GLY	ILE	THR	THR	VAL	LEU	PRO	LYS	LYS	MET	GLY	SER	HIS	GLU	PRO	THR	THR	ILE	SER	PRO	PRO	LEU	THR	PRO	VAL	SER	VAL	SER	PRO	ALA	ALA	ASN	ARG	SER	SER
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VAL	HIS	PRO	ALA	PRO	PRO	LEU	HIS	GLU	SER	MET	ALA	LEU	GLU	HIS	PHE
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.51Å 106.29Å 214.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.61 – 3.70 50.08 – 3.70	Depositor EDS
% Data completeness (in resolution range)	71.9 (47.61-3.70) 72.1 (50.08-3.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 3.67Å)	Xtrriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.268 , 0.322 0.268 , 0.322	Depositor DCC
R_{free} test set	883 reflections (5.21%)	wwPDB-VP
Wilson B-factor (Å ²)	55.0	Xtrriage
Anisotropy	0.443	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 132.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.26$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.78	EDS
Total number of atoms	7586	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.48% 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 i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: GOL

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	0.82	5/1982 (0.3%)	0.99	6/2702 (0.2%)
1	B	0.56	1/1946 (0.1%)	0.78	1/2652 (0.0%)
1	C	0.81	3/1951 (0.2%)	1.07	5/2661 (0.2%)
1	D	0.52	0/1918	0.81	1/2617 (0.0%)
All	All	0.69	9/7797 (0.1%)	0.92	13/10632 (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	2
1	B	0	1
1	C	0	1
1	D	0	2
All	All	0	6

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	89	SER	CA-CB	8.38	1.65	1.52
1	C	256	VAL	C-N	6.59	1.46	1.34
1	A	40	GLU	CG-CD	6.09	1.61	1.51
1	C	164	ASP	CB-CG	5.97	1.64	1.51
1	B	185	CYS	CB-SG	-5.35	1.73	1.81
1	C	185	CYS	CB-SG	-5.31	1.73	1.81
1	A	135	TYR	CD1-CE1	5.26	1.47	1.39
1	A	135	TYR	CG-CD2	5.01	1.45	1.39
1	A	27	GLU	CG-CD	5.00	1.59	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	231	LEU	CB-CG-CD2	7.76	124.20	111.00
1	C	267	LEU	CA-CB-CG	-6.08	101.31	115.30
1	A	60	LEU	CA-CB-CG	5.87	128.79	115.30
1	C	231	LEU	CA-CB-CG	5.81	128.67	115.30
1	A	121	LEU	CB-CG-CD1	5.79	120.84	111.00
1	A	135	TYR	CB-CG-CD1	5.72	124.43	121.00
1	C	267	LEU	CB-CG-CD2	-5.64	101.41	111.00
1	A	38	LEU	CB-CG-CD2	-5.60	101.48	111.00
1	C	229	ARG	NE-CZ-NH1	-5.57	117.51	120.30
1	D	182	LEU	CA-CB-CG	5.50	127.94	115.30
1	A	206	ILE	CG1-CB-CG2	-5.50	99.31	111.40
1	A	135	TYR	CA-CB-CG	5.41	123.68	113.40
1	B	52	LEU	CA-CB-CG	5.33	127.55	115.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	120	PHE	Peptide
1	A	251	GLU	Peptide
1	B	119	GLN	Peptide
1	C	224	ALA	Peptide
1	D	221	THR	Peptide
1	D	86	GLY	Peptide

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	1925	0	1930	184	0
1	B	1890	0	1888	173	0
1	C	1894	0	1891	230	0
1	D	1865	0	1856	199	0
2	A	6	0	8	1	0
2	C	6	0	8	1	0
All	All	7586	0	7581	694	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 46.

All (694) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:177:TRP:CZ3	1:D:129:THR:HB	1.89	1.07
1:B:38:LEU:HD23	1:D:275:PHE:HA	1.34	1.07
1:A:31:ARG:O	1:A:32:LYS:HG2	1.62	1.00
1:D:41:PHE:HZ	1:D:125:LEU:HD12	1.27	0.99
1:D:33:MET:HA	1:D:36:GLU:HG3	1.42	0.98
1:C:163:PRO:HD2	1:C:166:MET:HG3	1.46	0.93
1:A:166:MET:HE1	1:A:220:ASN:HB3	1.52	0.92
1:D:75:GLY:HA2	1:D:210:VAL:HB	1.51	0.91
1:A:192:GLN:HA	1:A:196:PRO:HG3	1.50	0.91
1:C:227:PRO:HB3	1:C:258:VAL:HA	1.52	0.91
1:C:68:LEU:HA	1:C:71:ASN:HD21	1.36	0.90
1:C:157:ILE:HG13	1:C:158:PHE:CD1	2.06	0.90
1:C:96:ALA:HB2	1:C:227:PRO:HD2	1.54	0.89
1:C:48:MET:HE1	1:C:229:ARG:HA	1.54	0.89
1:A:147:MET:HG2	1:A:152:VAL:HG23	1.52	0.89
1:B:38:LEU:HB3	1:D:275:PHE:HD1	1.39	0.88
1:B:219:MET:HB2	1:C:57:HIS:CE1	2.09	0.86
1:D:68:LEU:O	1:D:70:VAL:N	2.08	0.86
1:A:177:TRP:HH2	1:D:129:THR:HG21	1.39	0.86
1:B:94:ASN:HB2	1:B:97:VAL:HG22	1.58	0.86
1:C:192:GLN:HA	1:C:196:PRO:HG3	1.57	0.85
1:A:177:TRP:CZ3	1:D:129:THR:CB	2.60	0.85
1:D:100:ALA:HB2	1:D:265:ALA:HB1	1.58	0.85
1:A:204:LEU:HD13	1:C:205:VAL:HG12	1.59	0.84
1:C:157:ILE:HG13	1:C:158:PHE:HD1	1.41	0.84
1:D:186:LEU:O	1:D:190:THR:OG1	1.97	0.83
1:A:178:LEU:HG	1:A:217:LEU:HD23	1.60	0.82
1:D:96:ALA:HB2	1:D:227:PRO:HD2	1.61	0.82
1:C:37:PHE:O	1:C:41:PHE:N	2.13	0.81
1:C:233:PRO:HA	1:C:236:PHE:HB3	1.62	0.81
1:A:177:TRP:CH2	1:D:129:THR:HB	2.17	0.80
1:C:95:ALA:HB1	1:C:116:VAL:HG22	1.64	0.80
1:A:231:LEU:HD22	1:A:235:ILE:HD11	1.64	0.79
1:A:177:TRP:CH2	1:D:129:THR:CB	2.65	0.79
1:D:102:CYS:SG	1:D:112:PHE:HB2	2.22	0.79
1:A:57:HIS:O	1:A:65:GLY:HA3	1.82	0.78
1:C:80:MET:SD	1:C:80:MET:N	2.57	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:163:PRO:HD2	1:C:166:MET:CG	2.12	0.78
1:D:95:ALA:HA	1:D:116:VAL:HG22	1.65	0.78
1:A:177:TRP:CH2	1:D:129:THR:HG21	2.18	0.78
1:A:51:GLY:HA3	1:A:74:PHE:CD1	2.19	0.77
1:A:175:GLU:O	1:A:179:THR:OG1	2.01	0.77
1:D:79:THR:HG22	1:D:203:ALA:O	1.85	0.77
1:B:37:PHE:HE2	1:B:118:GLY:HA3	1.49	0.76
1:A:100:ALA:HB2	1:A:265:ALA:HB1	1.67	0.76
1:C:61:ASN:OD1	1:C:64:TYR:N	2.18	0.76
1:D:148:VAL:HG23	1:D:155:ALA:HB3	1.67	0.76
1:D:37:PHE:O	1:D:41:PHE:N	2.17	0.75
1:B:197:ALA:HB1	1:B:201:THR:O	1.87	0.75
1:A:80:MET:HE2	1:C:209:LEU:HA	1.69	0.75
1:A:219:MET:HB2	1:D:57:HIS:HD1	1.52	0.74
1:B:160:THR:HG23	1:B:253:TRP:HE1	1.53	0.74
1:D:227:PRO:HG3	1:D:258:VAL:HA	1.69	0.74
1:D:216:SER:HB2	1:D:217:LEU:HD12	1.68	0.74
1:B:72:LEU:HA	1:B:211:VAL:HG22	1.70	0.74
1:B:83:HIS:CD2	1:D:189:ILE:HG12	2.22	0.74
1:A:116:VAL:O	1:A:120:PHE:HB3	1.87	0.74
1:B:73:GLY:HA2	1:D:212:ILE:HD11	1.70	0.74
1:A:224:ALA:HB1	1:A:230:ASP:OD2	1.88	0.73
1:B:202:GLU:O	1:B:206:ILE:HG12	1.88	0.73
1:D:72:LEU:HA	1:D:211:VAL:HG22	1.70	0.73
1:A:37:PHE:HD1	1:A:38:LEU:HD12	1.53	0.73
1:A:129:THR:HB	1:C:177:TRP:CZ3	2.23	0.73
1:C:197:ALA:HB1	1:C:201:THR:HB	1.68	0.73
1:B:41:PHE:HZ	1:B:125:LEU:HD11	1.53	0.73
1:A:42:MET:HB2	1:A:84:VAL:HG11	1.71	0.72
1:C:40:GLU:OE1	1:C:93:MET:N	2.23	0.72
1:B:178:LEU:HD21	1:B:217:LEU:HB2	1.71	0.71
1:C:44:THR:HG21	1:C:119:GLN:O	1.89	0.71
1:D:41:PHE:CZ	1:D:125:LEU:HD12	2.18	0.71
1:D:55:VAL:HG22	1:D:70:VAL:HG21	1.71	0.71
1:B:219:MET:HB2	1:C:57:HIS:ND1	2.05	0.71
1:A:177:TRP:CH2	1:D:129:THR:CG2	2.74	0.71
1:A:219:MET:HB2	1:D:57:HIS:ND1	2.05	0.71
1:B:38:LEU:HD23	1:D:275:PHE:CA	2.15	0.71
1:A:121:LEU:HD13	1:A:125:LEU:HD23	1.71	0.70
1:D:94:ASN:HB3	1:D:226:ASN:HD22	1.54	0.70
1:A:98:THR:HG22	1:A:112:PHE:CD1	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:275:PHE:HB2	1:C:38:LEU:HB3	1.72	0.69
1:C:223:TYR:HB2	1:C:225:ILE:HG23	1.74	0.69
1:D:189:ILE:HD13	1:D:205:VAL:HG12	1.75	0.69
1:B:38:LEU:CD2	1:D:275:PHE:HA	2.17	0.69
1:D:102:CYS:O	1:D:109:TRP:NE1	2.25	0.69
1:B:212:ILE:HD13	1:C:76:PHE:HB3	1.73	0.68
1:C:272:TYR:CD1	1:C:273:LEU:HD23	2.28	0.68
1:C:120:PHE:O	1:C:123:SER:OG	2.09	0.68
1:D:79:THR:HG23	1:D:207:GLY:HA3	1.73	0.68
1:C:98:THR:O	1:C:102:CYS:HB2	1.93	0.68
1:B:75:GLY:O	1:B:78:VAL:HG12	1.94	0.68
1:C:214:GLY:HA2	1:C:223:TYR:CE1	2.29	0.68
1:D:198:LEU:H	1:D:201:THR:HB	1.59	0.68
1:C:127:ALA:HB2	1:C:233:PRO:HB3	1.74	0.68
1:B:37:PHE:CZ	1:B:114:VAL:HG22	2.29	0.67
1:C:54:SER:OG	1:C:69:GLY:O	2.11	0.67
1:A:200:GLY:HA3	1:C:198:LEU:HG	1.77	0.67
1:C:154:THR:OG1	1:C:242:TRP:NE1	2.27	0.67
1:C:246:VAL:HG23	1:C:247:PHE:CD1	2.29	0.67
1:B:158:PHE:HB3	1:B:233:PRO:HB2	1.77	0.67
1:B:163:PRO:O	1:B:166:MET:SD	2.53	0.66
1:B:37:PHE:CE2	1:B:118:GLY:HA3	2.31	0.66
1:C:68:LEU:HA	1:C:71:ASN:ND2	2.08	0.66
1:C:56:ALA:HA	1:C:59:VAL:HG12	1.76	0.66
1:D:53:GLY:O	1:D:57:HIS:HB3	1.97	0.65
1:C:205:VAL:HA	1:C:208:ILE:HG22	1.77	0.65
1:A:205:VAL:HG12	1:A:206:ILE:HD12	1.76	0.65
1:C:175:GLU:OE1	1:C:221:THR:HG21	1.96	0.65
1:D:75:GLY:HA2	1:D:210:VAL:CB	2.24	0.65
1:D:75:GLY:O	1:D:78:VAL:HB	1.97	0.65
1:A:98:THR:HG21	1:A:115:TYR:HB3	1.79	0.65
1:C:78:VAL:O	1:C:81:GLY:N	2.29	0.65
1:C:48:MET:CE	1:C:229:ARG:HA	2.26	0.64
1:D:53:GLY:HA2	1:D:56:ALA:HB3	1.77	0.64
1:D:104:LEU:HD23	1:D:273:LEU:HD12	1.79	0.64
1:C:51:GLY:O	1:C:54:SER:N	2.29	0.64
1:C:116:VAL:O	1:C:120:PHE:N	2.31	0.64
1:A:37:PHE:CD1	1:A:38:LEU:HD12	2.32	0.64
1:B:209:LEU:HA	1:C:80:MET:HE2	1.80	0.64
1:C:94:ASN:HB2	1:C:226:ASN:CB	2.27	0.64
1:B:85:ALA:HB1	1:B:90:GLY:O	1.98	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:139:LEU:HD12	1:C:144:GLY:HA2	1.78	0.64
1:C:71:ASN:HB2	1:C:214:GLY:HA3	1.79	0.64
1:C:216:SER:HB3	1:C:217:LEU:HD13	1.79	0.64
1:C:178:LEU:CD2	1:C:217:LEU:HD23	2.28	0.63
1:B:38:LEU:HB3	1:D:275:PHE:CD1	2.30	0.63
1:A:95:ALA:HB1	1:A:116:VAL:HG22	1.80	0.63
1:B:212:ILE:HA	1:B:215:VAL:HG22	1.80	0.63
1:D:37:PHE:O	1:D:40:GLU:N	2.32	0.63
1:B:231:LEU:HD12	1:B:258:VAL:HG21	1.79	0.62
1:D:60:LEU:HD11	1:D:137:ALA:O	2.00	0.62
1:D:37:PHE:CE1	1:D:114:VAL:HB	2.33	0.62
1:A:129:THR:HB	1:C:177:TRP:HZ3	1.64	0.62
1:D:178:LEU:HD22	1:D:225:ILE:HD11	1.80	0.62
1:D:37:PHE:HE1	1:D:114:VAL:HB	1.65	0.62
1:A:165:HIS:O	1:D:136:THR:OG1	2.17	0.62
1:C:56:ALA:HB2	1:C:157:ILE:HD12	1.81	0.62
1:C:272:TYR:O	1:C:274:VAL:N	2.33	0.62
1:D:95:ALA:HB2	1:D:116:VAL:HG13	1.80	0.62
1:A:98:THR:HG22	1:A:112:PHE:HD1	1.64	0.62
1:A:60:LEU:HD11	1:A:138:ILE:HG22	1.82	0.62
1:D:94:ASN:CB	1:D:226:ASN:HD22	2.13	0.62
1:B:114:VAL:HG13	1:B:115:TYR:CD1	2.35	0.61
1:C:201:THR:O	1:C:205:VAL:HG22	1.99	0.61
1:B:212:ILE:HG13	1:C:50:PHE:HE2	1.65	0.61
1:B:227:PRO:HG2	1:B:262:LEU:HD21	1.82	0.61
1:C:274:VAL:HG23	1:C:275:PHE:N	2.15	0.61
1:D:78:VAL:HG21	1:D:210:VAL:HG21	1.81	0.61
1:B:220:ASN:O	1:B:222:GLY:N	2.34	0.61
1:C:272:TYR:HD1	1:C:273:LEU:HD23	1.65	0.61
1:D:81:GLY:O	1:D:84:VAL:N	2.27	0.61
1:B:189:ILE:HG21	1:B:206:ILE:HD11	1.80	0.61
1:A:235:ILE:O	1:A:239:ILE:HG13	2.00	0.61
1:A:109:TRP:O	1:A:111:LYS:N	2.34	0.61
1:A:116:VAL:HG12	1:A:117:LEU:HD23	1.83	0.61
1:A:215:VAL:HG11	1:D:72:LEU:HD21	1.83	0.61
1:D:79:THR:CG2	1:D:207:GLY:HA3	2.30	0.60
1:D:255:TRP:CE3	1:D:259:VAL:HG21	2.36	0.60
1:C:71:ASN:ND2	1:C:71:ASN:H	1.97	0.60
1:D:198:LEU:HB3	1:D:199:PRO:HD2	1.83	0.60
1:B:75:GLY:HA2	1:B:210:VAL:HB	1.83	0.60
1:B:156:GLY:HA2	1:B:161:TYR:CE2	2.35	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:212:ILE:HD13	1:C:76:PHE:CB	2.30	0.60
1:B:253:TRP:O	1:B:255:TRP:N	2.34	0.60
1:D:60:LEU:HD21	1:D:138:ILE:HG12	1.82	0.60
1:A:54:SER:HB2	1:A:70:VAL:HG22	1.83	0.60
1:B:43:SER:OG	1:B:93:MET:SD	2.59	0.60
1:A:51:GLY:HA3	1:A:74:PHE:CE1	2.36	0.60
1:B:45:TYR:HE1	1:B:129:THR:HG21	1.67	0.60
1:B:195:ASN:CG	1:C:87:ARG:HG2	2.22	0.60
1:C:157:ILE:HG13	1:C:158:PHE:CE1	2.36	0.60
1:C:224:ALA:O	1:C:226:ASN:N	2.35	0.60
1:A:36:GLU:O	1:A:40:GLU:N	2.34	0.59
1:A:148:VAL:HG12	1:A:149:THR:HG23	1.83	0.59
1:C:70:VAL:O	1:C:74:PHE:HB2	2.01	0.59
1:C:94:ASN:O	1:C:96:ALA:N	2.35	0.59
1:B:58:MET:HG3	1:B:59:VAL:N	2.17	0.59
1:B:124:PHE:HD1	1:B:236:PHE:HB2	1.66	0.59
1:B:228:SER:HA	1:B:232:PRO:HG2	1.84	0.59
1:C:226:ASN:HD22	1:C:228:SER:HB2	1.66	0.59
1:A:83:HIS:O	1:C:188:ALA:HB1	2.02	0.59
1:B:80:MET:HG2	1:D:185:CYS:SG	2.43	0.59
1:B:100:ALA:O	1:B:102:CYS:N	2.30	0.59
1:A:172:PHE:CZ	1:A:259:VAL:HG12	2.37	0.59
1:B:138:ILE:O	1:B:142:SER:N	2.20	0.59
1:A:138:ILE:HG13	1:A:139:LEU:HD23	1.84	0.59
1:B:217:LEU:HD23	1:C:133:LEU:HD22	1.85	0.59
1:D:55:VAL:C	1:D:57:HIS:H	2.06	0.59
1:D:178:LEU:HB3	1:D:225:ILE:HG12	1.85	0.59
1:A:34:VAL:O	1:A:38:LEU:HD13	2.02	0.58
1:A:138:ILE:O	1:A:141:PHE:N	2.35	0.58
1:C:85:ALA:O	1:C:91:ALA:HB2	2.02	0.58
1:C:114:VAL:HG23	1:C:115:TYR:HD1	1.67	0.58
1:B:163:PRO:HD2	1:B:166:MET:CE	2.33	0.58
1:D:138:ILE:HA	1:D:141:PHE:HB3	1.85	0.58
1:C:75:GLY:HA3	1:C:211:VAL:CG1	2.32	0.58
1:B:129:THR:HB	1:D:177:TRP:CZ3	2.39	0.58
1:D:179:THR:HB	1:D:261:PRO:HA	1.84	0.58
1:D:189:ILE:HD12	1:D:206:ILE:CD1	2.34	0.58
1:A:175:GLU:HB3	1:A:260:ALA:HB1	1.86	0.58
1:D:76:PHE:O	1:D:79:THR:OG1	2.12	0.58
1:C:76:PHE:O	1:C:79:THR:HB	2.04	0.57
1:D:205:VAL:HA	1:D:208:ILE:HG22	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:268:GLY:O	1:D:271:ILE:N	2.36	0.57
1:B:35:ARG:HH11	1:D:276:ILE:HD11	1.69	0.57
1:B:35:ARG:HE	1:D:276:ILE:CD1	2.17	0.57
1:C:41:PHE:O	1:C:45:TYR:N	2.33	0.57
1:D:185:CYS:O	1:D:189:ILE:HG13	2.05	0.57
1:D:189:ILE:HD12	1:D:206:ILE:HD13	1.85	0.57
1:A:202:GLU:O	1:A:206:ILE:HD13	2.05	0.57
1:C:159:ALA:HB1	1:C:234:ARG:CZ	2.35	0.57
1:D:194:ASN:ND2	1:D:272:TYR:OH	2.23	0.57
1:B:205:VAL:O	1:B:209:LEU:N	2.37	0.56
1:A:94:ASN:O	1:A:96:ALA:N	2.39	0.56
1:B:57:HIS:NE2	1:B:65:GLY:HA2	2.21	0.56
1:D:234:ARG:HD2	1:D:247:PHE:HD1	1.71	0.56
1:B:40:GLU:OE2	1:B:115:TYR:CD2	2.58	0.56
1:C:68:LEU:O	1:C:72:LEU:HD23	2.06	0.56
1:C:162:LEU:HD11	1:C:250:GLY:HA2	1.85	0.56
1:C:185:CYS:HB2	1:C:209:LEU:HD11	1.87	0.56
1:D:68:LEU:HB3	1:D:72:LEU:HD22	1.87	0.56
1:A:184:LEU:HD13	1:A:268:GLY:O	2.06	0.56
1:A:160:THR:HG23	1:A:253:TRP:HE1	1.71	0.56
1:C:48:MET:HE3	1:C:123:SER:HB2	1.86	0.56
1:C:85:ALA:HB1	1:C:90:GLY:O	2.05	0.56
1:A:138:ILE:HG13	1:A:139:LEU:CD2	2.36	0.56
1:A:238:PHE:HB2	1:A:246:VAL:HG21	1.87	0.56
1:B:41:PHE:CZ	1:B:125:LEU:HD11	2.39	0.56
1:C:160:THR:HG21	1:C:222:GLY:O	2.06	0.56
1:A:120:PHE:HE2	1:A:227:PRO:O	1.88	0.56
1:B:111:LYS:O	1:B:114:VAL:HG12	2.05	0.56
1:C:231:LEU:HD22	1:C:235:ILE:CD1	2.36	0.56
1:D:68:LEU:HD22	1:D:71:ASN:HB2	1.86	0.56
1:B:54:SER:O	1:B:57:HIS:HB3	2.06	0.56
1:A:136:THR:HG22	1:C:170:ARG:HG3	1.87	0.56
1:B:57:HIS:O	1:B:65:GLY:HA3	2.06	0.56
1:C:41:PHE:O	1:C:45:TYR:HB2	2.05	0.56
1:C:237:THR:HA	1:C:240:ALA:HB3	1.87	0.56
1:B:104:LEU:HG	1:B:106:ARG:H	1.71	0.56
1:D:209:LEU:O	1:D:212:ILE:N	2.39	0.55
1:B:230:ASP:CB	1:B:257:PRO:HB2	2.37	0.55
1:C:256:VAL:HB	1:C:257:PRO:CD	2.36	0.55
1:C:80:MET:O	1:C:84:VAL:HG23	2.06	0.55
1:C:106:ARG:O	1:C:107:VAL:HG23	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:205:VAL:HG12	1:D:205:VAL:O	2.06	0.55
1:A:109:TRP:O	1:A:112:PHE:N	2.34	0.55
1:C:209:LEU:O	1:C:212:ILE:N	2.27	0.55
1:C:142:SER:OG	1:C:145:GLN:O	2.23	0.55
1:D:175:GLU:HG2	1:D:257:PRO:HB3	1.88	0.55
1:A:225:ILE:O	1:A:227:PRO:HD3	2.07	0.55
1:A:226:ASN:HB3	1:A:229:ARG:HG2	1.89	0.55
1:C:179:THR:HG22	1:C:265:ALA:HB2	1.89	0.55
1:D:257:PRO:HA	1:D:261:PRO:HD3	1.89	0.55
1:B:234:ARG:NH1	1:B:246:VAL:O	2.36	0.55
1:C:162:LEU:HB2	1:C:166:MET:HB2	1.88	0.55
1:A:30:GLN:HA	1:A:30:GLN:OE1	2.07	0.55
1:A:58:MET:SD	1:A:67:TYR:HA	2.46	0.55
1:A:129:THR:HB	1:C:177:TRP:CH2	2.41	0.55
1:B:126:ALA:O	1:B:129:THR:N	2.40	0.55
1:D:120:PHE:CZ	1:D:232:PRO:HD3	2.42	0.55
1:D:275:PHE:CD2	1:D:276:ILE:HG22	2.42	0.55
1:A:189:ILE:HB	1:A:206:ILE:HD11	1.89	0.54
1:B:75:GLY:CA	1:B:210:VAL:HB	2.37	0.54
1:B:109:TRP:O	1:B:112:PHE:HB3	2.07	0.54
1:B:124:PHE:CD1	1:B:236:PHE:HB2	2.42	0.54
1:C:256:VAL:HB	1:C:257:PRO:HD3	1.87	0.54
1:D:230:ASP:OD1	1:D:234:ARG:NH2	2.35	0.54
1:A:76:PHE:CE2	1:C:208:ILE:HD11	2.41	0.54
1:A:240:ALA:HB3	1:A:242:TRP:HZ3	1.72	0.54
1:B:133:LEU:HD11	1:D:174:ASN:HA	1.88	0.54
1:A:181:MET:HE2	1:D:46:VAL:HG22	1.88	0.54
1:B:231:LEU:HD12	1:B:258:VAL:HG11	1.90	0.54
1:D:49:VAL:HG23	1:D:126:ALA:HB1	1.88	0.54
1:D:223:TYR:HB2	1:D:225:ILE:HG13	1.89	0.54
1:A:121:LEU:HD22	1:A:124:PHE:HD2	1.72	0.54
1:B:100:ALA:C	1:B:102:CYS:H	2.09	0.54
1:B:103:ALA:CB	1:B:266:TYR:HD1	2.21	0.54
1:A:200:GLY:HA3	1:C:198:LEU:CG	2.37	0.54
1:B:67:TYR:O	1:B:71:ASN:ND2	2.40	0.54
1:A:58:MET:HB3	1:A:66:SER:O	2.07	0.54
1:A:219:MET:SD	1:D:57:HIS:HA	2.48	0.54
1:C:202:GLU:O	1:C:206:ILE:HG13	2.08	0.54
1:D:71:ASN:HB3	1:D:211:VAL:HG13	1.90	0.54
1:A:96:ALA:O	1:A:99:PHE:N	2.41	0.54
2:A:401:GOL:H11	1:D:64:TYR:CE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:ASN:HA	1:B:223:TYR:OH	2.08	0.54
1:D:130:ILE:HD11	1:D:134:PHE:HE2	1.71	0.54
1:C:94:ASN:HB2	1:C:226:ASN:HB3	1.88	0.53
1:C:231:LEU:CD2	1:C:235:ILE:HD11	2.37	0.53
1:A:75:GLY:O	1:A:207:GLY:HA3	2.08	0.53
1:C:112:PHE:HB3	1:C:113:PRO:HD3	1.89	0.53
1:D:123:SER:HB2	1:D:232:PRO:CG	2.38	0.53
1:B:35:ARG:HE	1:D:276:ILE:HD11	1.73	0.53
1:B:102:CYS:HB3	1:B:109:TRP:CD1	2.43	0.53
1:D:123:SER:HB2	1:D:232:PRO:HG2	1.91	0.53
1:B:114:VAL:HG13	1:B:115:TYR:HD1	1.72	0.53
1:B:227:PRO:HB3	1:B:258:VAL:HA	1.91	0.53
1:C:139:LEU:O	1:C:143:GLY:N	2.42	0.53
1:C:94:ASN:HB2	1:C:226:ASN:CG	2.29	0.53
1:C:204:LEU:O	1:C:208:ILE:HB	2.09	0.53
1:D:178:LEU:HD21	1:D:217:LEU:HB2	1.90	0.53
1:B:216:SER:OG	1:C:54:SER:HB2	2.08	0.52
1:A:40:GLU:OE1	1:A:92:HIS:N	2.42	0.52
1:A:214:GLY:HA2	1:A:223:TYR:HE2	1.74	0.52
1:A:237:THR:O	1:A:242:TRP:HE3	1.92	0.52
1:B:128:ALA:O	1:B:131:TYR:N	2.42	0.52
1:B:275:PHE:HA	1:C:38:LEU:HD22	1.92	0.52
1:C:75:GLY:HA3	1:C:211:VAL:HG12	1.90	0.52
1:D:138:ILE:CG2	1:D:154:THR:HG21	2.39	0.52
1:A:136:THR:CG2	1:C:170:ARG:HG3	2.40	0.52
1:A:275:PHE:HA	1:D:38:LEU:HD23	1.92	0.52
1:C:37:PHE:N	1:C:37:PHE:CD1	2.77	0.52
1:C:130:ILE:HD11	1:C:134:PHE:CE2	2.44	0.52
1:B:45:TYR:HA	1:B:122:GLY:O	2.10	0.52
1:B:73:GLY:HA2	1:D:212:ILE:CD1	2.38	0.52
1:B:231:LEU:CD1	1:B:258:VAL:HG21	2.39	0.52
1:C:55:VAL:HG22	1:C:157:ILE:HG22	1.92	0.52
1:C:256:VAL:C	1:C:258:VAL:H	2.13	0.52
1:C:271:ILE:O	1:C:274:VAL:HG22	2.09	0.52
1:D:62:LYS:HA	1:D:65:GLY:O	2.10	0.52
1:A:177:TRP:HH2	1:D:129:THR:CG2	2.11	0.52
1:A:33:MET:SD	1:A:111:LYS:HB3	2.49	0.51
1:B:87:ARG:HB2	1:D:195:ASN:CG	2.30	0.51
1:B:148:VAL:HB	1:B:245:GLN:OE1	2.10	0.51
1:B:275:PHE:HB2	1:C:38:LEU:CB	2.39	0.51
1:B:160:THR:CG2	1:B:253:TRP:HE1	2.22	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:VAL:HG23	1:C:115:TYR:CD1	2.44	0.51
1:A:104:LEU:HD21	1:A:270:ILE:HG13	1.93	0.51
1:C:82:VAL:CG1	1:C:203:ALA:HB2	2.40	0.51
1:C:33:MET:CE	1:C:111:LYS:HD2	2.41	0.51
1:D:117:LEU:O	1:D:121:LEU:HG	2.10	0.51
1:B:162:LEU:HD23	1:B:162:LEU:H	1.75	0.51
1:B:148:VAL:HG21	1:B:245:GLN:HB2	1.91	0.51
1:B:272:TYR:CE1	1:B:275:PHE:HE1	2.29	0.51
1:C:226:ASN:O	1:C:228:SER:N	2.42	0.51
1:C:33:MET:O	1:C:36:GLU:HB2	2.10	0.51
1:D:138:ILE:HG21	1:D:154:THR:HG21	1.93	0.51
1:A:189:ILE:HD13	1:A:205:VAL:CG1	2.40	0.51
1:B:172:PHE:HD1	1:B:256:VAL:HG23	1.76	0.51
1:B:182:LEU:O	1:B:186:LEU:HB2	2.11	0.51
1:B:217:LEU:HD12	1:B:217:LEU:N	2.26	0.51
1:D:198:LEU:HB2	1:D:201:THR:OG1	2.11	0.51
1:B:272:TYR:CZ	1:B:275:PHE:HE1	2.29	0.51
1:C:178:LEU:HD21	1:C:217:LEU:HD23	1.91	0.51
1:C:183:GLN:HA	1:C:183:GLN:OE1	2.10	0.50
1:D:172:PHE:CD2	1:D:260:ALA:HB2	2.45	0.50
1:A:50:PHE:HD2	1:A:77:GLY:HA2	1.75	0.50
1:A:82:VAL:C	1:A:84:VAL:H	2.15	0.50
1:A:159:ALA:HB2	1:A:234:ARG:HB2	1.94	0.50
1:D:75:GLY:HA2	1:D:210:VAL:CG1	2.41	0.50
1:D:116:VAL:O	1:D:120:PHE:HB2	2.11	0.50
1:A:56:ALA:O	1:A:60:LEU:HB3	2.10	0.50
1:A:98:THR:HG21	1:A:115:TYR:CB	2.42	0.50
1:A:135:TYR:HB3	1:C:170:ARG:NH2	2.26	0.50
1:D:103:ALA:HB2	1:D:109:TRP:HZ2	1.75	0.50
1:B:225:ILE:HD12	1:B:226:ASN:N	2.26	0.50
1:C:48:MET:HG3	1:C:123:SER:HA	1.94	0.50
1:D:32:LYS:HD3	1:D:33:MET:H	1.76	0.50
1:A:71:ASN:HA	1:A:223:TYR:OH	2.11	0.50
1:B:115:TYR:O	1:B:119:GLN:HB2	2.12	0.50
1:B:227:PRO:HG2	1:B:262:LEU:CD2	2.41	0.50
1:C:55:VAL:HB	1:C:70:VAL:HG13	1.94	0.50
1:A:60:LEU:HD21	1:A:137:ALA:O	2.11	0.50
1:B:51:GLY:HA2	1:B:74:PHE:HA	1.94	0.50
1:B:124:PHE:HE1	1:B:236:PHE:HD1	1.59	0.50
1:D:33:MET:CA	1:D:36:GLU:HG3	2.28	0.50
1:D:234:ARG:HD3	1:D:246:VAL:O	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:205:VAL:HA	1:A:208:ILE:HG22	1.93	0.49
1:B:76:PHE:C	1:D:212:ILE:HG12	2.32	0.49
1:A:157:ILE:HB	1:A:158:PHE:CD1	2.47	0.49
1:A:189:ILE:HG21	1:A:205:VAL:HG11	1.94	0.49
1:A:202:GLU:OE1	1:A:202:GLU:N	2.42	0.49
1:C:208:ILE:O	1:C:212:ILE:HG12	2.11	0.49
1:A:120:PHE:CE2	1:A:227:PRO:O	2.65	0.49
1:A:189:ILE:HD13	1:A:205:VAL:HG11	1.94	0.49
1:B:226:ASN:O	1:B:228:SER:N	2.42	0.49
1:C:124:PHE:HE1	1:C:236:PHE:HD1	1.60	0.49
1:D:212:ILE:HD12	1:D:215:VAL:HG21	1.94	0.49
1:B:55:VAL:HA	1:B:70:VAL:HG22	1.94	0.49
1:D:245:GLN:HA	1:D:248:SER:OG	2.11	0.49
1:A:33:MET:O	1:A:36:GLU:N	2.39	0.49
1:A:75:GLY:O	1:A:79:THR:HG23	2.13	0.49
1:B:45:TYR:CE1	1:B:129:THR:HG21	2.47	0.49
1:C:67:TYR:O	1:C:70:VAL:N	2.43	0.49
1:C:85:ALA:HB3	1:C:91:ALA:HA	1.94	0.49
1:D:117:LEU:O	1:D:121:LEU:N	2.27	0.49
1:A:90:GLY:HA2	1:A:115:TYR:OH	2.13	0.49
1:B:100:ALA:HB2	1:B:265:ALA:HB1	1.95	0.49
1:D:226:ASN:N	1:D:226:ASN:OD1	2.45	0.49
1:A:31:ARG:O	1:A:32:LYS:CG	2.49	0.49
1:A:57:HIS:HA	1:C:219:MET:HE2	1.93	0.49
1:B:37:PHE:HZ	1:B:114:VAL:O	1.96	0.49
1:D:45:TYR:HA	1:D:126:ALA:HB2	1.94	0.49
1:A:231:LEU:O	1:A:235:ILE:HG13	2.13	0.49
1:B:181:MET:O	1:B:185:CYS:HB2	2.12	0.49
1:C:118:GLY:H	1:C:120:PHE:H	1.60	0.49
1:C:194:ASN:CG	1:C:276:ILE:HD11	2.32	0.49
1:C:211:VAL:HG23	1:C:212:ILE:HD13	1.95	0.49
1:A:75:GLY:HA2	1:A:210:VAL:HB	1.94	0.48
1:B:128:ALA:HA	1:B:131:TYR:HB3	1.94	0.48
1:D:267:LEU:O	1:D:271:ILE:HG12	2.13	0.48
1:A:121:LEU:HD22	1:A:124:PHE:CD2	2.47	0.48
1:B:131:TYR:CD2	1:B:236:PHE:HZ	2.30	0.48
1:D:252:ASN:OD1	1:D:252:ASN:N	2.47	0.48
1:C:72:LEU:HA	1:C:211:VAL:HG12	1.94	0.48
1:C:162:LEU:O	1:C:162:LEU:HD12	2.13	0.48
1:C:226:ASN:ND2	1:C:228:SER:HB2	2.29	0.48
1:D:163:PRO:HD2	1:D:166:MET:SD	2.54	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:THR:HG22	1:A:207:GLY:H	1.79	0.48
1:C:172:PHE:CD2	1:C:256:VAL:HG13	2.49	0.48
1:C:182:LEU:O	1:C:186:LEU:HB2	2.14	0.48
1:A:128:ALA:HB2	1:A:236:PHE:CE1	2.49	0.48
1:A:275:PHE:CE2	1:A:276:ILE:HB	2.49	0.48
1:B:50:PHE:O	1:B:54:SER:OG	2.17	0.48
1:B:76:PHE:O	1:D:212:ILE:HG12	2.13	0.48
1:C:68:LEU:CA	1:C:71:ASN:HD21	2.18	0.48
1:D:250:GLY:C	1:D:252:ASN:H	2.16	0.48
1:A:228:SER:O	1:A:232:PRO:HG2	2.14	0.48
1:C:37:PHE:O	1:C:41:PHE:HB2	2.14	0.48
1:C:255:TRP:CD1	1:C:256:VAL:N	2.82	0.48
1:D:122:GLY:O	1:D:125:LEU:N	2.47	0.47
1:D:192:GLN:HA	1:D:196:PRO:HG3	1.95	0.47
1:A:60:LEU:CD1	1:A:138:ILE:HG22	2.43	0.47
1:C:231:LEU:O	1:C:235:ILE:HG13	2.14	0.47
1:A:256:VAL:O	1:A:260:ALA:N	2.33	0.47
1:C:71:ASN:OD1	1:C:215:VAL:CG1	2.62	0.47
1:A:95:ALA:CB	1:A:116:VAL:HG22	2.44	0.47
1:A:172:PHE:HZ	1:A:259:VAL:HG12	1.75	0.47
1:C:231:LEU:HD23	1:C:235:ILE:HG13	1.96	0.47
1:A:107:VAL:HG12	1:A:108:PRO:O	2.15	0.47
1:A:177:TRP:HZ3	1:D:129:THR:CB	2.24	0.47
1:C:161:TYR:OH	1:C:246:VAL:HG12	2.15	0.47
1:C:171:GLY:O	1:C:256:VAL:HG11	2.14	0.47
1:A:80:MET:HE2	1:C:209:LEU:CA	2.44	0.47
1:A:219:MET:HE2	1:D:134:PHE:HE1	1.80	0.47
1:C:78:VAL:HB	1:C:207:GLY:HA2	1.96	0.47
1:D:123:SER:CB	1:D:232:PRO:HG2	2.44	0.47
1:C:162:LEU:HB2	1:C:166:MET:CB	2.44	0.47
1:C:269:GLY:O	1:C:272:TYR:HB3	2.15	0.47
1:D:117:LEU:C	1:D:121:LEU:HG	2.36	0.47
1:D:179:THR:OG1	1:D:225:ILE:HG23	2.15	0.47
1:A:204:LEU:HD21	1:C:204:LEU:HD12	1.96	0.47
1:B:45:TYR:O	1:B:45:TYR:CG	2.68	0.47
1:A:85:ALA:O	1:A:91:ALA:HB2	2.16	0.47
1:D:234:ARG:HD2	1:D:247:PHE:CD1	2.48	0.47
1:A:76:PHE:HD2	1:C:212:ILE:HD11	1.80	0.46
1:B:223:TYR:C	1:B:225:ILE:H	2.17	0.46
1:A:254:TRP:CD1	1:A:255:TRP:N	2.83	0.46
1:B:172:PHE:HD1	1:B:256:VAL:CG2	2.28	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:208:ILE:HD12	1:C:204:LEU:HD21	1.97	0.46
1:C:42:MET:O	1:C:46:VAL:HG23	2.16	0.46
1:A:162:LEU:HD23	1:A:253:TRP:CE3	2.51	0.46
1:B:40:GLU:OE1	1:B:119:GLN:HG3	2.16	0.46
1:C:186:LEU:HA	1:C:186:LEU:HD22	1.75	0.46
1:D:227:PRO:HB3	1:D:258:VAL:HG13	1.96	0.46
1:B:46:VAL:HG22	1:D:181:MET:CE	2.46	0.46
1:D:142:SER:OG	1:D:145:GLN:O	2.20	0.46
1:A:46:VAL:HG13	1:C:181:MET:CE	2.46	0.46
1:B:83:HIS:CE1	1:D:205:VAL:HG11	2.50	0.46
1:C:56:ALA:HB2	1:C:157:ILE:CD1	2.45	0.46
1:A:84:VAL:O	1:A:84:VAL:HG12	2.15	0.46
1:A:85:ALA:O	1:A:87:ARG:N	2.49	0.46
1:A:183:GLN:OE1	1:A:183:GLN:HA	2.16	0.46
1:C:154:THR:OG1	1:C:155:ALA:N	2.49	0.46
1:D:157:ILE:HG13	1:D:158:PHE:H	1.81	0.46
1:B:160:THR:HG23	1:B:253:TRP:NE1	2.26	0.46
1:D:198:LEU:N	1:D:201:THR:HB	2.28	0.46
1:A:74:PHE:O	1:A:78:VAL:HG23	2.16	0.46
1:D:76:PHE:HA	1:D:79:THR:HG23	1.98	0.46
1:D:275:PHE:CE2	1:D:276:ILE:HG22	2.51	0.46
1:A:200:GLY:HA3	1:C:198:LEU:CD2	2.45	0.45
1:C:134:PHE:O	1:C:138:ILE:HG12	2.16	0.45
1:B:85:ALA:HB1	1:B:91:ALA:HA	1.97	0.45
1:C:41:PHE:O	1:C:45:TYR:CB	2.64	0.45
1:C:184:LEU:HD12	1:C:268:GLY:O	2.15	0.45
1:D:95:ALA:CB	1:D:116:VAL:HG13	2.45	0.45
1:D:107:VAL:HG12	1:D:111:LYS:HB2	1.97	0.45
1:A:92:HIS:CE1	1:A:115:TYR:HE2	2.34	0.45
1:A:126:ALA:HA	1:A:129:THR:OG1	2.17	0.45
1:A:159:ALA:HB1	1:A:234:ARG:NH2	2.32	0.45
1:C:52:LEU:HA	1:C:55:VAL:HG12	1.98	0.45
1:C:71:ASN:HA	1:C:223:TYR:OH	2.17	0.45
1:C:148:VAL:HG22	1:C:242:TRP:HD1	1.81	0.45
1:D:34:VAL:C	1:D:36:GLU:H	2.19	0.45
1:A:162:LEU:O	1:A:162:LEU:HD12	2.17	0.45
1:A:216:SER:HA	1:D:54:SER:HA	1.98	0.45
1:B:46:VAL:HG22	1:D:181:MET:HE3	1.97	0.45
1:C:95:ALA:CB	1:C:116:VAL:HG22	2.42	0.45
1:C:104:LEU:CD2	1:C:266:TYR:HE1	2.30	0.45
1:C:227:PRO:HD3	1:C:261:PRO:CB	2.47	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:79:THR:CG2	1:A:207:GLY:HA3	2.47	0.45
1:A:205:VAL:O	1:A:208:ILE:HG22	2.17	0.45
1:C:117:LEU:HA	1:C:120:PHE:HB2	1.99	0.45
1:D:193:GLU:HG3	1:D:194:ASN:H	1.80	0.45
1:A:184:LEU:HD21	1:A:271:ILE:HG22	1.98	0.45
1:B:225:ILE:CD1	1:B:226:ASN:HD22	2.30	0.45
1:C:75:GLY:HA3	1:C:211:VAL:HG13	1.97	0.45
1:C:205:VAL:HA	1:C:208:ILE:CG2	2.44	0.45
1:B:41:PHE:HZ	1:B:125:LEU:CD1	2.25	0.45
1:C:272:TYR:CD1	1:C:276:ILE:HG23	2.52	0.45
1:A:170:ARG:HG3	1:D:136:THR:CG2	2.47	0.45
1:B:116:VAL:HG12	1:B:120:PHE:CZ	2.51	0.45
1:B:45:TYR:CD1	1:B:126:ALA:HB2	2.52	0.45
1:B:208:ILE:HD13	1:C:76:PHE:CZ	2.52	0.45
1:C:222:GLY:HA2	2:C:400:GOL:H2	1.98	0.45
1:D:71:ASN:HD21	1:D:215:VAL:HA	1.82	0.45
1:D:112:PHE:CZ	1:D:116:VAL:HG21	2.52	0.45
1:D:231:LEU:O	1:D:235:ILE:N	2.42	0.45
1:A:171:GLY:O	1:A:256:VAL:HG11	2.16	0.44
1:B:148:VAL:HG11	1:B:245:GLN:HB3	2.00	0.44
1:B:170:ARG:HG2	1:C:136:THR:HG23	1.99	0.44
1:B:219:MET:HB3	1:B:219:MET:HE2	1.70	0.44
1:D:271:ILE:O	1:D:275:PHE:HB3	2.17	0.44
1:A:46:VAL:HG13	1:C:181:MET:HE3	1.99	0.44
1:B:100:ALA:HB2	1:B:265:ALA:CB	2.46	0.44
1:B:230:ASP:CB	1:B:257:PRO:HG2	2.48	0.44
1:C:58:MET:HG3	1:C:59:VAL:N	2.32	0.44
1:C:232:PRO:HB2	1:C:233:PRO:HD3	2.00	0.44
1:D:127:ALA:HA	1:D:130:ILE:HG22	2.00	0.44
1:A:213:ILE:HA	1:A:213:ILE:HD13	1.85	0.44
1:C:231:LEU:HD22	1:C:235:ILE:HD11	1.96	0.44
1:B:189:ILE:HG21	1:B:206:ILE:CD1	2.45	0.44
1:B:266:TYR:CE1	1:B:270:ILE:HD11	2.52	0.44
1:C:168:LEU:HD21	1:C:253:TRP:HE3	1.83	0.44
1:B:195:ASN:CB	1:C:87:ARG:HG2	2.48	0.44
1:D:60:LEU:HD13	1:D:60:LEU:O	2.17	0.44
1:B:127:ALA:HB2	1:B:233:PRO:HB3	2.00	0.44
1:B:206:ILE:O	1:B:210:VAL:HG23	2.17	0.44
1:B:221:THR:HB	1:B:253:TRP:CH2	2.53	0.44
1:C:231:LEU:CD2	1:C:235:ILE:HG13	2.47	0.44
1:A:68:LEU:O	1:A:71:ASN:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88:ILE:HD11	1:A:190:THR:CG2	2.48	0.44
1:B:256:VAL:HG12	1:B:257:PRO:HD3	2.00	0.44
1:C:148:VAL:HG22	1:C:242:TRP:CD1	2.53	0.44
1:A:42:MET:HB2	1:A:84:VAL:CG1	2.45	0.44
1:B:83:HIS:HB3	1:D:188:ALA:HB1	1.98	0.44
1:B:206:ILE:O	1:B:209:LEU:HB3	2.18	0.44
1:C:168:LEU:HA	1:C:171:GLY:HA3	2.00	0.44
1:B:45:TYR:HD1	1:B:126:ALA:HB2	1.81	0.44
1:B:68:LEU:HA	1:B:71:ASN:OD1	2.18	0.44
1:C:37:PHE:CE1	1:C:114:VAL:HB	2.53	0.44
1:C:37:PHE:HE1	1:C:114:VAL:HB	1.81	0.44
1:C:71:ASN:CB	1:C:214:GLY:HA3	2.47	0.44
1:C:157:ILE:CD1	1:C:158:PHE:HE1	2.31	0.44
1:D:127:ALA:O	1:D:130:ILE:HG22	2.18	0.44
1:A:207:GLY:O	1:A:210:VAL:N	2.51	0.43
1:A:208:ILE:O	1:A:212:ILE:HG13	2.17	0.43
1:C:252:ASN:OD1	1:C:252:ASN:N	2.50	0.43
1:C:274:VAL:CG2	1:C:275:PHE:N	2.80	0.43
1:D:212:ILE:HA	1:D:215:VAL:HG22	1.99	0.43
1:C:226:ASN:O	1:C:226:ASN:ND2	2.51	0.43
1:D:208:ILE:HG13	1:D:208:ILE:O	2.18	0.43
1:A:76:PHE:CB	1:C:212:ILE:HG13	2.47	0.43
1:D:212:ILE:HD12	1:D:212:ILE:HA	1.83	0.43
1:B:79:THR:HG22	1:B:203:ALA:O	2.18	0.43
1:D:113:PRO:HA	1:D:116:VAL:HB	1.99	0.43
1:D:195:ASN:H	1:D:195:ASN:ND2	2.15	0.43
1:D:230:ASP:O	1:D:234:ARG:HB2	2.18	0.43
1:A:181:MET:HE1	1:D:46:VAL:HA	2.00	0.43
1:A:205:VAL:O	1:A:209:LEU:N	2.51	0.43
1:A:236:PHE:O	1:A:239:ILE:N	2.46	0.43
1:C:85:ALA:HB3	1:C:91:ALA:CB	2.49	0.43
1:D:142:SER:CB	1:D:152:VAL:HG11	2.48	0.43
1:D:175:GLU:HG3	1:D:261:PRO:HG3	2.00	0.43
1:D:209:LEU:O	1:D:212:ILE:HG22	2.19	0.43
1:D:238:PHE:CD1	1:D:244:LYS:HA	2.54	0.43
1:B:68:LEU:HD12	1:B:71:ASN:OD1	2.18	0.43
1:C:35:ARG:HA	1:C:38:LEU:HD13	2.00	0.43
1:D:43:SER:OG	1:D:93:MET:HG2	2.19	0.43
1:D:94:ASN:HD22	1:D:226:ASN:ND2	2.17	0.43
1:D:104:LEU:HD21	1:D:269:GLY:C	2.39	0.43
1:B:228:SER:HA	1:B:232:PRO:CG	2.49	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:78:VAL:O	1:C:79:THR:C	2.56	0.43
1:C:114:VAL:HG23	1:C:115:TYR:H	1.82	0.43
1:C:154:THR:O	1:C:157:ILE:HG12	2.18	0.43
1:A:32:LYS:HD3	1:A:32:LYS:HA	1.55	0.43
1:B:162:LEU:HD22	1:B:253:TRP:CE3	2.53	0.43
1:C:231:LEU:CD2	1:C:235:ILE:CD1	2.96	0.43
1:D:81:GLY:H	1:D:84:VAL:HG23	1.84	0.43
1:C:183:GLN:HB2	1:C:268:GLY:HA3	2.01	0.43
1:C:230:ASP:OD2	1:C:257:PRO:CG	2.67	0.43
1:A:208:ILE:HA	1:A:211:VAL:HG23	2.01	0.42
1:B:160:THR:O	1:B:253:TRP:CD1	2.72	0.42
1:C:52:LEU:HB2	1:C:130:ILE:HG21	2.01	0.42
1:C:55:VAL:HG13	1:C:157:ILE:HB	2.01	0.42
1:C:250:GLY:C	1:C:252:ASN:H	2.22	0.42
1:D:189:ILE:CD1	1:D:205:VAL:HG12	2.46	0.42
1:D:201:THR:HG22	1:D:201:THR:O	2.19	0.42
1:A:208:ILE:HA	1:A:211:VAL:CG2	2.49	0.42
1:A:263:LEU:O	1:A:267:LEU:HD22	2.19	0.42
1:A:57:HIS:HA	1:C:219:MET:CE	2.50	0.42
1:A:163:PRO:C	1:A:165:HIS:H	2.21	0.42
1:B:50:PHE:CZ	1:D:212:ILE:HG23	2.54	0.42
1:B:148:VAL:HA	1:B:155:ALA:HB2	2.01	0.42
1:D:175:GLU:HB3	1:D:260:ALA:HB3	2.00	0.42
1:A:71:ASN:O	1:A:211:VAL:HA	2.19	0.42
1:A:163:PRO:O	1:A:165:HIS:N	2.53	0.42
1:B:163:PRO:HD2	1:B:166:MET:HE1	2.00	0.42
1:C:60:LEU:HD21	1:C:137:ALA:O	2.20	0.42
1:C:63:LYS:O	1:C:64:TYR:HD1	2.02	0.42
1:D:130:ILE:HD12	1:D:130:ILE:HA	1.90	0.42
1:D:205:VAL:HA	1:D:208:ILE:CG2	2.50	0.42
1:C:38:LEU:HD12	1:C:38:LEU:H	1.85	0.42
1:C:104:LEU:HD21	1:C:266:TYR:HE1	1.84	0.42
1:C:178:LEU:HB3	1:C:225:ILE:HG22	2.00	0.42
1:D:120:PHE:CE1	1:D:232:PRO:HD3	2.55	0.42
1:B:266:TYR:O	1:B:270:ILE:HG13	2.18	0.42
1:D:112:PHE:HB3	1:D:113:PRO:HD3	2.01	0.42
1:A:219:MET:HE2	1:D:134:PHE:CE1	2.55	0.42
1:A:219:MET:CB	1:D:57:HIS:HD1	2.27	0.42
1:C:124:PHE:C	1:C:126:ALA:H	2.22	0.42
1:A:72:LEU:HB3	1:A:211:VAL:HG13	2.02	0.42
1:A:85:ALA:HB3	1:A:91:ALA:HB2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:120:PHE:CD2	1:A:228:SER:HA	2.55	0.42
1:B:162:LEU:HD13	1:B:253:TRP:CZ3	2.55	0.42
1:C:71:ASN:H	1:C:71:ASN:HD22	1.68	0.42
1:B:227:PRO:HD3	1:B:261:PRO:HG2	2.01	0.42
1:D:36:GLU:O	1:D:115:TYR:HE1	2.02	0.42
1:D:165:HIS:CE1	1:D:166:MET:HG2	2.55	0.42
1:A:85:ALA:HB1	1:A:90:GLY:O	2.19	0.42
1:A:159:ALA:HB1	1:A:234:ARG:CZ	2.50	0.41
1:A:198:LEU:HD21	1:D:200:GLY:H	1.85	0.41
1:B:73:GLY:CA	1:D:212:ILE:HD11	2.45	0.41
1:D:58:MET:HG3	1:D:66:SER:O	2.20	0.41
1:D:117:LEU:HD23	1:D:117:LEU:HA	1.80	0.41
1:A:208:ILE:O	1:A:208:ILE:HG23	2.19	0.41
1:B:41:PHE:CE2	1:B:121:LEU:HB2	2.55	0.41
1:B:219:MET:HE2	1:C:134:PHE:HE1	1.86	0.41
1:B:272:TYR:O	1:B:275:PHE:HD1	2.02	0.41
1:A:189:ILE:O	1:A:196:PRO:HB2	2.20	0.41
1:B:76:PHE:CE1	1:D:208:ILE:HG12	2.55	0.41
1:C:231:LEU:N	1:C:232:PRO:CD	2.83	0.41
1:D:76:PHE:HZ	1:D:208:ILE:HD13	1.85	0.41
1:A:179:THR:HG21	1:A:261:PRO:O	2.21	0.41
1:B:85:ALA:CB	1:B:91:ALA:HA	2.50	0.41
1:D:68:LEU:HD23	1:D:68:LEU:HA	1.90	0.41
1:C:63:LYS:HB2	1:C:63:LYS:HE2	1.67	0.41
1:C:142:SER:OG	1:C:142:SER:O	2.37	0.41
1:D:174:ASN:O	1:D:174:ASN:ND2	2.53	0.41
1:B:41:PHE:HA	1:B:119:GLN:OE1	2.20	0.41
1:A:44:THR:CG2	1:A:123:SER:HB3	2.50	0.41
1:A:212:ILE:HD11	1:D:76:PHE:HB3	2.01	0.41
1:B:75:GLY:HA2	1:B:78:VAL:HG12	2.02	0.41
1:C:102:CYS:SG	1:C:112:PHE:HB2	2.61	0.41
1:A:121:LEU:HD13	1:A:125:LEU:CD2	2.45	0.41
1:A:177:TRP:CZ3	1:D:129:THR:OG1	2.73	0.41
1:C:42:MET:O	1:C:46:VAL:N	2.46	0.41
1:C:207:GLY:O	1:C:211:VAL:HG13	2.21	0.41
1:C:234:ARG:NH1	1:C:246:VAL:O	2.53	0.41
1:A:58:MET:HG3	1:A:59:VAL:N	2.36	0.41
1:A:236:PHE:O	1:A:239:ILE:HB	2.21	0.41
1:B:40:GLU:HB3	1:B:119:GLN:CG	2.51	0.41
1:B:103:ALA:HB2	1:B:266:TYR:HD1	1.86	0.41
1:B:118:GLY:O	1:B:119:GLN:NE2	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:SER:HB2	1:B:154:THR:HG21	2.02	0.41
1:B:233:PRO:O	1:B:237:THR:HG23	2.20	0.41
1:C:55:VAL:HA	1:C:70:VAL:HG22	2.03	0.41
1:C:83:HIS:NE2	1:C:203:ALA:HB3	2.36	0.41
1:C:148:VAL:CG2	1:C:242:TRP:HD1	2.34	0.41
1:C:174:ASN:O	1:C:178:LEU:HG	2.21	0.41
1:D:76:PHE:CZ	1:D:208:ILE:HD13	2.56	0.41
1:D:148:VAL:CG2	1:D:155:ALA:HB3	2.44	0.41
1:D:267:LEU:O	1:D:267:LEU:HD23	2.20	0.41
1:A:76:PHE:HB2	1:C:212:ILE:HG13	2.03	0.41
1:A:114:VAL:H	1:A:114:VAL:HG22	1.49	0.41
1:B:175:GLU:OE2	1:B:225:ILE:HA	2.20	0.41
1:C:183:GLN:O	1:C:184:LEU:C	2.58	0.41
1:D:50:PHE:HB3	1:D:77:GLY:HA3	2.03	0.41
1:D:96:ALA:HB2	1:D:227:PRO:CD	2.40	0.41
1:D:136:THR:OG1	1:D:136:THR:O	2.37	0.41
1:A:177:TRP:HZ3	1:D:129:THR:OG1	2.03	0.40
1:A:202:GLU:HG2	1:A:203:ALA:N	2.36	0.40
1:A:213:ILE:HD12	1:A:213:ILE:HG23	1.88	0.40
1:B:62:LYS:HA	1:B:65:GLY:O	2.20	0.40
1:C:85:ALA:O	1:C:87:ARG:N	2.54	0.40
1:C:238:PHE:HB2	1:C:246:VAL:HG21	2.03	0.40
1:A:80:MET:HG2	1:C:185:CYS:SG	2.61	0.40
1:A:160:THR:HG21	1:A:224:ALA:HB2	2.03	0.40
1:B:76:PHE:HE1	1:B:204:LEU:HD12	1.87	0.40
1:B:165:HIS:ND1	1:C:137:ALA:HA	2.37	0.40
1:B:231:LEU:HA	1:B:234:ARG:HB3	2.04	0.40
1:C:32:LYS:HG3	1:C:34:VAL:HG22	2.02	0.40
1:C:158:PHE:HE2	1:C:236:PHE:CE2	2.39	0.40
1:B:272:TYR:CE1	1:B:275:PHE:CE1	3.09	0.40
1:C:48:MET:HE3	1:C:123:SER:CB	2.51	0.40
1:C:96:ALA:CB	1:C:227:PRO:HD2	2.39	0.40
1:C:162:LEU:HD11	1:C:250:GLY:CA	2.50	0.40
1:D:226:ASN:OD1	1:D:229:ARG:HB3	2.20	0.40
1:A:60:LEU:HD22	1:C:219:MET:SD	2.61	0.40
1:B:103:ALA:HB1	1:B:266:TYR:HD1	1.86	0.40
1:C:162:LEU:HA	1:C:163:PRO:HD3	1.76	0.40
1:A:270:ILE:O	1:A:274:VAL:HB	2.22	0.40
1:B:96:ALA:HB2	1:B:227:PRO:HD3	2.04	0.40
1:B:124:PHE:CE1	1:B:236:PHE:HD1	2.39	0.40
1:B:253:TRP:C	1:B:255:TRP:H	2.24	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:232:PRO:HG2	1:D:233:PRO:HD3	2.03	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	250/342 (73%)	185 (74%)	60 (24%)	5 (2%)	7	39
1	B	247/342 (72%)	176 (71%)	66 (27%)	5 (2%)	7	39
1	C	247/342 (72%)	174 (70%)	67 (27%)	6 (2%)	6	35
1	D	247/342 (72%)	189 (76%)	55 (22%)	3 (1%)	13	48
All	All	991/1368 (72%)	724 (73%)	248 (25%)	19 (2%)	8	40

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	95	ALA
1	A	86	GLY
1	C	86	GLY
1	A	95	ALA
1	B	254	TRP
1	C	240	ALA
1	A	32	LYS
1	A	110	ARG
1	B	221	THR
1	C	101	ASN
1	C	225	ILE
1	A	87	ARG
1	B	196	PRO
1	C	88	ILE

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Mol	Chain	Res	Type
1	D	56	ALA
1	B	88	ILE
1	B	225	ILE
1	D	196	PRO
1	D	69	GLY

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	195/278 (70%)	182 (93%)	13 (7%)	16	47
1	B	189/278 (68%)	178 (94%)	11 (6%)	20	52
1	C	191/278 (69%)	178 (93%)	13 (7%)	16	47
1	D	187/278 (67%)	173 (92%)	14 (8%)	13	43
All	All	762/1112 (68%)	711 (93%)	51 (7%)	16	47

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	PHE
1	A	80	MET
1	A	110	ARG
1	A	135	TYR
1	A	175	GLU
1	A	177	TRP
1	A	181	MET
1	A	187	PHE
1	A	191	ASP
1	A	231	LEU
1	A	254	TRP
1	A	255	TRP
1	A	275	PHE
1	B	32	LYS
1	B	80	MET
1	B	87	ARG

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Mol	Chain	Res	Type
1	B	112	PHE
1	B	166	MET
1	B	223	TYR
1	B	238	PHE
1	B	242	TRP
1	B	247	PHE
1	B	252	ASN
1	B	275	PHE
1	C	41	PHE
1	C	74	PHE
1	C	80	MET
1	C	120	PHE
1	C	124	PHE
1	C	131	TYR
1	C	135	TYR
1	C	141	PHE
1	C	147	MET
1	C	162	LEU
1	C	169	TRP
1	C	174	ASN
1	C	255	TRP
1	D	32	LYS
1	D	40	GLU
1	D	42	MET
1	D	45	TYR
1	D	80	MET
1	D	115	TYR
1	D	131	TYR
1	D	135	TYR
1	D	145	GLN
1	D	183	GLN
1	D	229	ARG
1	D	255	TRP
1	D	266	TYR
1	D	275	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	71	ASN
1	D	71	ASN
1	D	195	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 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	GOL	C	400	-	5,5,5	1.68	2 (40%)	5,5,5	0.67	0
2	GOL	A	401	-	5,5,5	1.50	1 (20%)	5,5,5	0.80	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	GOL	C	400	-	-	2/4/4/4	-
2	GOL	A	401	-	-	1/4/4/4	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	GOL	C3-C2	2.67	1.62	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	400	GOL	C3-C2	2.41	1.61	1.51
2	C	400	GOL	C1-C2	2.39	1.61	1.51

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

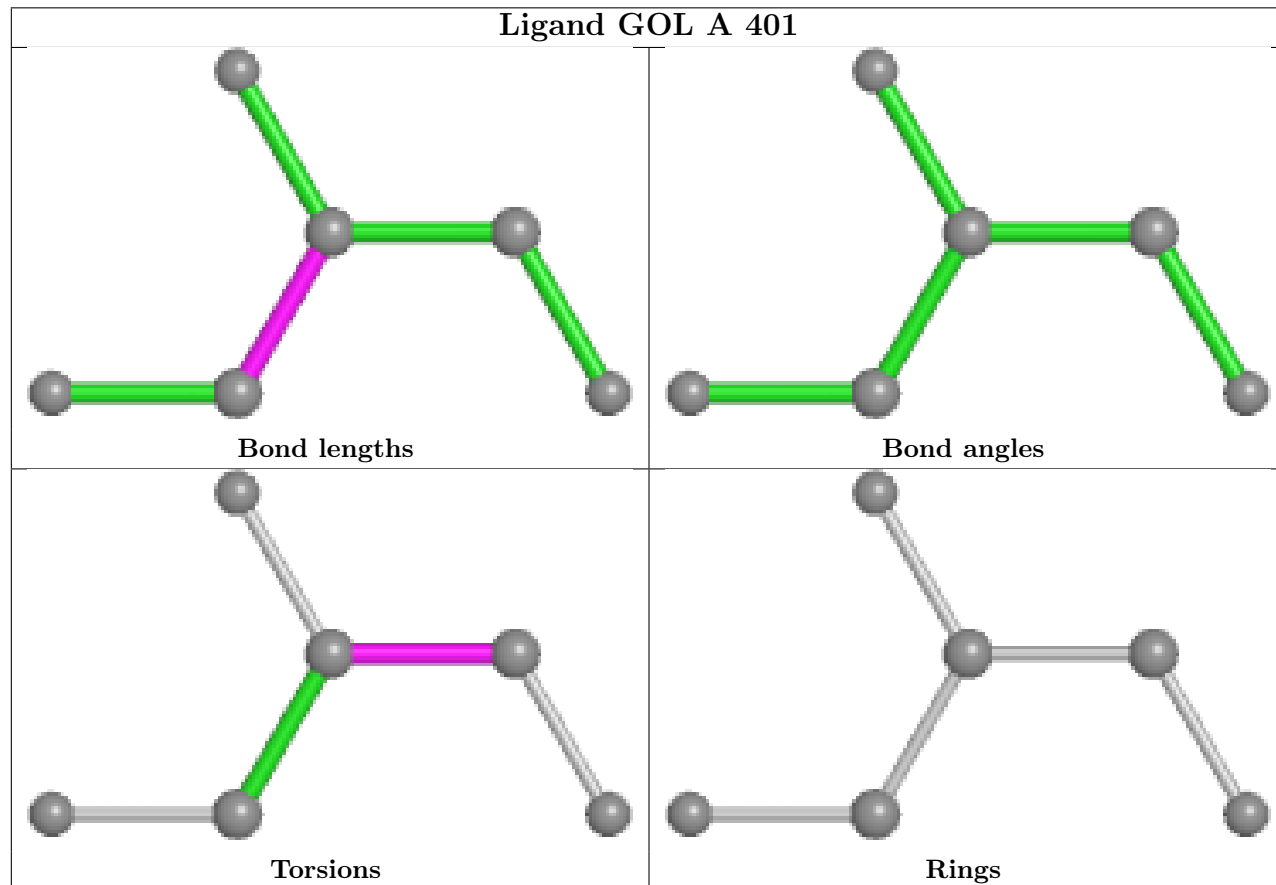
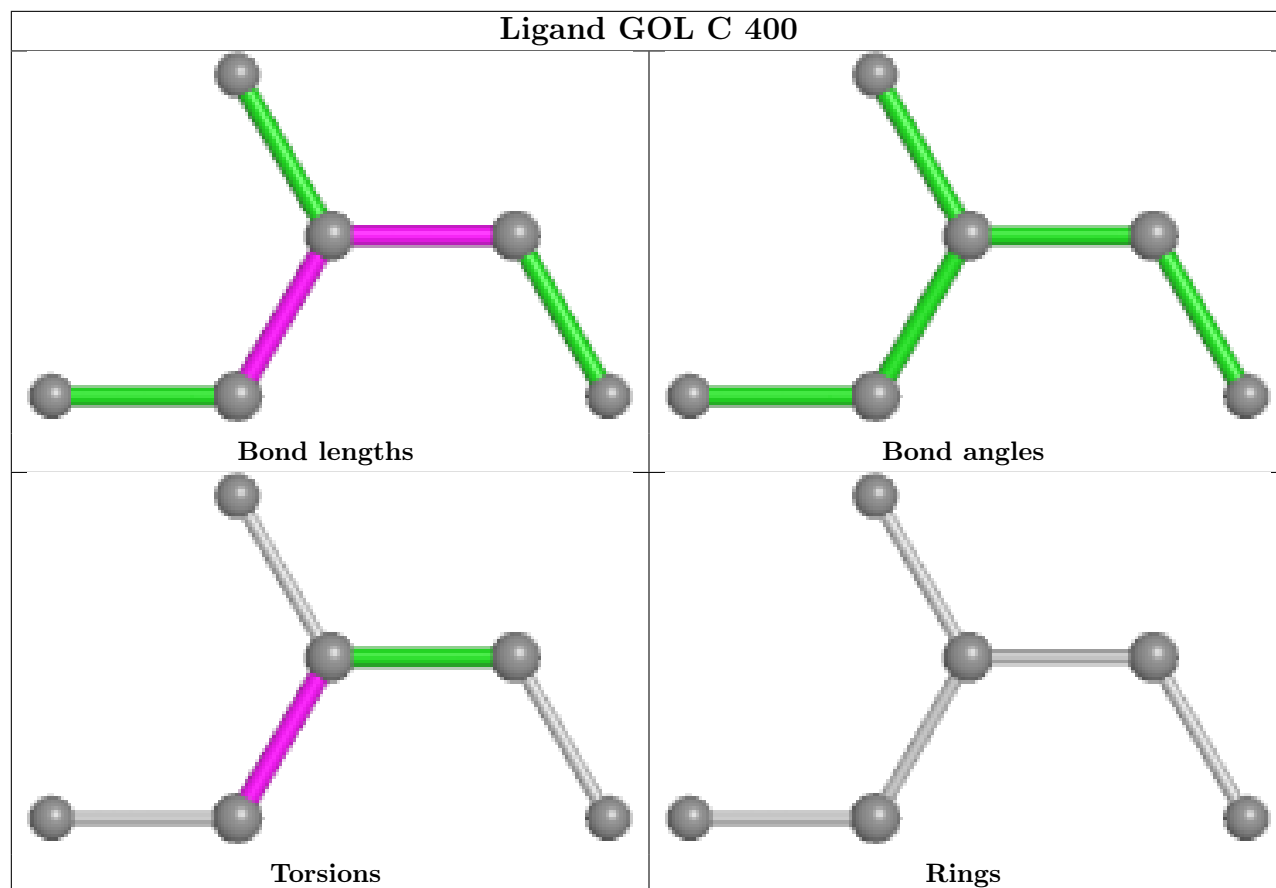
Mol	Chain	Res	Type	Atoms
2	C	400	GOL	C1-C2-C3-O3
2	C	400	GOL	O2-C2-C3-O3
2	A	401	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	400	GOL	1	0
2	A	401	GOL	1	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	252/342 (73%)	-0.09	8 (3%) 47 35	17, 71, 132, 174	0
1	B	249/342 (72%)	0.38	27 (10%) 5 4	60, 147, 218, 244	0
1	C	249/342 (72%)	-0.41	2 (0%) 86 78	8, 55, 121, 166	0
1	D	249/342 (72%)	0.41	22 (8%) 10 7	74, 153, 211, 252	0
All	All	999/1368 (73%)	0.07	59 (5%) 22 15	8, 102, 201, 252	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	278	SER	8.4
1	A	89	SER	6.5
1	D	277	GLY	6.4
1	B	238	PHE	4.9
1	B	246	VAL	4.7
1	D	89	SER	4.5
1	D	149	THR	4.5
1	B	237	THR	4.4
1	A	278	SER	4.3
1	A	88	ILE	4.3
1	D	252	ASN	4.2
1	B	277	GLY	4.2
1	B	239	ILE	4.0
1	D	167	THR	3.7
1	B	132	SER	3.7
1	D	224	ALA	3.6
1	D	278	SER	3.6
1	D	101	ASN	3.5
1	D	148	VAL	3.4
1	D	249	ASN	3.3
1	D	88	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	B	88	ILE	3.3
1	D	87	ARG	3.2
1	B	247	PHE	3.1
1	B	89	SER	3.1
1	B	240	ALA	3.1
1	B	140	HIS	3.0
1	B	161	TYR	2.9
1	D	230	ASP	2.9
1	D	242	TRP	2.9
1	D	86	GLY	2.7
1	A	160	THR	2.7
1	D	220	ASN	2.7
1	A	250	GLY	2.7
1	C	89	SER	2.6
1	B	139	LEU	2.6
1	D	162	LEU	2.6
1	B	165	HIS	2.5
1	B	241	GLY	2.5
1	B	146	LEU	2.5
1	B	110	ARG	2.4
1	A	277	GLY	2.4
1	B	242	TRP	2.4
1	D	106	ARG	2.4
1	B	134	PHE	2.4
1	B	113	PRO	2.3
1	A	249	ASN	2.3
1	C	66	SER	2.3
1	B	249	ASN	2.2
1	A	163	PRO	2.2
1	B	107	VAL	2.1
1	B	245	GLN	2.1
1	D	253	TRP	2.1
1	B	243	GLY	2.0
1	B	154	THR	2.0
1	B	135	TYR	2.0
1	D	180	GLY	2.0
1	D	153	ALA	2.0
1	D	105	GLY	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](#)

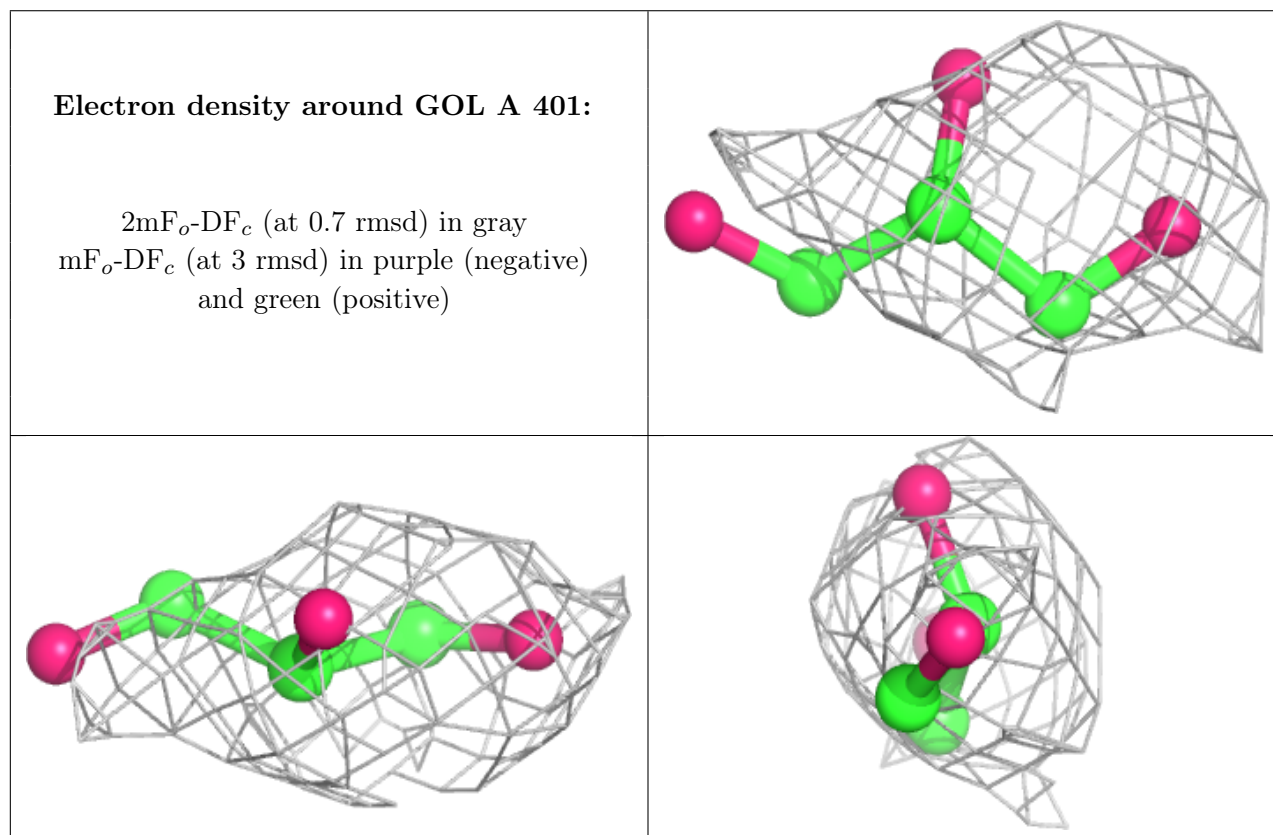
There are no monosaccharides in this entry.

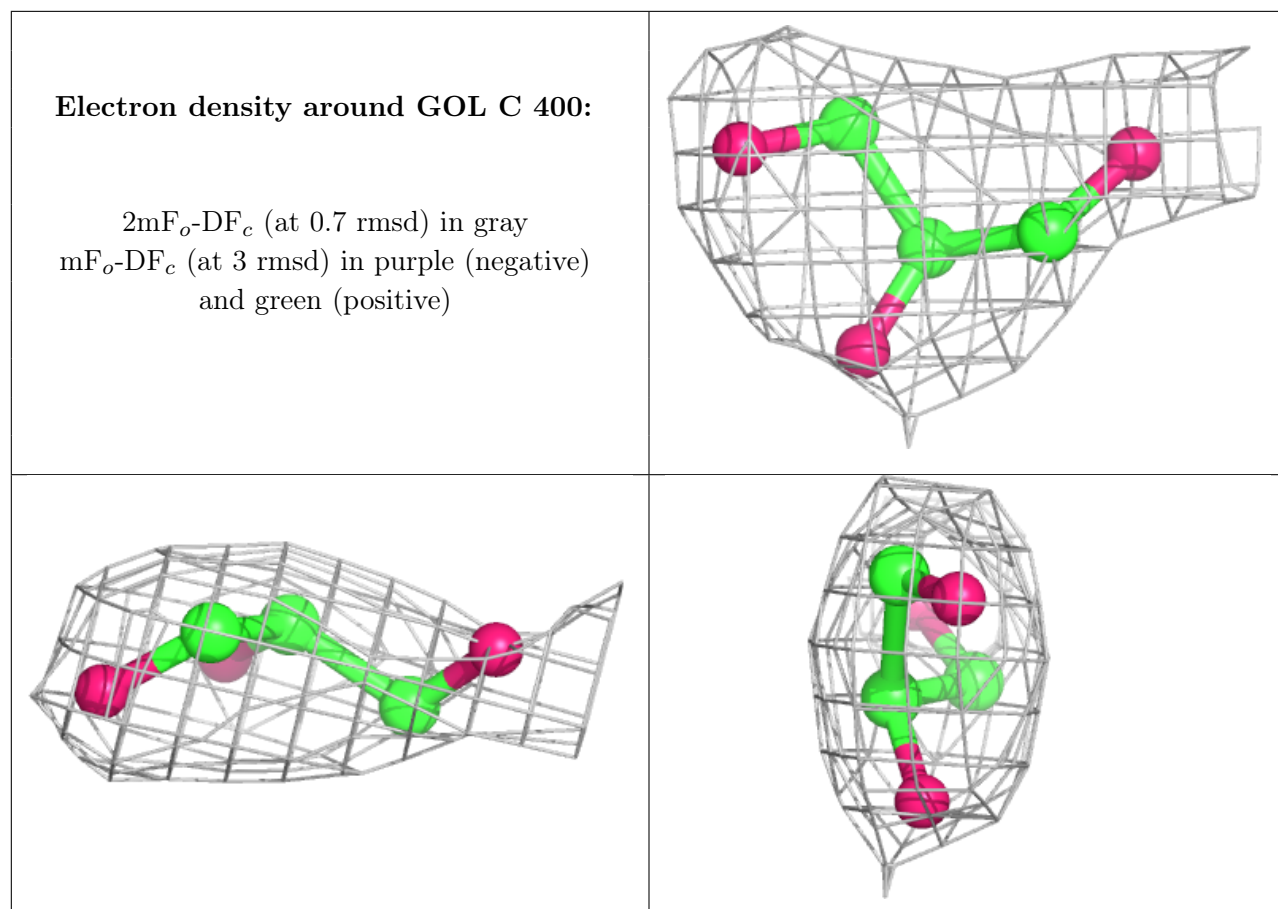
6.4 Ligands [i](#)

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. 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(Å ²)	Q<0.9
2	GOL	A	401	6/6	0.91	0.35	69,73,76,82	0
2	GOL	C	400	6/6	0.95	0.22	23,29,48,54	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.