



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 1, 2024 – 02:08 PM JST

PDB ID : 8ID1
Title : Crystal structure of N-Methyl-cis-4-hydroxy-L-proline dehydratase in *Intestinibacter bartlettii*
Authors : Jiang, L.; Zhang, Y.
Deposited on : 2023-02-11
Resolution : 3.12 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 : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

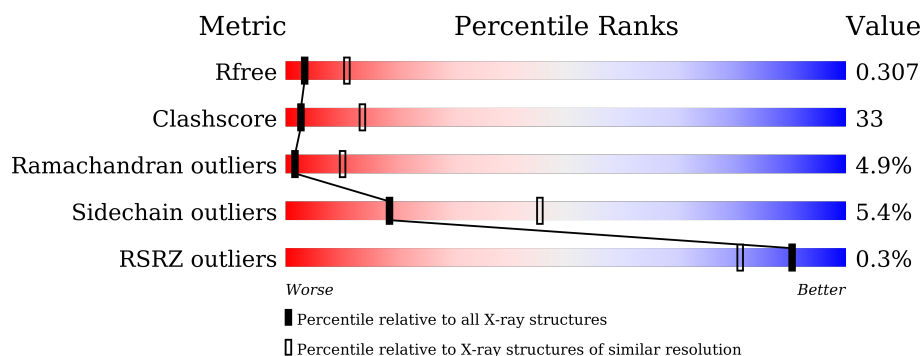
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.12 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}	164625	1668 (3.14-3.10)
Clashscore	180529	1788 (3.14-3.10)
Ramachandran outliers	177936	1696 (3.14-3.10)
Sidechain outliers	177891	1696 (3.14-3.10)
RSRZ outliers	164620	1668 (3.14-3.10)

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 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	792	<div> <div style="width: 48%; background-color: green;"></div> <div style="width: 44%; background-color: yellow;"></div> <div style="width: 6%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> <div style="width: 2%; background-color: grey;"></div> </div> <div>48% 44% 6% ..</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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	6IW	A	801	-	X	X	-

2 Entry composition [i](#)

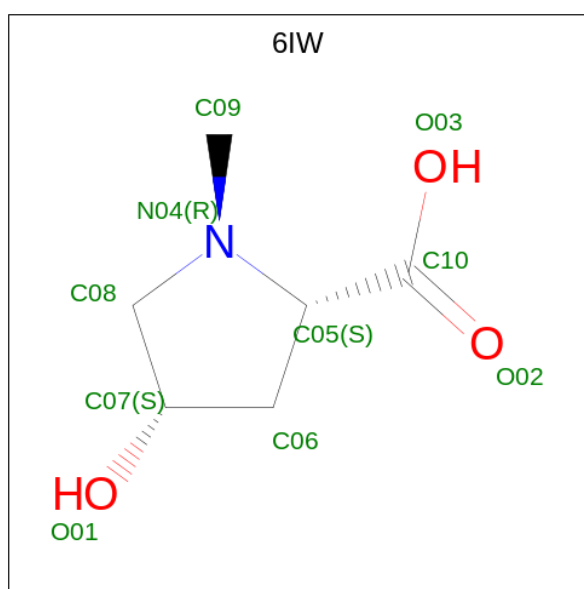
There are 2 unique types of molecules in this entry. The entry contains 6195 atoms, of which 10 are hydrogens and 0 are deuteriums.

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 Formate C-acetyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	780	6175	3924	1042	1172	37	0	0	0

- Molecule 2 is (2S,4S)-1-methyl-4-oxidanyl-pyrrolidine-2-carboxylic acid (three-letter code: 6IW) (formula: $C_6H_{11}NO_3$) (labeled as "Ligand of Interest" by depositor).

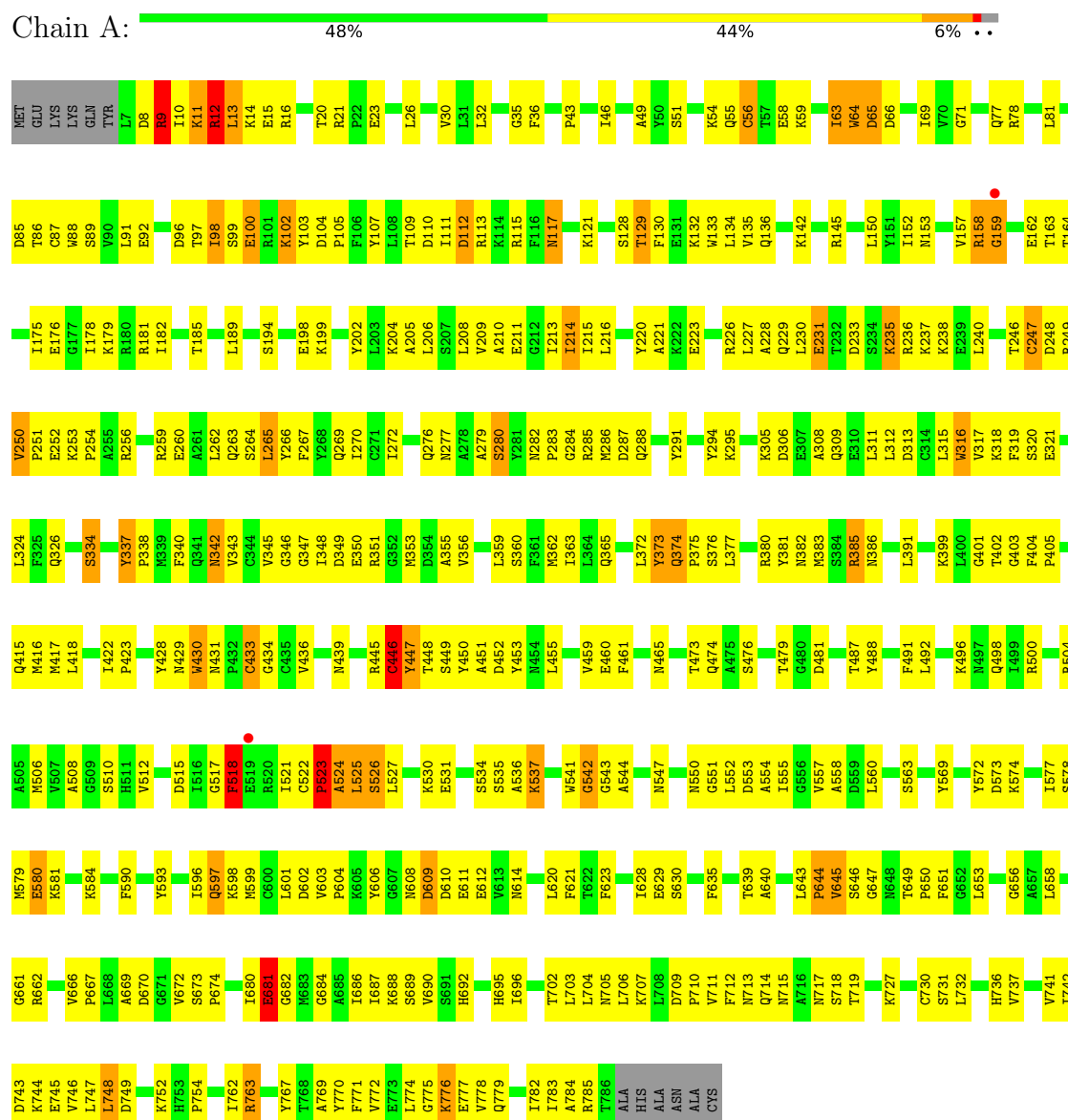


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	H	N	O		
2	A	1	20	6	10	1	3	0	0

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: Formate C-acetyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 21 2	Depositor
Cell constants a, b, c, α , β , γ	142.75Å 142.75Å 101.03Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.52 – 3.12 50.52 – 3.12	Depositor EDS
% Data completeness (in resolution range)	93.8 (50.52-3.12) 91.2 (50.52-3.12)	Depositor EDS
R_{merge}	0.24	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 3.13Å)	Xtriage
Refinement program	PHENIX 1.14	Depositor
R, R_{free}	0.211 , 0.309 0.211 , 0.307	Depositor DCC
R_{free} test set	17322 reflections (9.98%)	wwPDB-VP
Wilson B-factor (Å ²)	74.4	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 43.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6195	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.26% 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: 6IW

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	0.63	3/6295 (0.0%)	0.80	9/8497 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	446	CYS	CB-SG	-6.45	1.71	1.82
1	A	526	SER	C-O	-5.73	1.12	1.23
1	A	64	TRP	CB-CG	-5.62	1.40	1.50

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	522	CYS	C-N-CD	-19.85	76.94	120.60
1	A	15	GLU	N-CA-C	-8.10	89.14	111.00
1	A	748	LEU	CA-CB-CG	-7.57	97.90	115.30
1	A	373	TYR	C-N-CA	-7.28	103.49	121.70
1	A	158	ARG	NE-CZ-NH1	-6.48	117.06	120.30
1	A	523	PRO	N-CA-C	6.42	128.78	112.10
1	A	65	ASP	N-CA-C	6.32	128.06	111.00
1	A	158	ARG	NE-CZ-NH2	5.92	123.26	120.30
1	A	63	ILE	CG1-CB-CG2	-5.01	100.37	111.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6175	0	6138	401	0
2	A	10	10	0	6	0
All	All	6185	10	6138	401	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 33.

All (401) 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:158:ARG:NH2	2:A:801:6IW:O03	1.57	1.35
1:A:517:GLY:O	1:A:521:ILE:HG22	1.26	1.30
1:A:209:VAL:HG11	1:A:524:ALA:CB	1.73	1.18
1:A:158:ARG:NH2	2:A:801:6IW:C10	2.08	1.14
1:A:415:GLN:HG3	1:A:696:ILE:HD13	1.30	1.13
1:A:209:VAL:HG11	1:A:524:ALA:HB1	1.11	1.08
1:A:158:ARG:NH2	2:A:801:6IW:O02	1.87	1.02
1:A:164:THR:HG21	1:A:431:ASN:HD21	1.22	1.02
1:A:517:GLY:O	1:A:521:ILE:CG2	2.09	1.01
1:A:158:ARG:HH22	2:A:801:6IW:C10	1.71	1.00
1:A:164:THR:HG21	1:A:431:ASN:ND2	1.79	0.96
1:A:383:MET:CE	1:A:730:CYS:HB2	1.97	0.95
1:A:185:THR:HG21	1:A:534:SER:HA	1.47	0.93
1:A:35:GLY:HA3	1:A:51:SER:HB3	1.50	0.93
1:A:236:ARG:O	1:A:240:LEU:HD23	1.69	0.92
1:A:383:MET:HE3	1:A:730:CYS:HB2	1.52	0.91
1:A:743:ASP:HB2	1:A:746:VAL:HG23	1.54	0.87
1:A:249:ARG:NE	1:A:256:ARG:HD2	1.90	0.84
1:A:403:GLY:O	1:A:763:ARG:NH1	2.10	0.84
1:A:763:ARG:HD2	1:A:767:TYR:O	1.75	0.84
1:A:315:LEU:HD22	1:A:319:PHE:CE2	2.14	0.83
1:A:415:GLN:HA	1:A:418:LEU:HD12	1.61	0.82
1:A:383:MET:HE2	1:A:727:LYS:HA	1.59	0.82
1:A:347:GLY:HA3	1:A:380:ARG:NH1	1.96	0.81
1:A:130:PHE:CZ	1:A:134:LEU:HD11	2.15	0.81
1:A:246:THR:HG22	1:A:250:VAL:CG1	2.10	0.81
1:A:703:LEU:HA	1:A:736:HIS:CD2	2.15	0.80
1:A:351:ARG:NH1	1:A:353:MET:SD	2.54	0.80
1:A:681:GLU:OE1	1:A:682:GLY:N	2.15	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:THR:HG23	1:A:404:PHE:H	1.47	0.79
1:A:11:LYS:C	1:A:13:LEU:H	1.86	0.79
1:A:209:VAL:CG1	1:A:524:ALA:HB1	2.04	0.79
1:A:517:GLY:C	1:A:521:ILE:HG22	2.03	0.78
1:A:769:ALA:CB	1:A:774:LEU:HD11	2.14	0.78
1:A:653:LEU:O	1:A:653:LEU:HG	1.83	0.77
1:A:150:LEU:HD22	1:A:506:MET:HG2	1.67	0.77
1:A:703:LEU:HA	1:A:736:HIS:HD2	1.47	0.77
1:A:316:TRP:CD1	1:A:375:PRO:HG2	2.20	0.76
1:A:703:LEU:HD22	1:A:736:HIS:NE2	2.02	0.75
1:A:227:LEU:HB2	1:A:240:LEU:CD1	2.16	0.74
1:A:649:THR:HB	1:A:650:PRO:HD3	1.69	0.74
1:A:55:GLN:O	1:A:59:LYS:HB2	1.89	0.73
1:A:316:TRP:CG	1:A:375:PRO:HG2	2.23	0.73
1:A:349:ASP:OD1	1:A:350:GLU:N	2.22	0.72
1:A:453:TYR:CZ	1:A:554:ALA:HB2	2.23	0.72
1:A:383:MET:CE	1:A:727:LYS:HA	2.18	0.72
1:A:347:GLY:HA3	1:A:380:ARG:HH12	1.52	0.72
1:A:346:GLY:HA2	1:A:356:VAL:HG22	1.72	0.72
1:A:246:THR:HG23	1:A:260:GLU:HG2	1.71	0.72
1:A:769:ALA:HB1	1:A:774:LEU:HD11	1.71	0.71
1:A:313:ASP:O	1:A:317:VAL:HG23	1.90	0.71
1:A:320:SER:HA	1:A:374:GLN:HB3	1.72	0.71
1:A:383:MET:HE3	1:A:730:CYS:CB	2.21	0.71
1:A:445:ARG:HG2	1:A:446:CYS:N	2.04	0.70
1:A:451:ALA:HB3	1:A:506:MET:CE	2.21	0.70
1:A:383:MET:HE1	1:A:730:CYS:HB2	1.74	0.69
1:A:777:GLU:OE1	1:A:777:GLU:N	2.24	0.69
1:A:628:ILE:HD12	1:A:640:ALA:HB2	1.72	0.69
1:A:250:VAL:HG23	1:A:251:PRO:CD	2.23	0.69
1:A:92:GLU:OE2	1:A:121:LYS:NZ	2.21	0.69
1:A:263:GLN:HG3	1:A:267:PHE:CD2	2.28	0.69
1:A:433:CYS:SG	1:A:439:ASN:ND2	2.66	0.69
1:A:558:ALA:HB3	1:A:669:ALA:CB	2.23	0.69
1:A:249:ARG:HD3	1:A:256:ARG:NH1	2.08	0.68
1:A:102:LYS:H	1:A:102:LYS:HD2	1.58	0.68
1:A:382:ASN:N	1:A:386:ASN:OD1	2.19	0.67
1:A:227:LEU:HB2	1:A:240:LEU:HD12	1.74	0.67
1:A:417:MET:HE3	1:A:422:ILE:HD12	1.76	0.67
1:A:506:MET:HE2	1:A:552:LEU:HD22	1.74	0.67
1:A:288:GLN:NE2	1:A:355:ALA:O	2.26	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:359:LEU:HD13	1:A:359:LEU:O	1.94	0.67
1:A:459:VAL:HG12	1:A:658:LEU:HD22	1.77	0.66
1:A:262:LEU:HD22	1:A:315:LEU:HD12	1.78	0.66
1:A:453:TYR:OH	1:A:554:ALA:HB2	1.96	0.66
1:A:164:THR:HG23	1:A:439:ASN:OD1	1.96	0.66
1:A:451:ALA:HB3	1:A:506:MET:HE3	1.78	0.65
1:A:445:ARG:O	1:A:446:CYS:HB2	1.96	0.65
1:A:704:LEU:HD23	1:A:737:VAL:HG23	1.78	0.65
1:A:164:THR:CG2	1:A:431:ASN:HD21	2.02	0.65
1:A:704:LEU:H	1:A:736:HIS:CD2	2.15	0.65
1:A:672:VAL:HG22	1:A:703:LEU:O	1.97	0.64
1:A:318:LYS:O	1:A:321:GLU:HB2	1.97	0.63
1:A:460:GLU:OE2	1:A:656:GLY:N	2.30	0.63
1:A:9:ARG:HH11	1:A:9:ARG:HG2	1.63	0.63
1:A:315:LEU:HD22	1:A:319:PHE:CD2	2.34	0.63
1:A:762:ILE:HD13	1:A:771:PHE:CD1	2.33	0.63
1:A:23:GLU:HB3	1:A:107:TYR:HB3	1.81	0.63
1:A:558:ALA:HB3	1:A:669:ALA:HB2	1.81	0.63
1:A:762:ILE:HD13	1:A:771:PHE:HD1	1.64	0.63
1:A:508:ALA:O	1:A:512:VAL:HG23	1.97	0.62
1:A:102:LYS:H	1:A:102:LYS:CD	2.13	0.62
1:A:742:ILE:CD1	1:A:747:LEU:HD21	2.29	0.62
1:A:479:THR:HG21	1:A:498:GLN:HG2	1.80	0.62
1:A:402:THR:HG23	1:A:404:PHE:N	2.14	0.62
1:A:606:TYR:OH	1:A:690:VAL:HG22	2.00	0.62
1:A:10:ILE:HG23	1:A:10:ILE:O	2.00	0.62
1:A:401:GLY:HA2	1:A:741:VAL:HB	1.82	0.61
1:A:603:VAL:HG12	1:A:604:PRO:HD2	1.82	0.61
1:A:56:CYS:HB2	1:A:216:LEU:HB2	1.81	0.61
1:A:542:GLY:O	1:A:544:ALA:N	2.33	0.61
1:A:747:LEU:HD22	1:A:771:PHE:CE1	2.36	0.61
1:A:778:VAL:O	1:A:782:ILE:HG13	2.01	0.61
1:A:12:ARG:C	1:A:14:LYS:H	2.02	0.61
1:A:603:VAL:CG1	1:A:604:PRO:HD2	2.31	0.61
1:A:247:CYS:HA	1:A:250:VAL:HG21	1.81	0.60
1:A:238:LYS:O	1:A:238:LYS:HG2	2.00	0.60
1:A:249:ARG:HE	1:A:256:ARG:HD2	1.63	0.60
1:A:250:VAL:CG2	1:A:251:PRO:HD3	2.31	0.60
1:A:455:LEU:HD22	1:A:560:LEU:CD1	2.31	0.60
1:A:645:VAL:HG21	2:A:801:6IW:C09	2.31	0.60
1:A:680:ILE:HD12	1:A:681:GLU:N	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:712:PHE:CE2	1:A:718:SER:HB2	2.38	0.59
1:A:246:THR:O	1:A:248:ASP:N	2.36	0.59
1:A:628:ILE:CD1	1:A:640:ALA:HB2	2.31	0.59
1:A:346:GLY:HA2	1:A:356:VAL:CG2	2.31	0.59
1:A:249:ARG:NH1	1:A:253:LYS:HE3	2.18	0.59
1:A:645:VAL:CG2	2:A:801:6IW:C09	2.81	0.59
1:A:107:TYR:CE2	1:A:109:THR:HA	2.37	0.59
1:A:555:ILE:HG21	1:A:644:PRO:HA	1.85	0.59
1:A:670:ASP:OD1	1:A:673:SER:OG	2.19	0.58
1:A:11:LYS:C	1:A:13:LEU:N	2.53	0.58
1:A:517:GLY:HA2	1:A:521:ILE:CG2	2.34	0.58
1:A:16:ARG:HG3	1:A:16:ARG:HH11	1.68	0.58
1:A:107:TYR:HE2	1:A:109:THR:HA	1.67	0.58
1:A:521:ILE:HG23	1:A:521:ILE:O	2.02	0.58
1:A:164:THR:HG22	1:A:282:ASN:HB2	1.86	0.57
1:A:359:LEU:CD1	1:A:363:ILE:HD11	2.34	0.57
1:A:250:VAL:HG23	1:A:251:PRO:HD3	1.86	0.57
1:A:359:LEU:O	1:A:363:ILE:HG13	2.04	0.57
1:A:291:TYR:OH	1:A:295:LYS:HD2	2.04	0.57
1:A:743:ASP:HB3	1:A:745:GLU:HG2	1.86	0.57
1:A:309:GLN:OE1	1:A:365:GLN:HG2	2.05	0.57
1:A:488:TYR:O	1:A:491:PHE:HB3	2.05	0.57
1:A:687:ILE:HG22	1:A:732:LEU:HD13	1.87	0.57
1:A:276:GLN:O	1:A:277:ASN:HB3	2.03	0.57
1:A:282:ASN:HD22	1:A:342:ASN:H	1.52	0.57
1:A:9:ARG:H	1:A:9:ARG:HD3	1.69	0.57
1:A:130:PHE:CE2	1:A:134:LEU:HD11	2.40	0.57
1:A:102:LYS:HD2	1:A:102:LYS:N	2.21	0.56
1:A:577:ILE:HG22	1:A:578:SER:O	2.05	0.56
1:A:500:ARG:O	1:A:504:ARG:HG3	2.04	0.56
1:A:779:GLN:O	1:A:783:ILE:HD13	2.06	0.56
1:A:176:GLU:HB2	1:A:252:GLU:O	2.06	0.56
1:A:742:ILE:HD11	1:A:747:LEU:HD21	1.87	0.56
1:A:246:THR:HG22	1:A:250:VAL:HG11	1.87	0.56
1:A:287:ASP:HA	1:A:359:LEU:HD12	1.87	0.56
1:A:492:LEU:HG	1:A:496:LYS:HE3	1.87	0.56
1:A:666:VAL:HG13	1:A:667:PRO:HD2	1.87	0.56
1:A:643:LEU:HD12	1:A:643:LEU:O	2.06	0.55
1:A:69:ILE:O	1:A:318:LYS:HD2	2.07	0.55
1:A:279:ALA:O	1:A:280:SER:HB2	2.06	0.55
1:A:666:VAL:HG12	1:A:667:PRO:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:209:VAL:CG1	1:A:524:ALA:CB	2.67	0.55
1:A:214:ILE:HD12	1:A:252:GLU:HB2	1.89	0.55
1:A:399:LYS:HZ3	1:A:719:THR:HG1	1.50	0.55
1:A:417:MET:CE	1:A:422:ILE:HD12	2.37	0.55
1:A:649:THR:HG23	1:A:667:PRO:HG3	1.88	0.55
1:A:599:MET:O	1:A:603:VAL:HG23	2.07	0.55
1:A:209:VAL:O	1:A:213:ILE:HG13	2.06	0.55
1:A:415:GLN:HG3	1:A:696:ILE:CD1	2.19	0.55
1:A:381:TYR:CE1	1:A:391:LEU:HD13	2.42	0.55
1:A:49:ALA:HB1	1:A:209:VAL:HG23	1.88	0.55
1:A:680:ILE:HD12	1:A:680:ILE:C	2.27	0.55
1:A:747:LEU:HD22	1:A:771:PHE:CD1	2.42	0.55
1:A:97:THR:O	1:A:100:GLU:N	2.33	0.54
1:A:250:VAL:CB	1:A:251:PRO:HD3	2.37	0.54
1:A:11:LYS:O	1:A:11:LYS:HG2	2.05	0.54
1:A:10:ILE:O	1:A:13:LEU:CD1	2.55	0.54
1:A:97:THR:O	1:A:99:SER:N	2.40	0.54
1:A:447:TYR:HB2	1:A:550:ASN:OD1	2.06	0.54
1:A:449:SER:OG	1:A:553:ASP:OD1	2.15	0.54
1:A:601:LEU:HD21	1:A:661:GLY:HA3	1.88	0.54
1:A:551:GLY:O	1:A:552:LEU:HD23	2.08	0.54
1:A:687:ILE:HG22	1:A:732:LEU:CD1	2.37	0.54
1:A:263:GLN:HG3	1:A:267:PHE:CE2	2.44	0.53
1:A:401:GLY:CA	1:A:741:VAL:HB	2.38	0.53
1:A:277:ASN:CG	1:A:277:ASN:O	2.47	0.53
1:A:372:LEU:HD22	1:A:770:TYR:OH	2.07	0.53
1:A:10:ILE:O	1:A:13:LEU:HD13	2.08	0.53
1:A:221:ALA:HB2	1:A:247:CYS:HB2	1.89	0.53
1:A:578:SER:HG	1:A:581:LYS:HG3	1.74	0.53
1:A:175:ILE:CD1	1:A:175:ILE:N	2.70	0.53
1:A:250:VAL:HB	1:A:251:PRO:HD3	1.91	0.53
1:A:674:PRO:HG2	1:A:686:ILE:CD1	2.38	0.53
1:A:754:PRO:O	1:A:772:VAL:HG11	2.09	0.53
1:A:246:THR:HG22	1:A:250:VAL:HG13	1.89	0.53
1:A:132:LYS:O	1:A:136:GLN:HG3	2.09	0.53
1:A:96:ASP:N	1:A:96:ASP:OD1	2.41	0.52
1:A:620:LEU:O	1:A:623:PHE:HB3	2.09	0.52
1:A:517:GLY:CA	1:A:521:ILE:CG2	2.87	0.52
1:A:776:LYS:HD2	1:A:779:GLN:OE1	2.09	0.52
1:A:11:LYS:HD3	1:A:11:LYS:N	2.23	0.52
1:A:555:ILE:HG21	1:A:644:PRO:CA	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:ASN:O	1:A:609:ASP:HB3	2.09	0.52
1:A:86:THR:O	1:A:128:SER:HB2	2.09	0.52
1:A:695:HIS:CD2	1:A:702:THR:HG21	2.45	0.52
1:A:604:PRO:HB3	1:A:610:ASP:OD2	2.10	0.52
1:A:709:ASP:CG	1:A:710:PRO:HD2	2.30	0.52
1:A:228:ALA:O	1:A:230:LEU:N	2.43	0.52
1:A:88:TRP:CG	1:A:89:SER:N	2.78	0.51
1:A:517:GLY:HA2	1:A:521:ILE:HG21	1.90	0.51
1:A:11:LYS:O	1:A:13:LEU:N	2.43	0.51
1:A:614:ASN:HB3	1:A:692:HIS:CG	2.45	0.51
1:A:455:LEU:HD22	1:A:560:LEU:HD11	1.92	0.51
1:A:16:ARG:HG3	1:A:16:ARG:NH1	2.26	0.51
1:A:707:LYS:HD2	1:A:785:ARG:HB2	1.92	0.51
1:A:227:LEU:HB2	1:A:240:LEU:HD11	1.89	0.51
1:A:705:ASN:O	1:A:706:LEU:HD23	2.10	0.51
1:A:709:ASP:OD2	1:A:711:VAL:HG22	2.10	0.51
1:A:744:LYS:HE3	1:A:783:ILE:HG23	1.93	0.51
1:A:263:GLN:O	1:A:267:PHE:HB2	2.10	0.50
1:A:85:ASP:OD1	1:A:85:ASP:N	2.43	0.50
1:A:611:GLU:HG3	1:A:612:GLU:H	1.76	0.50
1:A:43:PRO:O	1:A:46:ILE:N	2.39	0.50
1:A:11:LYS:O	1:A:14:LYS:HG2	2.12	0.50
1:A:214:ILE:HD11	1:A:252:GLU:HA	1.94	0.50
1:A:227:LEU:CB	1:A:240:LEU:HD11	2.42	0.50
1:A:709:ASP:OD1	1:A:710:PRO:HD2	2.11	0.50
1:A:231:GLU:HB2	1:A:237:LYS:HG3	1.94	0.50
1:A:707:LYS:HD3	1:A:785:ARG:O	2.12	0.50
1:A:175:ILE:N	1:A:175:ILE:HD12	2.26	0.49
1:A:175:ILE:O	1:A:179:LYS:HG3	2.11	0.49
1:A:459:VAL:CG1	1:A:658:LEU:HD22	2.42	0.49
1:A:12:ARG:C	1:A:14:LYS:N	2.65	0.49
1:A:233:ASP:OD2	1:A:235:LYS:HB2	2.12	0.49
1:A:284:GLY:O	1:A:286:MET:N	2.44	0.49
1:A:9:ARG:HG2	1:A:9:ARG:NH1	2.27	0.49
1:A:16:ARG:O	1:A:20:THR:OG1	2.30	0.49
1:A:593:TYR:N	1:A:593:TYR:CD2	2.80	0.49
1:A:117:ASN:HA	1:A:121:LYS:HB3	1.93	0.49
1:A:282:ASN:ND2	1:A:434:GLY:H	2.10	0.49
1:A:686:ILE:HG21	1:A:706:LEU:HD21	1.94	0.49
1:A:163:THR:HA	1:A:439:ASN:ND2	2.28	0.48
1:A:283:PRO:HB2	1:A:286:MET:CE	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:267:PHE:O	1:A:270:ILE:HG12	2.13	0.48
1:A:451:ALA:HB3	1:A:506:MET:HE1	1.94	0.48
1:A:54:LYS:HE3	1:A:58:GLU:OE2	2.14	0.48
1:A:294:TYR:OH	1:A:362:MET:CE	2.62	0.48
1:A:662:ARG:NH1	1:A:666:VAL:O	2.47	0.48
1:A:517:GLY:CA	1:A:521:ILE:HG22	2.44	0.48
1:A:199:LYS:HB3	1:A:536:ALA:CB	2.44	0.48
1:A:334:SER:HA	1:A:646:SER:HB3	1.96	0.48
1:A:487:THR:O	1:A:572:TYR:CE1	2.66	0.48
1:A:551:GLY:HA2	1:A:639:THR:O	2.14	0.48
1:A:741:VAL:O	1:A:741:VAL:HG12	2.14	0.48
1:A:71:GLY:HA2	1:A:220:TYR:CE2	2.49	0.47
1:A:429:ASN:O	1:A:430:TRP:C	2.52	0.47
1:A:312:LEU:HD12	1:A:312:LEU:H	1.79	0.47
1:A:712:PHE:C	1:A:714:GLN:H	2.17	0.47
1:A:555:ILE:HG21	1:A:644:PRO:HB3	1.95	0.47
1:A:315:LEU:CD2	1:A:319:PHE:CE2	2.92	0.47
1:A:305:LYS:O	1:A:308:ALA:HB3	2.14	0.47
1:A:145:ARG:NH1	1:A:153:ASN:HD21	2.13	0.47
1:A:337:TYR:N	1:A:338:PRO:HD3	2.30	0.47
1:A:294:TYR:OH	1:A:362:MET:HE1	2.14	0.47
1:A:518:PHE:CE2	1:A:541:TRP:HA	2.49	0.47
1:A:611:GLU:HG3	1:A:612:GLU:N	2.29	0.47
1:A:684:GLY:O	1:A:688:LYS:HG3	2.15	0.47
1:A:102:LYS:CD	1:A:102:LYS:N	2.77	0.46
1:A:517:GLY:CA	1:A:521:ILE:HG21	2.46	0.46
1:A:30:VAL:HG21	1:A:115:ARG:HD2	1.97	0.46
1:A:185:THR:O	1:A:189:LEU:HD13	2.16	0.46
1:A:228:ALA:C	1:A:230:LEU:H	2.18	0.46
1:A:557:VAL:HG13	1:A:621:PHE:CZ	2.50	0.46
1:A:647:GLY:O	1:A:651:PHE:HB2	2.15	0.46
1:A:747:LEU:HD13	1:A:783:ILE:HD12	1.97	0.46
1:A:13:LEU:HD22	1:A:66:ASP:OD2	2.16	0.46
1:A:86:THR:HG21	1:A:276:GLN:OE1	2.16	0.46
1:A:445:ARG:CG	1:A:446:CYS:N	2.76	0.46
1:A:599:MET:HA	1:A:602:ASP:HB2	1.97	0.46
1:A:449:SER:CB	1:A:553:ASP:OD1	2.63	0.46
1:A:687:ILE:CG2	1:A:732:LEU:HD12	2.46	0.46
1:A:769:ALA:HB1	1:A:774:LEU:CD1	2.44	0.46
1:A:96:ASP:HB3	1:A:113:ARG:HH22	1.81	0.46
1:A:164:THR:CG2	1:A:439:ASN:OD1	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:181:ARG:NH2	1:A:530:LYS:HD3	2.31	0.46
1:A:763:ARG:HD2	1:A:763:ARG:HA	1.69	0.46
1:A:133:TRP:CZ2	1:A:152:ILE:HG21	2.51	0.46
1:A:266:TYR:O	1:A:270:ILE:HG23	2.16	0.46
1:A:152:ILE:HG12	1:A:451:ALA:CB	2.45	0.46
1:A:763:ARG:CD	1:A:767:TYR:O	2.58	0.45
1:A:320:SER:HA	1:A:374:GLN:CB	2.45	0.45
1:A:269:GLN:O	1:A:272:ILE:HG12	2.17	0.45
1:A:383:MET:HE2	1:A:727:LYS:CA	2.39	0.45
1:A:710:PRO:C	1:A:712:PHE:H	2.20	0.45
1:A:286:MET:HE3	1:A:343:VAL:HG22	1.99	0.45
1:A:11:LYS:HA	1:A:13:LEU:HD13	1.98	0.45
1:A:316:TRP:CH2	1:A:363:ILE:HG23	2.51	0.45
1:A:145:ARG:HH11	1:A:153:ASN:HD21	1.64	0.45
1:A:178:ILE:HG21	1:A:527:LEU:HD22	1.99	0.45
1:A:265:LEU:C	1:A:265:LEU:HD23	2.36	0.45
1:A:547:ASN:HB3	1:A:635:PHE:HB3	1.99	0.45
1:A:198:GLU:H	1:A:198:GLU:HG3	1.61	0.45
1:A:359:LEU:HD11	1:A:363:ILE:HD11	1.99	0.45
1:A:158:ARG:O	1:A:159:GLY:O	2.35	0.45
1:A:202:TYR:O	1:A:205:ALA:N	2.50	0.45
1:A:311:LEU:HA	1:A:311:LEU:HD23	1.73	0.45
1:A:359:LEU:HD13	1:A:363:ILE:HG13	1.99	0.45
1:A:747:LEU:HD13	1:A:783:ILE:CD1	2.48	0.44
1:A:81:LEU:HD23	1:A:81:LEU:HA	1.72	0.44
1:A:87:CYS:O	1:A:87:CYS:SG	2.75	0.44
1:A:63:ILE:HD13	1:A:223:GLU:HG2	1.98	0.44
1:A:305:LYS:HG3	1:A:362:MET:HE1	1.99	0.44
1:A:374:GLN:HA	1:A:374:GLN:NE2	2.32	0.44
1:A:749:ASP:O	1:A:752:LYS:HB2	2.18	0.44
1:A:204:LYS:HE3	1:A:208:LEU:HD21	1.99	0.44
1:A:150:LEU:HD22	1:A:506:MET:CG	2.41	0.44
1:A:253:LYS:HB3	1:A:254:PRO:CD	2.47	0.44
1:A:569:TYR:O	1:A:574:LYS:HB2	2.16	0.44
1:A:259:ARG:HG2	1:A:311:LEU:HD11	2.00	0.44
1:A:157:VAL:HG23	1:A:158:ARG:HG3	2.00	0.44
1:A:209:VAL:HG21	1:A:524:ALA:HB2	2.00	0.44
1:A:227:LEU:CB	1:A:240:LEU:CD1	2.92	0.44
1:A:449:SER:OG	1:A:449:SER:O	2.35	0.44
1:A:535:SER:O	1:A:536:ALA:HB3	2.17	0.44
1:A:465:ASN:HB2	1:A:481:ASP:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:LEU:O	1:A:91:LEU:HD23	2.19	0.43
1:A:687:ILE:HG21	1:A:732:LEU:HD12	2.00	0.43
1:A:26:LEU:O	1:A:30:VAL:HG23	2.18	0.43
1:A:334:SER:HB3	1:A:645:VAL:HG11	1.99	0.43
1:A:337:TYR:N	1:A:338:PRO:CD	2.81	0.43
1:A:237:LYS:HE2	1:A:237:LYS:HB3	1.76	0.43
1:A:162:GLU:HG2	1:A:448:THR:OG1	2.19	0.43
1:A:710:PRO:HG3	1:A:743:ASP:OD1	2.18	0.43
1:A:182:ILE:HD13	1:A:206:LEU:HB3	2.01	0.43
1:A:348:ILE:HD13	1:A:385:ARG:HG3	2.00	0.43
1:A:428:TYR:CE2	1:A:429:ASN:OD1	2.72	0.43
1:A:228:ALA:O	1:A:231:GLU:HB2	2.18	0.43
1:A:103:TYR:OH	1:A:777:GLU:HB2	2.18	0.43
1:A:105:PRO:HD2	1:A:337:TYR:OH	2.19	0.43
1:A:228:ALA:O	1:A:231:GLU:N	2.48	0.43
1:A:86:THR:HA	1:A:129:THR:HB	2.01	0.42
1:A:142:LYS:CG	1:A:145:ARG:HH21	2.32	0.42
1:A:645:VAL:HB	1:A:646:SER:H	1.71	0.42
1:A:142:LYS:HG3	1:A:145:ARG:HH21	1.83	0.42
1:A:523:PRO:HB3	1:A:525:LEU:H	1.83	0.42
1:A:531:GLU:H	1:A:531:GLU:HG2	1.66	0.42
1:A:535:SER:HB3	1:A:537:LYS:HB2	2.01	0.42
1:A:769:ALA:HB3	1:A:774:LEU:HD11	1.98	0.42
1:A:251:PRO:O	1:A:252:GLU:C	2.57	0.42
1:A:416:MET:HE2	1:A:695:HIS:O	2.18	0.42
1:A:628:ILE:O	1:A:630:SER:N	2.53	0.42
1:A:77:GLN:O	1:A:78:ARG:C	2.57	0.42
1:A:175:ILE:HG23	1:A:210:ALA:HB1	2.01	0.42
1:A:579:MET:O	1:A:581:LYS:N	2.53	0.42
1:A:417:MET:HG3	1:A:430:TRP:CB	2.49	0.42
1:A:748:LEU:HA	1:A:748:LEU:HD23	1.60	0.42
1:A:111:ILE:HG13	1:A:112:ASP:N	2.35	0.42
1:A:133:TRP:CH2	1:A:152:ILE:HG21	2.54	0.42
1:A:150:LEU:HB2	1:A:452:ASP:O	2.19	0.42
1:A:249:ARG:O	1:A:250:VAL:C	2.58	0.42
1:A:250:VAL:CG2	1:A:251:PRO:CD	2.92	0.42
1:A:450:TYR:CE2	1:A:510:SER:HA	2.55	0.42
1:A:338:PRO:HG2	1:A:340:PHE:CE2	2.54	0.42
1:A:666:VAL:CG1	1:A:667:PRO:N	2.83	0.42
1:A:152:ILE:O	1:A:152:ILE:HG22	2.20	0.42
1:A:422:ILE:HG23	1:A:423:PRO:HD2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:ILE:C	1:A:598:LYS:N	2.73	0.42
1:A:601:LEU:CD2	1:A:661:GLY:HA3	2.50	0.42
1:A:348:ILE:HD12	1:A:348:ILE:HA	1.90	0.41
1:A:103:TYR:CE1	1:A:775:GLY:HA3	2.55	0.41
1:A:265:LEU:HD23	1:A:266:TYR:N	2.35	0.41
1:A:584:LYS:HD2	1:A:584:LYS:HA	1.80	0.41
1:A:596:ILE:O	1:A:598:LYS:N	2.53	0.41
1:A:35:GLY:CA	1:A:51:SER:HB3	2.36	0.41
1:A:305:LYS:HE2	1:A:305:LYS:HB3	1.71	0.41
1:A:318:LYS:HE2	1:A:321:GLU:OE2	2.20	0.41
1:A:461:PHE:O	1:A:465:ASN:N	2.53	0.41
1:A:356:VAL:HG13	1:A:360:SER:HB2	2.02	0.41
1:A:13:LEU:CD2	1:A:66:ASP:OD2	2.69	0.41
1:A:246:THR:C	1:A:248:ASP:H	2.24	0.41
1:A:596:ILE:HD12	1:A:596:ILE:N	2.35	0.41
1:A:97:THR:O	1:A:98:ILE:C	2.58	0.41
1:A:152:ILE:O	1:A:152:ILE:CG2	2.69	0.41
1:A:181:ARG:HH21	1:A:530:LYS:HD3	1.85	0.41
1:A:11:LYS:C	1:A:11:LYS:HD3	2.41	0.41
1:A:32:LEU:HD13	1:A:36:PHE:CD1	2.55	0.41
1:A:158:ARG:HD2	1:A:324:LEU:HD11	2.02	0.41
1:A:158:ARG:HD3	1:A:326:GLN:HG2	2.03	0.41
1:A:211:GLU:O	1:A:215:ILE:HG13	2.21	0.41
1:A:579:MET:O	1:A:580:GLU:C	2.59	0.41
1:A:453:TYR:CE1	1:A:554:ALA:HB2	2.55	0.41
1:A:473:THR:HG22	1:A:474:GLN:N	2.36	0.41
1:A:590:PHE:CG	1:A:597:GLN:HB2	2.56	0.41
1:A:64:TRP:O	1:A:66:ASP:N	2.54	0.41
1:A:133:TRP:CZ2	1:A:152:ILE:CG2	3.03	0.41
1:A:135:VAL:O	1:A:135:VAL:HG12	2.21	0.41
1:A:603:VAL:HG12	1:A:604:PRO:CD	2.50	0.40
1:A:783:ILE:HG22	1:A:784:ALA:N	2.35	0.40
1:A:312:LEU:HD12	1:A:312:LEU:N	2.37	0.40
1:A:362:MET:HA	1:A:365:GLN:HB3	2.03	0.40
1:A:506:MET:HE2	1:A:506:MET:HB3	1.92	0.40
1:A:695:HIS:NE2	1:A:702:THR:HG21	2.35	0.40
1:A:14:LYS:HB3	1:A:317:VAL:HG11	2.03	0.40
1:A:345:VAL:HG11	1:A:363:ILE:HB	2.01	0.40
1:A:460:GLU:HG2	1:A:460:GLU:O	2.21	0.40
1:A:715:ASN:C	1:A:717:ASN:H	2.25	0.40
1:A:134:LEU:HD23	1:A:134:LEU:HA	1.54	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:287:ASP:HB3	1:A:345:VAL:HG12	2.03	0.40
1:A:551:GLY:C	1:A:552:LEU:HD23	2.42	0.40
1:A:717:ASN:O	1:A:718:SER:C	2.60	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	778/792 (98%)	646 (83%)	94 (12%)	38 (5%)	2	10

All (38) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	ARG
1	A	12	ARG
1	A	65	ASP
1	A	110	ASP
1	A	250	VAL
1	A	446	CYS
1	A	518	PHE
1	A	523	PRO
1	A	580	GLU
1	A	98	ILE
1	A	159	GLY
1	A	229	GLN
1	A	247	CYS
1	A	285	ARG
1	A	334	SER
1	A	337	TYR
1	A	376	SER
1	A	524	ALA

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Mol	Chain	Res	Type
1	A	543	GLY
1	A	645	VAL
1	A	194	SER
1	A	430	TRP
1	A	597	GLN
1	A	609	ASP
1	A	629	GLU
1	A	713	ASN
1	A	129	THR
1	A	265	LEU
1	A	681	GLU
1	A	280	SER
1	A	385	ARG
1	A	573	ASP
1	A	644	PRO
1	A	13	LEU
1	A	374	GLN
1	A	436	VAL
1	A	542	GLY
1	A	214	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	667/678 (98%)	631 (95%)	36 (5%)	18	45

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	8	ASP
1	A	9	ARG
1	A	11	LYS
1	A	12	ARG
1	A	21	ARG
1	A	56	CYS

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Mol	Chain	Res	Type
1	A	100	GLU
1	A	102	LYS
1	A	104	ASP
1	A	112	ASP
1	A	117	ASN
1	A	226	ARG
1	A	231	GLU
1	A	235	LYS
1	A	264	SER
1	A	306	ASP
1	A	316	TRP
1	A	342	ASN
1	A	373	TYR
1	A	377	LEU
1	A	405	PRO
1	A	433	CYS
1	A	447	TYR
1	A	476	SER
1	A	515	ASP
1	A	518	PHE
1	A	523	PRO
1	A	525	LEU
1	A	526	SER
1	A	537	LYS
1	A	563	SER
1	A	681	GLU
1	A	689	SER
1	A	731	SER
1	A	763	ARG
1	A	776	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	282	ASN
1	A	288	GLN
1	A	431	ASN
1	A	439	ASN
1	A	444	GLN
1	A	736	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

1 ligand is 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	6IW	A	801	-	9,10,10	7.14	6 (66%)	12,14,14	4.40	8 (66%)

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	6IW	A	801	-	-	4/4/16/16	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	6IW	C08-C07	-18.34	1.25	1.52
2	A	801	6IW	C08-N04	9.35	1.59	1.47
2	A	801	6IW	O03-C10	-3.32	1.19	1.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	6IW	C09-N04	-3.07	1.40	1.46
2	A	801	6IW	C06-C07	-2.67	1.47	1.52
2	A	801	6IW	C06-C05	-2.29	1.49	1.53

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	6IW	O01-C07-C06	-7.04	92.62	110.03
2	A	801	6IW	C09-N04-C08	-6.63	103.46	112.45
2	A	801	6IW	C07-C06-C05	-6.57	95.54	103.97
2	A	801	6IW	C06-C05-N04	-5.66	91.58	103.88
2	A	801	6IW	O03-C10-O02	-5.56	111.45	124.09
2	A	801	6IW	C06-C05-C10	-3.91	105.45	110.92
2	A	801	6IW	O03-C10-C05	2.91	123.46	113.38
2	A	801	6IW	C06-C07-C08	-2.17	100.64	103.31

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	801	6IW	C06-C05-C10-O02
2	A	801	6IW	N04-C05-C10-O02
2	A	801	6IW	C06-C05-C10-O03
2	A	801	6IW	N04-C05-C10-O03

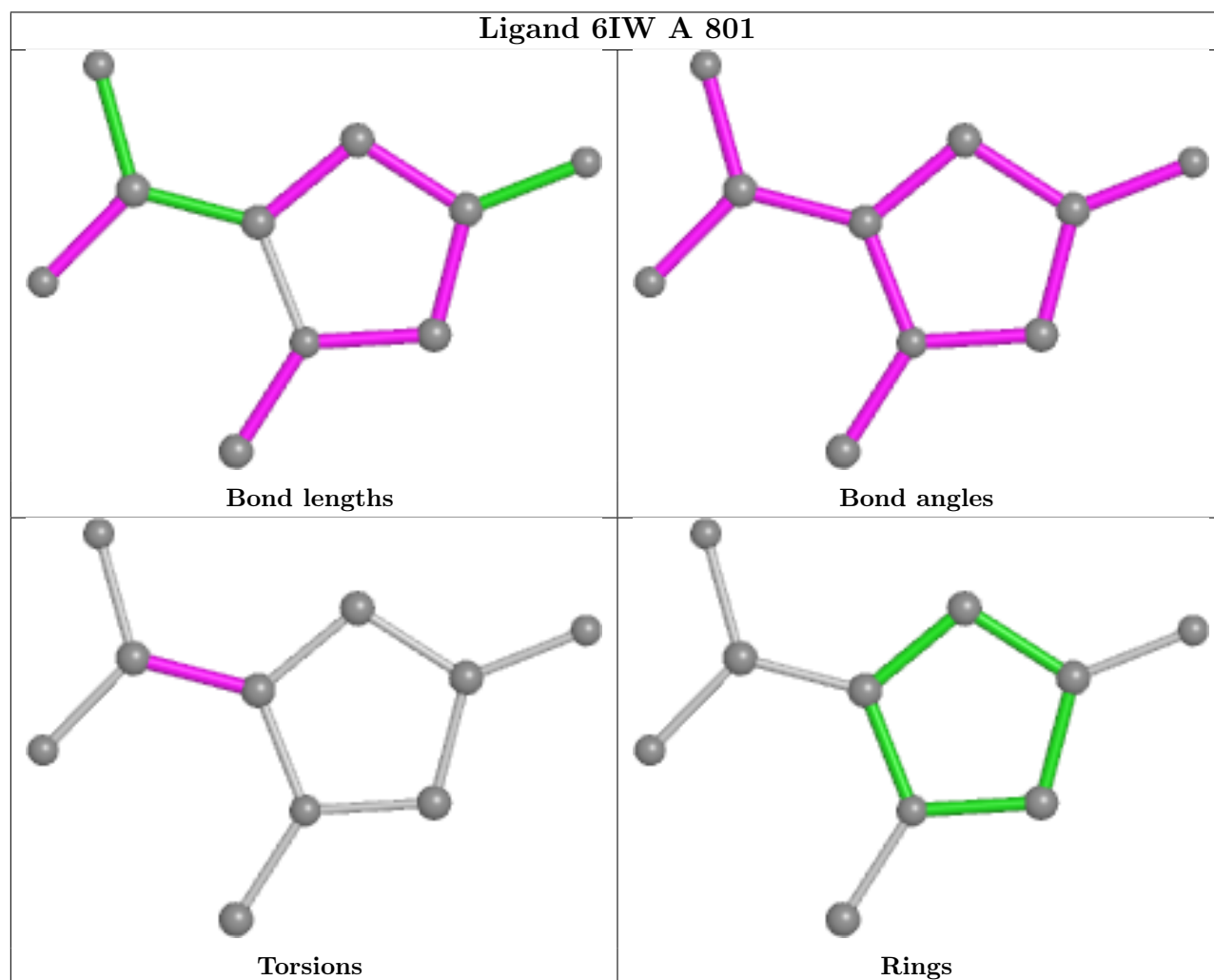
There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	6IW	6	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	780/792 (98%)	-0.64	2 (0%) 90 81	39, 58, 78, 95	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	519	GLU	4.6
1	A	159	GLY	2.1

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](#)

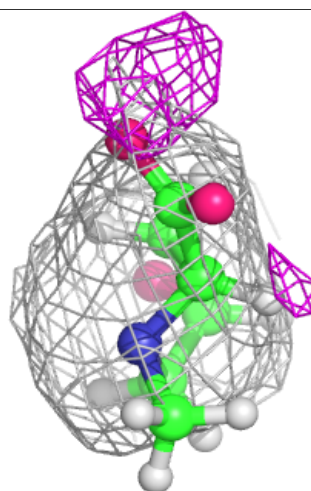
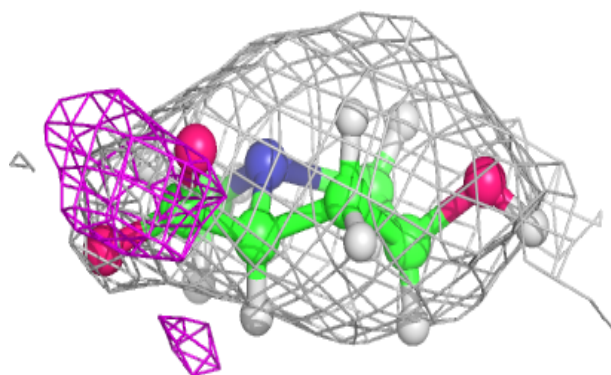
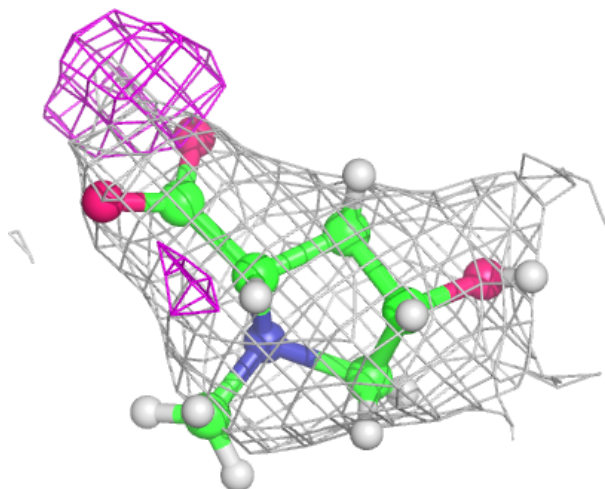
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists 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	6IW	A	801	10/10	0.90	0.15	57,71,85,85	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 6IW A 801:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.