



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 28, 2023 – 02:21 AM EDT

PDB ID : 3LPF
Title : Structure of E. coli beta-Glucuronidase bound with a novel, potent inhibitor 1-((6,7-dimethyl-2-oxo-1,2-dihydroquinolin-3-yl)methyl)-1-(2-hydroxyethyl)-3-(3-methoxyphenyl)thiourea
Authors : Wallace, B.D.; Redinbo, M.R.
Deposited on : 2010-02-05
Resolution : 2.26 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)
Xtrriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

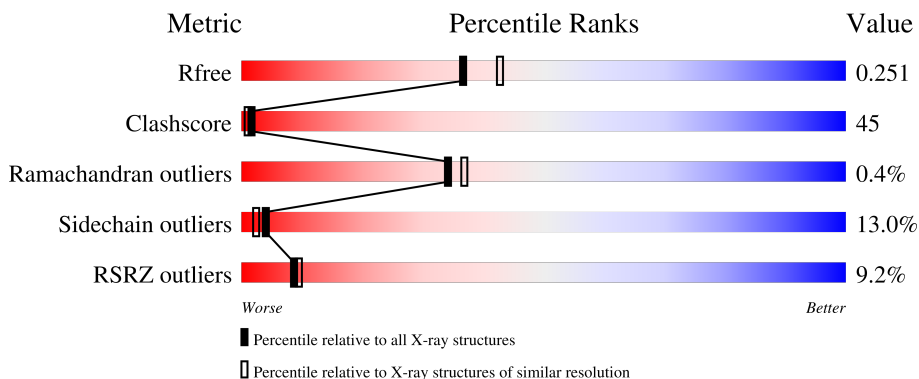
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.26 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	1377 (2.26-2.26)
Clashscore	141614	1487 (2.26-2.26)
Ramachandran outliers	138981	1449 (2.26-2.26)
Sidechain outliers	138945	1450 (2.26-2.26)
RSRZ outliers	127900	1356 (2.26-2.26)

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	605	
1	B	605	

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	Z77	B	604	-	-	X	-

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 10100 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.

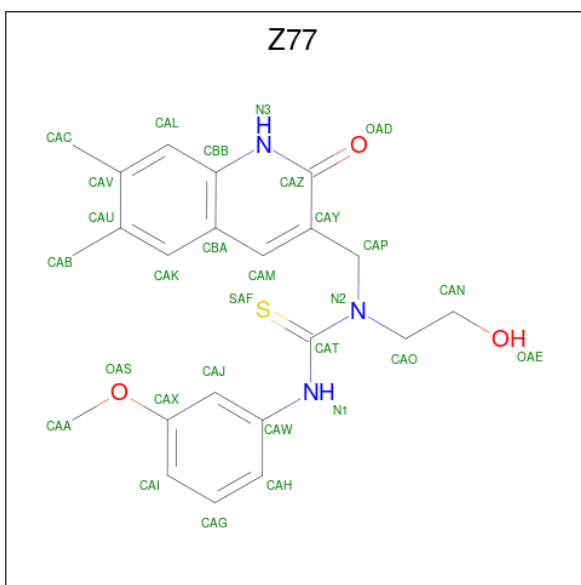
- Molecule 1 is a protein called Beta-glucuronidase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	603	4822	3060	833	907	9	13	0	0	0
1	B	603	4822	3060	833	907	9	13	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP P05804
A	0	HIS	-	expression tag	UNP P05804
B	-1	SER	-	expression tag	UNP P05804
B	0	HIS	-	expression tag	UNP P05804

- Molecule 2 is 1-[(6,7-dimethyl-2-oxo-1,2-dihydroquinolin-3-yl)methyl]-1-(2-hydroxyethyl)-3-(3-methoxyphenyl)thiourea (three-letter code: Z77) (formula: C₂₂H₂₅N₃O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			29	22	3	3	1		
2	B	1	Total	C	N	O	S	0	0
			29	22	3	3	1		

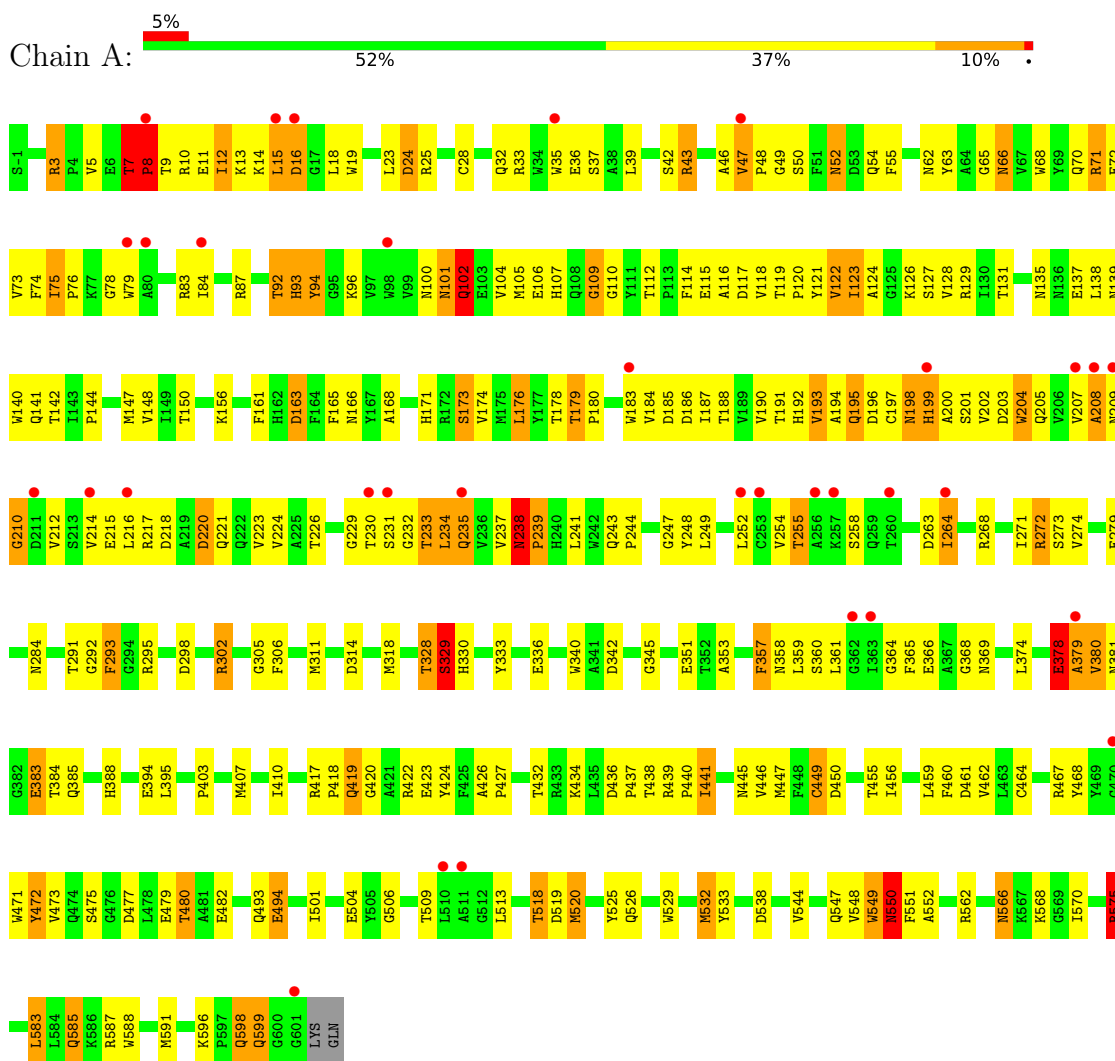
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	269	Total	O	0	0
			269	269		
3	B	129	Total	O	0	0
			129	129		

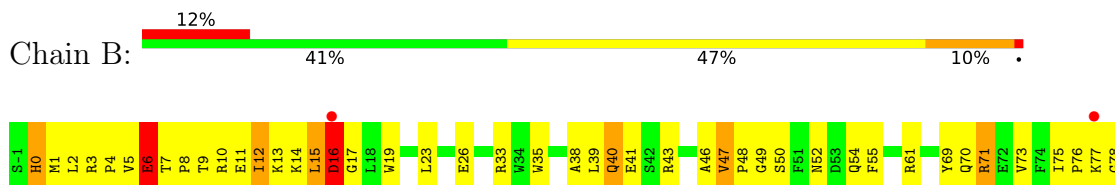
3 Residue-property plots i

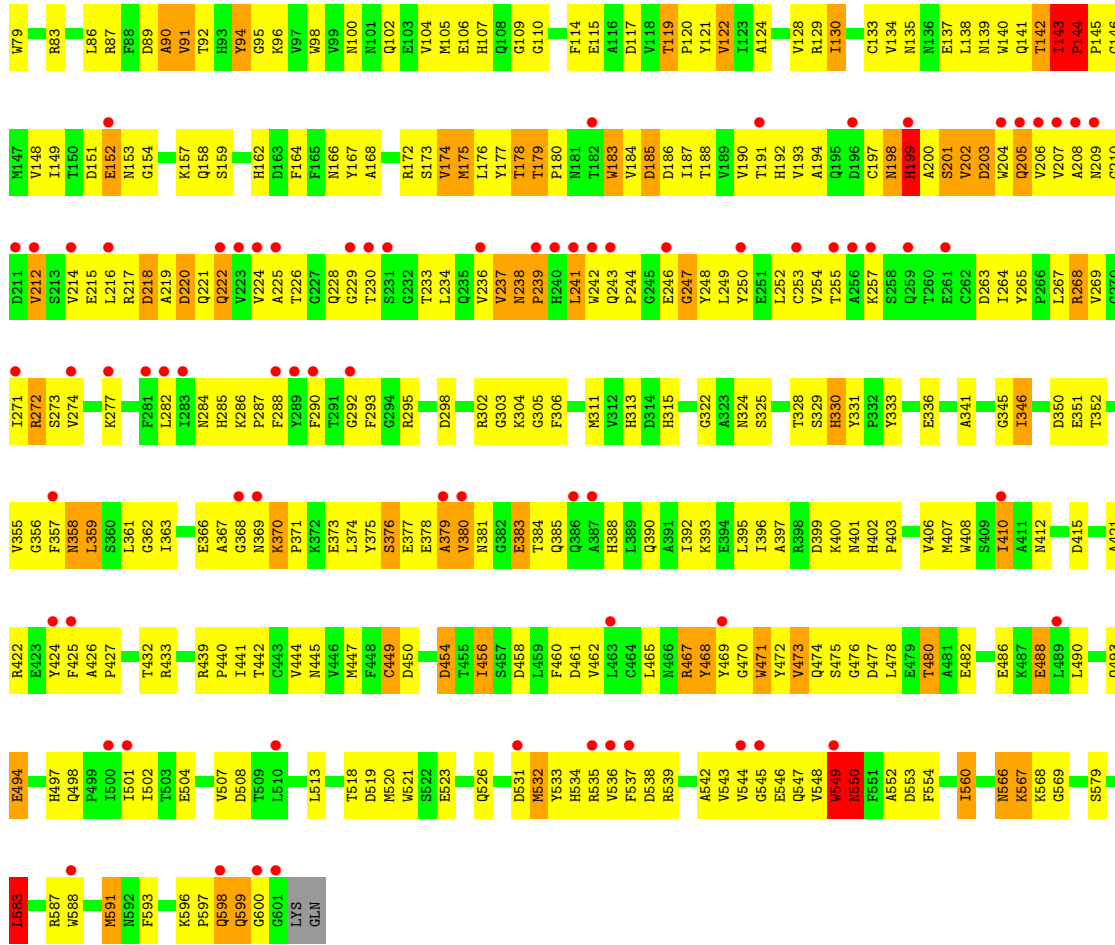
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Beta-glucuronidase



- Molecule 1: Beta-glucuronidase





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	168.06Å 77.41Å 126.15Å 90.00° 124.66° 90.00°	Depositor
Resolution (Å)	50.00 – 2.26 48.11 – 2.26	Depositor EDS
% Data completeness (in resolution range)	94.6 (50.00-2.26) 94.4 (48.11-2.26)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.88 (at 2.27Å)	Xtrriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.209 , 0.249 0.214 , 0.251	Depositor DCC
R_{free} test set	2982 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	38.8	Xtrriage
Anisotropy	0.589	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 62.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	10100	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.65% 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:
Z77

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	0.60	0/4939	1.05	41/6700 (0.6%)
1	B	0.54	2/4939 (0.0%)	0.98	35/6700 (0.5%)
All	All	0.57	2/9878 (0.0%)	1.02	76/13400 (0.6%)

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	6
1	B	0	2
All	All	0	8

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	239	PRO	N-CD	-7.47	1.37	1.47
1	B	144	PRO	N-CD	6.81	1.57	1.47

All (76) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	549	TRP	CB-CA-C	17.72	145.84	110.40
1	A	329	SER	CB-CA-C	14.82	138.26	110.10
1	A	379	ALA	N-CA-C	11.13	141.06	111.00
1	A	208	ALA	CB-CA-C	-10.96	93.66	110.10
1	B	549	TRP	N-CA-C	-10.54	82.55	111.00
1	A	449	CYS	N-CA-C	-9.89	84.29	111.00
1	A	358	ASN	N-CA-CB	-9.33	93.80	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	8	PRO	CB-CA-C	8.72	133.80	112.00
1	B	363	ILE	CB-CA-C	-8.69	94.23	111.60
1	A	209	ASN	N-CA-CB	8.67	126.21	110.60
1	A	24	ASP	N-CA-C	-8.56	87.89	111.00
1	A	329	SER	N-CA-C	-8.31	88.57	111.00
1	B	554	PHE	N-CA-CB	-8.30	95.67	110.60
1	A	549	TRP	C-N-CA	-8.12	101.40	121.70
1	B	379	ALA	N-CA-C	8.01	132.62	111.00
1	B	239	PRO	N-CA-CB	-7.95	93.77	103.30
1	A	8	PRO	N-CA-C	-7.86	91.67	112.10
1	B	583	LEU	CA-CB-CG	7.75	133.12	115.30
1	B	90	ALA	CB-CA-C	7.67	121.60	110.10
1	A	93	HIS	CB-CA-C	7.64	125.67	110.40
1	A	583	LEU	CA-CB-CG	7.41	132.34	115.30
1	A	378	GLU	CB-CA-C	7.39	125.18	110.40
1	A	598	GLN	CB-CA-C	-7.32	95.76	110.40
1	B	143	ILE	N-CA-C	7.22	130.49	111.00
1	B	468	TYR	N-CA-C	-7.18	91.61	111.00
1	B	471	TRP	N-CA-C	7.17	130.37	111.00
1	A	7	THR	N-CA-C	7.17	130.37	111.00
1	A	450	ASP	N-CA-CB	7.12	123.42	110.60
1	A	328	THR	N-CA-C	-7.02	92.06	111.00
1	B	16	ASP	N-CA-C	-6.96	92.22	111.00
1	A	379	ALA	CB-CA-C	-6.85	99.83	110.10
1	B	379	ALA	N-CA-CB	-6.80	100.58	110.10
1	A	209	ASN	N-CA-C	6.76	129.26	111.00
1	B	380	VAL	N-CA-C	-6.74	92.80	111.00
1	B	154	GLY	N-CA-C	6.34	128.94	113.10
1	B	109	GLY	N-CA-C	-6.20	97.60	113.10
1	A	101	ASN	CB-CA-C	-6.20	98.01	110.40
1	A	199	HIS	N-CA-C	6.13	127.55	111.00
1	B	379	ALA	CB-CA-C	-6.10	100.94	110.10
1	B	449	CYS	N-CA-C	-6.09	94.55	111.00
1	A	94	TYR	N-CA-CB	-6.06	99.69	110.60
1	A	16	ASP	N-CA-C	-6.05	94.66	111.00
1	A	109	GLY	N-CA-C	-6.05	97.97	113.10
1	A	520	MSE	N-CA-C	6.03	127.29	111.00
1	B	6	GLU	N-CA-C	5.99	127.17	111.00
1	A	575	ARG	NE-CZ-NH2	-5.94	117.33	120.30
1	A	471	TRP	N-CA-C	5.91	126.95	111.00
1	A	472	TYR	N-CA-CB	5.80	121.04	110.60
1	A	102	GLN	N-CA-CB	5.80	121.03	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	554	PHE	N-CA-C	5.79	126.64	111.00
1	B	246	GLU	N-CA-C	5.74	126.49	111.00
1	B	247	GLY	N-CA-C	5.67	127.28	113.10
1	A	379	ALA	N-CA-CB	-5.67	102.16	110.10
1	B	239	PRO	N-CD-CG	-5.65	94.73	103.20
1	A	209	ASN	CB-CA-C	-5.62	99.16	110.40
1	A	550	ASN	N-CA-C	5.62	126.16	111.00
1	A	293	PHE	N-CA-CB	-5.60	100.51	110.60
1	B	358	ASN	N-CA-CB	-5.57	100.57	110.60
1	B	239	PRO	N-CA-C	5.55	126.54	112.10
1	A	380	VAL	N-CA-C	-5.53	96.08	111.00
1	A	365	PHE	N-CA-C	5.50	125.85	111.00
1	A	50	SER	N-CA-C	-5.43	96.35	111.00
1	B	376	SER	CB-CA-C	5.41	120.37	110.10
1	B	549	TRP	N-CA-CB	5.36	120.24	110.60
1	A	210	GLY	N-CA-C	5.26	126.25	113.10
1	A	357	PHE	CB-CA-C	5.24	120.88	110.40
1	B	560	ILE	CB-CA-C	-5.24	101.12	111.60
1	A	380	VAL	N-CA-CB	5.22	123.00	111.50
1	B	144	PRO	N-CD-CG	-5.20	95.40	103.20
1	A	25	ARG	N-CA-CB	5.17	119.90	110.60
1	B	550	ASN	N-CA-CB	5.17	119.90	110.60
1	B	246	GLU	CB-CA-C	-5.12	100.16	110.40
1	B	91	VAL	N-CA-CB	5.10	122.72	111.50
1	B	549	TRP	CA-C-N	-5.09	105.99	117.20
1	B	199	HIS	N-CA-C	5.06	124.67	111.00
1	B	92	THR	CA-C-N	-5.02	106.15	117.20

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	195	GLN	Peptide
1	A	238	ASN	Peptide
1	A	329	SER	Peptide
1	A	364	GLY	Peptide
1	A	519	ASP	Peptide
1	A	92	THR	Peptide
1	B	143	ILE	Peptide
1	B	549	TRP	Peptide

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4822	0	4593	356	1
1	B	4822	0	4593	489	1
2	A	29	0	25	6	0
2	B	29	0	25	10	0
3	A	269	0	0	38	0
3	B	129	0	0	34	0
All	All	10100	0	9236	845	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 45.

All (845) 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:B:548:VAL:HG12	1:B:549:TRP:O	1.23	1.32
1:A:598:GLN:O	1:A:598:GLN:CG	1.82	1.18
1:A:15:LEU:HD12	1:A:173:SER:CB	1.79	1.11
1:A:7:THR:HB	1:A:8:PRO:HD3	1.33	1.11
1:A:15:LEU:CD1	1:A:173:SER:HB3	1.80	1.09
1:B:482:GLU:HB2	1:B:532:MSE:HE1	1.17	1.09
1:A:147:MSE:HE3	1:A:161:PHE:CZ	1.88	1.08
1:B:216:LEU:HB3	1:B:225:ALA:HB3	1.37	1.07
1:B:151:ASP:OD1	1:B:153:ASN:O	1.71	1.06
1:B:207:VAL:HG12	1:B:208:ALA:O	1.54	1.06
1:A:147:MSE:HE3	1:A:161:PHE:HZ	1.15	1.05
1:B:407:MSE:HE1	1:B:462:VAL:HB	1.39	1.04
1:B:467:ARG:HH11	1:B:467:ARG:HG2	1.19	1.03
1:B:212:VAL:HG22	1:B:229:GLY:O	1.56	1.03
1:B:7:THR:HG23	1:B:8:PRO:HD3	1.38	1.02
1:B:598:GLN:O	1:B:598:GLN:HG2	1.56	1.02
1:A:15:LEU:HD23	1:A:15:LEU:O	1.58	1.01
1:B:1:MSE:HE1	1:B:87:ARG:NH1	1.76	1.00
1:A:7:THR:O	3:A:853:HOH:O	1.80	0.99
1:B:470:GLY:O	1:B:475:SER:HA	1.64	0.98
1:B:202:VAL:HG12	1:B:234:LEU:HD23	1.43	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:GLY:O	1:A:547:GLN:HA	1.64	0.97
1:A:247:GLY:O	1:A:249:LEU:CD1	2.13	0.97
1:B:547:GLN:HB2	3:B:606:HOH:O	1.61	0.97
1:B:447:MSE:HE1	1:B:468:TYR:O	1.62	0.97
1:A:212:VAL:CG2	1:A:230:THR:HA	1.94	0.97
1:A:3:ARG:NH2	3:A:872:HOH:O	1.96	0.96
1:B:205:GLN:NE2	1:B:207:VAL:HG23	1.79	0.96
1:B:295:ARG:O	1:B:329:SER:HB2	1.66	0.96
1:A:198:ASN:HA	1:A:239:PRO:HD3	1.46	0.94
1:B:202:VAL:HG12	1:B:234:LEU:CD2	1.97	0.94
1:A:318:MSE:SE	3:A:791:HOH:O	2.34	0.94
1:B:191:THR:HG21	1:B:271:ILE:HA	1.47	0.94
1:B:212:VAL:HG13	1:B:230:THR:HG23	1.50	0.94
1:B:10:ARG:HH22	1:B:79:TRP:HE1	1.15	0.93
1:B:244:PRO:HB2	1:B:593:PHE:CE1	2.03	0.93
1:B:83:ARG:HD3	1:B:179:THR:HG22	1.52	0.92
1:A:585:GLN:HG3	3:A:636:HOH:O	1.70	0.92
1:B:184:VAL:HG12	3:B:728:HOH:O	1.69	0.91
1:B:548:VAL:CG1	1:B:549:TRP:O	2.17	0.91
1:B:183:TRP:HA	1:B:263:ASP:OD2	1.70	0.91
1:B:142:THR:HG23	1:B:144:PRO:O	1.71	0.90
1:B:207:VAL:CG1	1:B:208:ALA:O	2.19	0.90
1:B:272:ARG:HA	1:B:284:ASN:HD21	1.35	0.90
1:A:436:ASP:OD1	1:A:438:THR:HG22	1.70	0.90
1:B:143:ILE:O	1:B:143:ILE:HG22	1.69	0.90
1:B:46:ALA:H	1:B:54:GLN:HE22	1.18	0.89
1:B:482:GLU:CB	1:B:532:MSE:HE1	2.01	0.89
2:A:604:Z77:SAF	2:A:604:Z77:HAJ	2.13	0.89
1:B:238:ASN:CG	1:B:238:ASN:O	2.10	0.89
1:B:105:MSE:CE	1:B:115:GLU:HA	2.04	0.88
1:A:199:HIS:ND1	1:A:200:ALA:N	2.21	0.88
1:B:362:GLY:HA3	3:B:733:HOH:O	1.72	0.88
1:B:33:ARG:HA	1:B:35:TRP:CZ3	2.09	0.88
1:B:83:ARG:HD3	1:B:179:THR:CG2	2.04	0.87
1:B:598:GLN:O	1:B:598:GLN:CG	2.22	0.87
1:B:212:VAL:CG1	1:B:230:THR:HG23	2.05	0.87
1:B:366:GLU:HG3	1:B:367:ALA:H	1.37	0.87
1:B:26:GLU:OE1	1:B:26:GLU:HA	1.72	0.87
1:A:306:PHE:O	3:A:868:HOH:O	1.91	0.87
1:A:247:GLY:O	1:A:249:LEU:HD12	1.73	0.86
1:A:7:THR:HB	1:A:8:PRO:CD	2.04	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:298:ASP:OD2	3:B:717:HOH:O	1.94	0.86
1:A:407:MSE:HE1	1:A:462:VAL:HB	1.57	0.86
1:A:139:ASN:H	1:A:142:THR:CG2	1.89	0.86
1:A:311:MSE:CE	1:A:340:TRP:HB2	2.06	0.86
1:A:9:THR:OG1	3:A:852:HOH:O	1.84	0.85
1:A:105:MSE:CE	1:A:115:GLU:HA	2.06	0.85
1:B:83:ARG:HH21	1:B:117:ASP:HB2	1.39	0.85
1:B:531:ASP:OD1	1:B:583:LEU:HD21	1.75	0.85
1:B:407:MSE:HE2	1:B:442:THR:HB	1.59	0.84
1:B:212:VAL:HA	1:B:255:THR:O	1.76	0.84
1:B:306:PHE:HZ	1:B:311:MSE:CE	1.89	0.84
1:A:441:ILE:HG22	1:A:461:ASP:OD2	1.77	0.84
1:B:376:SER:OG	1:B:378:GLU:HG2	1.78	0.84
1:A:13:LYS:HE2	1:A:15:LEU:HD13	1.61	0.83
1:A:139:ASN:H	1:A:142:THR:HG22	1.43	0.83
1:B:306:PHE:CZ	1:B:311:MSE:HE2	2.14	0.83
1:A:15:LEU:HD21	1:A:48:PRO:HD3	1.60	0.83
1:B:216:LEU:CB	1:B:225:ALA:HB3	2.08	0.83
1:B:306:PHE:HZ	1:B:311:MSE:HE2	1.44	0.83
1:B:467:ARG:HH11	1:B:467:ARG:CG	1.92	0.82
1:B:415:ASP:OD2	3:B:729:HOH:O	1.94	0.82
1:A:215:GLU:HG3	1:A:217:ARG:HH12	1.44	0.82
1:B:205:GLN:CD	1:B:207:VAL:HG23	1.99	0.82
1:A:598:GLN:O	1:A:598:GLN:HG2	0.94	0.82
1:B:119:THR:HB	1:B:120:PRO:HD3	1.62	0.82
1:B:550:ASN:O	1:B:569:GLY:HA2	1.80	0.82
1:A:83:ARG:HD3	1:A:179:THR:HG22	1.60	0.81
1:A:24:ASP:O	1:A:63:TYR:OH	1.98	0.81
1:A:72:GLU:OE1	3:A:857:HOH:O	1.98	0.81
1:B:15:LEU:HG	1:B:48:PRO:HD3	1.62	0.81
1:B:105:MSE:HE3	1:B:115:GLU:CA	2.10	0.81
1:B:7:THR:CG2	1:B:8:PRO:HD3	2.11	0.81
1:B:203:ASP:OD1	1:B:233:THR:OG1	1.99	0.81
1:A:550:ASN:N	3:A:832:HOH:O	2.11	0.81
1:A:7:THR:O	3:A:834:HOH:O	1.98	0.81
1:A:214:VAL:HG12	1:A:235:GLN:HE22	1.45	0.81
1:A:550:ASN:HD22	1:A:552:ALA:H	1.26	0.81
1:A:203:ASP:CG	1:A:233:THR:HG1	1.84	0.81
1:B:373:GLU:HA	3:B:702:HOH:O	1.80	0.81
1:A:479:GLU:OE1	3:A:784:HOH:O	1.97	0.80
1:B:152:GLU:HG2	1:B:153:ASN:H	1.47	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:ALA:H	1:A:54:GLN:HE22	1.28	0.80
1:B:15:LEU:HD12	1:B:173:SER:HA	1.61	0.80
1:A:208:ALA:HB1	3:A:839:HOH:O	1.80	0.80
1:B:10:ARG:HB2	1:B:10:ARG:CZ	2.10	0.80
1:B:14:LYS:HB2	1:B:174:VAL:CG2	2.11	0.80
1:A:357:PHE:O	1:A:374:LEU:HD21	1.81	0.79
1:A:179:THR:HG23	1:A:180:PRO:O	1.82	0.79
1:A:15:LEU:CD2	1:A:48:PRO:HD3	2.13	0.79
1:A:212:VAL:HG22	1:A:230:THR:HA	1.65	0.79
1:B:366:GLU:OE1	3:B:626:HOH:O	1.99	0.79
1:B:469:TYR:O	1:B:474:GLN:HB2	1.82	0.79
1:B:579:SER:O	3:B:724:HOH:O	2.00	0.79
1:B:191:THR:HG21	1:B:271:ILE:CA	2.13	0.79
1:A:62:ASN:ND2	3:A:701:HOH:O	2.17	0.78
1:A:214:VAL:HG13	1:A:252:LEU:HD11	1.65	0.78
1:B:12:ILE:HG22	1:B:14:LYS:HD2	1.66	0.78
1:A:203:ASP:OD2	1:A:233:THR:OG1	2.00	0.78
1:A:202:VAL:HG12	1:A:234:LEU:HG	1.64	0.78
1:B:193:VAL:HG13	1:B:285:HIS:NE2	1.99	0.78
1:B:445:ASN:ND2	1:B:467:ARG:HH22	1.81	0.78
1:A:142:THR:HG23	1:A:144:PRO:O	1.83	0.78
1:A:311:MSE:HE1	1:A:340:TRP:HB2	1.65	0.78
1:B:83:ARG:NH2	1:B:117:ASP:HB2	1.99	0.78
1:A:566:ASN:HD22	1:A:568:LYS:H	1.29	0.78
1:A:28:CYS:HB3	1:A:32:GLN:NE2	2.00	0.77
1:B:140:TRP:CE3	1:B:379:ALA:O	2.38	0.76
1:B:212:VAL:CG2	1:B:229:GLY:O	2.31	0.76
1:A:566:ASN:ND2	1:A:568:LYS:H	1.82	0.76
1:A:83:ARG:HD3	1:A:179:THR:CG2	2.13	0.76
1:B:369:ASN:HA	1:B:370:LYS:CB	2.16	0.76
1:B:122:VAL:HG23	1:B:128:VAL:HG11	1.67	0.76
1:A:247:GLY:O	1:A:249:LEU:HD11	1.85	0.76
1:B:14:LYS:HG2	1:B:175:MSE:HA	1.67	0.76
1:B:105:MSE:HE1	1:B:115:GLU:HA	1.65	0.76
1:A:140:TRP:HZ2	1:A:147:MSE:HE2	1.51	0.76
1:B:566:ASN:HD22	1:B:568:LYS:H	1.32	0.75
1:B:184:VAL:CG1	3:B:728:HOH:O	2.30	0.75
1:B:205:GLN:NE2	1:B:206:VAL:O	2.20	0.75
1:B:49:GLY:HA2	1:B:305:GLY:HA3	1.69	0.74
1:A:212:VAL:HG23	1:A:229:GLY:O	1.88	0.74
1:B:482:GLU:HB2	1:B:532:MSE:CE	2.09	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:139:ASN:O	1:A:142:THR:HG22	1.87	0.74
1:B:378:GLU:O	3:B:709:HOH:O	2.06	0.74
1:B:179:THR:HG23	1:B:180:PRO:O	1.88	0.74
1:B:185:ASP:N	3:B:728:HOH:O	2.20	0.73
1:B:184:VAL:HG21	1:B:254:VAL:HG12	1.70	0.73
1:A:119:THR:HB	1:A:120:PRO:HD3	1.70	0.73
1:A:342:ASP:OD1	1:A:403:PRO:HD2	1.87	0.73
1:A:243:GLN:OE1	3:A:819:HOH:O	2.06	0.73
1:A:482:GLU:HB2	1:A:532:MSE:CE	2.17	0.73
1:B:566:ASN:HD21	1:B:568:LYS:HB2	1.53	0.73
1:A:43:ARG:HD2	1:A:55:PHE:CE1	2.22	0.73
1:B:218:ASP:HB2	1:B:222:GLN:HG3	1.69	0.73
1:A:107:HIS:HE1	1:A:394:GLU:OE1	1.71	0.73
1:B:7:THR:OG1	3:B:707:HOH:O	2.06	0.73
1:B:83:ARG:CD	1:B:179:THR:HG22	2.18	0.72
1:B:83:ARG:NH1	1:B:183:TRP:CZ3	2.57	0.72
1:B:244:PRO:HB2	1:B:593:PHE:CZ	2.23	0.72
1:A:13:LYS:CE	1:A:15:LEU:HD13	2.19	0.72
1:A:165:PHE:O	3:A:666:HOH:O	2.07	0.72
1:A:183:TRP:CZ3	1:A:185:ASP:HB3	2.23	0.72
1:A:477:ASP:CG	1:A:480:THR:HG23	2.09	0.72
1:B:10:ARG:NH2	1:B:79:TRP:HE1	1.87	0.72
1:B:244:PRO:HB2	1:B:593:PHE:HE1	1.48	0.72
1:A:36:GLU:HA	1:A:101:ASN:ND2	2.04	0.72
1:B:19:TRP:CD1	1:B:47:VAL:HG13	2.25	0.72
1:A:191:THR:HG21	1:A:272:ARG:N	2.06	0.71
1:A:248:TYR:C	1:A:249:LEU:HD12	2.11	0.71
1:B:200:ALA:HB2	1:B:236:VAL:HG22	1.70	0.71
1:A:410:ILE:HD11	1:A:432:THR:HG21	1.70	0.71
1:B:83:ARG:CB	1:B:179:THR:HG22	2.21	0.71
1:A:52:ASN:H	1:A:52:ASN:HD22	1.39	0.71
1:B:244:PRO:CB	1:B:593:PHE:HE1	2.04	0.71
1:B:292:GLY:O	1:B:547:GLN:HA	1.90	0.71
1:A:15:LEU:O	1:A:15:LEU:CD2	2.37	0.71
1:B:33:ARG:HG2	1:B:35:TRP:CH2	2.26	0.71
1:B:105:MSE:HE3	1:B:115:GLU:HA	1.70	0.71
1:B:534:HIS:ND1	3:B:619:HOH:O	1.90	0.71
1:A:208:ALA:C	3:A:839:HOH:O	2.30	0.70
1:B:15:LEU:CD1	1:B:173:SER:HA	2.21	0.70
1:B:152:GLU:CG	1:B:153:ASN:H	2.03	0.70
1:B:186:ASP:N	3:B:728:HOH:O	1.97	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:MSE:CE	1:A:115:GLU:CA	2.69	0.70
1:B:218:ASP:CB	1:B:222:GLN:HG3	2.21	0.70
1:A:198:ASN:OD1	1:A:237:VAL:O	2.10	0.70
1:A:249:LEU:HD12	1:A:249:LEU:N	2.07	0.70
1:B:432:THR:CG2	1:B:441:ILE:HG21	2.21	0.70
1:A:10:ARG:HH12	1:A:79:TRP:HE1	1.37	0.70
1:A:272:ARG:HA	1:A:284:ASN:HD21	1.55	0.70
1:B:205:GLN:OE1	1:B:207:VAL:CG2	2.39	0.70
1:B:357:PHE:O	1:B:374:LEU:HD11	1.91	0.70
1:B:445:ASN:HD21	1:B:467:ARG:HH22	1.38	0.70
1:A:37:SER:O	3:A:795:HOH:O	2.09	0.70
1:A:198:ASN:HA	1:A:239:PRO:CD	2.21	0.70
1:B:14:LYS:HB2	1:B:174:VAL:HG22	1.74	0.70
1:B:14:LYS:HE3	1:B:73:VAL:HG21	1.74	0.70
1:B:166:ASN:O	3:B:608:HOH:O	2.09	0.69
1:A:36:GLU:HA	1:A:129:ARG:HH21	1.55	0.69
1:B:244:PRO:HG2	1:B:593:PHE:HE1	1.55	0.69
1:B:467:ARG:HG2	1:B:467:ARG:NH1	1.96	0.69
1:A:100:ASN:HD22	1:A:129:ARG:NH1	1.90	0.69
1:A:52:ASN:HD21	1:A:168:ALA:H	1.40	0.69
1:A:105:MSE:HE3	1:A:116:ALA:N	2.07	0.69
1:B:10:ARG:HB2	1:B:10:ARG:NH1	2.07	0.69
1:A:518:THR:O	1:A:525:TYR:HD1	1.76	0.69
1:B:141:GLN:HG2	1:B:383:GLU:HB3	1.74	0.69
1:A:191:THR:HG21	1:A:271:ILE:HA	1.73	0.68
1:A:135:ASN:ND2	1:A:137:GLU:H	1.91	0.68
1:A:190:VAL:HB	1:A:202:VAL:HG22	1.75	0.68
1:B:1:MSE:CE	1:B:87:ARG:NH1	2.54	0.68
1:B:532:MSE:HG3	1:B:533:TYR:N	2.08	0.68
1:B:186:ASP:HB3	1:B:206:VAL:HB	1.75	0.68
1:A:482:GLU:CG	1:A:532:MSE:HE1	2.23	0.68
1:B:139:ASN:O	1:B:142:THR:HG22	1.93	0.68
1:B:198:ASN:O	1:B:199:HIS:HB2	1.92	0.68
1:B:75:ILE:HD12	1:B:176:LEU:HD21	1.76	0.68
1:A:8:PRO:CA	3:A:853:HOH:O	2.41	0.68
1:A:195:GLN:N	1:A:195:GLN:OE1	2.27	0.68
1:A:238:ASN:HB2	3:A:789:HOH:O	1.94	0.68
1:B:205:GLN:CD	1:B:207:VAL:CG2	2.62	0.68
1:A:482:GLU:OE2	3:A:724:HOH:O	2.12	0.68
1:A:52:ASN:H	1:A:52:ASN:ND2	1.91	0.67
1:A:140:TRP:CE3	1:A:379:ALA:O	2.47	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:TRP:CZ2	1:A:147:MSE:HE2	2.28	0.67
1:B:368:GLY:O	1:B:370:LYS:CB	2.41	0.67
1:A:366:GLU:HG3	3:A:710:HOH:O	1.93	0.67
1:B:341:ALA:HB1	1:B:346:ILE:HG22	1.77	0.67
1:B:212:VAL:HG13	1:B:230:THR:CG2	2.24	0.67
1:B:467:ARG:HD2	1:B:469:TYR:CE1	2.30	0.67
1:A:73:VAL:HG22	1:A:74:PHE:N	2.10	0.67
1:A:216:LEU:O	1:A:224:VAL:HG12	1.95	0.67
1:B:244:PRO:CG	1:B:593:PHE:HE1	2.08	0.67
1:A:138:LEU:HA	1:A:142:THR:HG21	1.76	0.66
1:A:94:TYR:OH	1:A:96:LYS:HE3	1.95	0.66
1:B:282:LEU:HA	1:B:286:LYS:O	1.94	0.66
1:A:202:VAL:HG12	1:A:234:LEU:CG	2.26	0.66
1:A:419:GLN:O	3:A:810:HOH:O	2.13	0.66
1:B:238:ASN:O	3:B:701:HOH:O	2.13	0.66
1:A:191:THR:HG21	1:A:272:ARG:H	1.60	0.66
1:A:436:ASP:O	3:A:688:HOH:O	2.14	0.66
1:A:122:VAL:HG22	1:A:128:VAL:HG11	1.77	0.66
1:B:83:ARG:CG	1:B:179:THR:HG22	2.26	0.66
1:A:112:THR:O	3:A:628:HOH:O	2.14	0.65
1:A:482:GLU:HB2	1:A:532:MSE:HE1	1.78	0.65
1:B:362:GLY:CA	3:B:733:HOH:O	2.39	0.65
1:B:193:VAL:HG13	1:B:285:HIS:HE2	1.61	0.65
1:B:204:TRP:CH2	1:B:206:VAL:HG23	2.31	0.65
1:B:247:GLY:O	1:B:249:LEU:HD12	1.97	0.65
1:B:396:ILE:O	1:B:400:LYS:HG2	1.95	0.65
1:A:548:VAL:HG11	1:A:570:ILE:HD11	1.77	0.65
1:A:455:THR:O	1:A:456:ILE:HD13	1.97	0.64
1:B:183:TRP:O	1:B:208:ALA:HB3	1.97	0.64
1:A:342:ASP:CG	1:A:403:PRO:HD2	2.18	0.64
1:A:203:ASP:CG	1:A:233:THR:OG1	2.35	0.64
1:B:566:ASN:ND2	1:B:568:LYS:H	1.96	0.64
1:B:10:ARG:NH2	1:B:79:TRP:NE1	2.42	0.64
1:B:330:HIS:O	1:B:331:TYR:HD2	1.81	0.64
1:A:73:VAL:HG22	1:A:74:PHE:H	1.61	0.64
1:A:330:HIS:HD2	1:A:351:GLU:OE1	1.79	0.64
1:A:477:ASP:OD1	1:A:480:THR:HG23	1.97	0.64
1:B:50:SER:OG	1:B:303:GLY:HA3	1.97	0.64
1:B:183:TRP:H	1:B:208:ALA:HB3	1.63	0.64
1:A:8:PRO:HA	3:A:853:HOH:O	1.96	0.64
1:B:191:THR:CG2	1:B:271:ILE:HG23	2.29	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:548:VAL:C	1:B:549:TRP:O	2.25	0.63
1:A:202:VAL:HG12	1:A:234:LEU:CD1	2.29	0.63
1:A:75:ILE:HD11	1:A:128:VAL:HG13	1.80	0.63
1:A:214:VAL:CG1	1:A:235:GLN:HE22	2.11	0.63
1:A:328:THR:O	1:A:351:GLU:HB3	1.99	0.63
1:B:192:HIS:O	1:B:199:HIS:CG	2.51	0.63
1:B:193:VAL:HG12	1:B:273:SER:HB3	1.80	0.63
1:A:71:ARG:HD2	1:A:72:GLU:O	1.98	0.63
1:A:183:TRP:H	1:A:208:ALA:HB3	1.64	0.63
1:B:183:TRP:CD1	1:B:208:ALA:CB	2.81	0.63
1:B:447:MSE:CE	1:B:468:TYR:O	2.43	0.62
1:B:432:THR:HG21	1:B:441:ILE:HG21	1.80	0.62
1:A:105:MSE:HE3	1:A:115:GLU:C	2.19	0.62
1:B:14:LYS:CG	1:B:174:VAL:HG23	2.29	0.62
1:B:212:VAL:HG13	1:B:230:THR:HA	1.81	0.62
1:A:7:THR:CB	1:A:8:PRO:CD	2.78	0.62
1:B:76:PRO:HG2	1:B:79:TRP:CE2	2.34	0.62
1:B:141:GLN:HG2	1:B:383:GLU:CB	2.28	0.62
1:B:407:MSE:CE	1:B:442:THR:HB	2.27	0.62
1:A:200:ALA:HB1	1:A:234:LEU:HD23	1.81	0.62
1:B:366:GLU:HG3	1:B:367:ALA:N	2.13	0.61
1:A:93:HIS:HD2	3:A:833:HOH:O	1.81	0.61
1:B:19:TRP:CD1	1:B:47:VAL:CG1	2.83	0.61
1:A:33:ARG:HG2	1:A:35:TRP:CZ2	2.36	0.61
1:B:194:ALA:HB2	1:B:199:HIS:CD2	2.36	0.61
1:B:537:PHE:HB3	1:B:543:VAL:HG11	1.83	0.61
1:B:14:LYS:HG3	1:B:174:VAL:HG23	1.82	0.61
1:B:205:GLN:OE1	1:B:207:VAL:HG21	1.99	0.61
1:A:8:PRO:O	1:B:77:LYS:NZ	2.33	0.61
1:B:306:PHE:CZ	1:B:311:MSE:CE	2.75	0.61
1:A:232:GLY:O	1:A:233:THR:HG23	2.00	0.60
1:B:26:GLU:OE1	1:B:26:GLU:CA	2.47	0.60
1:A:36:GLU:HA	1:A:101:ASN:HD21	1.64	0.60
1:A:105:MSE:HE3	1:A:115:GLU:CA	2.31	0.60
1:B:361:LEU:HD12	2:B:604:Z77:N3	2.16	0.60
1:B:410:ILE:CD1	1:B:410:ILE:N	2.65	0.60
1:B:105:MSE:HE2	1:B:114:PHE:CD1	2.37	0.60
1:A:183:TRP:CE3	1:A:185:ASP:HB3	2.37	0.60
1:A:311:MSE:HE2	1:A:340:TRP:CE3	2.37	0.60
1:B:203:ASP:OD2	1:B:233:THR:HG23	2.01	0.60
1:A:378:GLU:O	3:A:610:HOH:O	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:604:Z77:SAF	2:A:604:Z77:CAJ	2.80	0.60
1:B:10:ARG:NH1	1:B:10:ARG:CB	2.65	0.60
1:B:15:LEU:O	1:B:16:ASP:C	2.39	0.60
1:A:123:ILE:O	1:A:123:ILE:HG22	2.01	0.60
1:A:192:HIS:O	1:A:199:HIS:HB3	2.01	0.60
1:A:311:MSE:CE	1:A:340:TRP:CB	2.79	0.60
1:A:330:HIS:O	1:A:353:ALA:HA	2.02	0.60
1:B:14:LYS:HA	1:B:71:ARG:NH2	2.17	0.59
1:B:100:ASN:HA	1:B:129:ARG:NH2	2.18	0.59
1:B:566:ASN:ND2	1:B:568:LYS:HB2	2.18	0.59
1:B:532:MSE:HG3	1:B:533:TYR:H	1.66	0.59
1:B:315:HIS:HE1	3:B:668:HOH:O	1.85	0.59
1:A:105:MSE:HE3	1:A:115:GLU:HA	1.82	0.59
1:A:238:ASN:HD22	1:A:239:PRO:CD	2.15	0.59
1:B:357:PHE:O	1:B:374:LEU:HD21	2.02	0.59
1:A:186:ASP:OD2	1:A:204:TRP:HH2	1.86	0.59
1:B:218:ASP:HB3	1:B:220:ASP:H	1.67	0.59
1:B:15:LEU:HD12	1:B:173:SER:CA	2.32	0.59
1:A:72:GLU:HA	1:A:128:VAL:O	2.03	0.58
1:A:75:ILE:HG13	1:A:122:VAL:HG13	1.85	0.58
1:A:139:ASN:H	1:A:142:THR:HG21	1.67	0.58
1:B:83:ARG:HD3	1:B:179:THR:HG21	1.85	0.58
1:B:83:ARG:HB2	1:B:179:THR:HG22	1.84	0.58
1:B:191:THR:HG21	1:B:271:ILE:HG23	1.83	0.58
1:A:203:ASP:OD1	1:A:233:THR:OG1	2.22	0.58
1:B:7:THR:HG23	1:B:8:PRO:CD	2.26	0.58
1:B:10:ARG:H	1:B:178:THR:HG22	1.68	0.58
1:B:330:HIS:O	1:B:331:TYR:CD2	2.57	0.58
1:B:202:VAL:HG12	1:B:234:LEU:HD21	1.81	0.58
2:B:604:Z77:HAI	2:B:604:Z77:SAF	2.43	0.58
1:A:105:MSE:HE1	1:A:115:GLU:HA	1.83	0.58
1:A:587:ARG:HG2	1:A:588:TRP:CD1	2.39	0.58
1:B:43:ARG:HD3	3:B:653:HOH:O	2.04	0.58
1:B:183:TRP:O	1:B:208:ALA:CB	2.52	0.58
1:A:199:HIS:CG	1:A:200:ALA:H	2.17	0.58
1:B:15:LEU:HD11	1:B:173:SER:OG	2.04	0.58
1:A:191:THR:HG23	1:A:271:ILE:HG23	1.85	0.58
1:B:214:VAL:HG13	1:B:252:LEU:HD11	1.85	0.58
1:B:537:PHE:O	1:B:596:LYS:NZ	2.37	0.58
1:B:355:VAL:HG23	1:B:412:ASN:HD22	1.69	0.58
1:A:314:ASP:OD1	1:A:575:ARG:HD2	2.03	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:482:GLU:CB	1:A:532:MSE:HE1	2.34	0.57
1:B:194:ALA:N	1:B:199:HIS:HD2	2.01	0.57
1:A:244:PRO:O	1:A:345:GLY:O	2.22	0.57
1:B:284:ASN:O	1:B:286:LYS:NZ	2.35	0.57
1:B:215:GLU:CD	1:B:217:ARG:NH2	2.58	0.57
1:A:36:GLU:CA	1:A:129:ARG:HH21	2.18	0.57
1:B:193:VAL:HG13	1:B:285:HIS:CD2	2.39	0.57
1:B:273:SER:H	1:B:284:ASN:ND2	2.03	0.57
1:A:138:LEU:CA	1:A:142:THR:HG21	2.34	0.57
1:B:144:PRO:O	1:B:144:PRO:HD2	2.03	0.57
1:B:241:LEU:HD12	1:B:241:LEU:H	1.70	0.57
1:B:471:TRP:CE3	1:B:520:MSE:HE3	2.39	0.57
1:B:224:VAL:HG22	1:B:237:VAL:HG11	1.86	0.57
1:B:388:HIS:HD2	1:B:424:TYR:OH	1.87	0.57
1:B:12:ILE:HG22	1:B:14:LYS:CD	2.34	0.57
1:B:152:GLU:HG2	1:B:153:ASN:N	2.17	0.57
1:B:272:ARG:NH1	1:B:274:VAL:HB	2.20	0.57
1:A:75:ILE:HD11	1:A:128:VAL:CG1	2.34	0.57
1:A:407:MSE:HE1	1:A:462:VAL:CB	2.31	0.57
1:B:11:GLU:HG3	1:B:177:TYR:HB2	1.87	0.57
1:B:14:LYS:HD3	1:B:176:LEU:HB2	1.87	0.57
1:B:290:PHE:HB2	1:B:545:GLY:HA2	1.87	0.57
1:B:350:ASP:OD2	1:B:399:ASP:OD2	2.23	0.56
1:B:396:ILE:HG12	1:B:408:TRP:CZ2	2.40	0.56
1:A:194:ALA:C	1:A:196:ASP:H	2.09	0.56
1:B:238:ASN:C	3:B:701:HOH:O	2.42	0.56
1:A:107:HIS:CE1	1:A:394:GLU:OE1	2.55	0.56
1:A:417:ARG:HB2	1:A:418:PRO:HD3	1.86	0.56
1:B:52:ASN:H	1:B:52:ASN:ND2	2.03	0.56
1:B:274:VAL:HG12	1:B:440:PRO:HD3	1.87	0.56
1:A:76:PRO:HG2	1:A:79:TRP:CE2	2.40	0.56
1:B:119:THR:CB	1:B:120:PRO:HD3	2.35	0.56
1:B:162:HIS:CD2	1:B:164:PHE:CZ	2.94	0.56
1:B:224:VAL:HG22	1:B:224:VAL:O	2.06	0.56
1:A:11:GLU:OE2	1:A:11:GLU:N	2.39	0.56
1:B:140:TRP:CD2	1:B:379:ALA:O	2.58	0.56
1:B:432:THR:HG22	1:B:441:ILE:HG21	1.87	0.56
1:B:15:LEU:CD1	1:B:173:SER:OG	2.54	0.55
1:B:102:GLN:HG2	1:B:121:TYR:CG	2.41	0.55
1:B:378:GLU:HG3	1:B:379:ALA:N	2.21	0.55
1:A:238:ASN:HD22	1:A:239:PRO:N	2.04	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:434:LYS:NZ	3:A:704:HOH:O	2.39	0.55
1:A:532:MSE:CA	1:A:532:MSE:HE2	2.34	0.55
1:B:17:GLY:O	1:B:19:TRP:HD1	1.88	0.55
1:B:83:ARG:HB2	1:B:179:THR:O	2.06	0.55
1:B:361:LEU:HD12	2:B:604:Z77:CAZ	2.37	0.55
1:B:193:VAL:C	1:B:199:HIS:CD2	2.79	0.55
1:B:553:ASP:OD2	3:B:710:HOH:O	2.18	0.55
1:B:205:GLN:NE2	1:B:207:VAL:CG2	2.64	0.55
1:B:306:PHE:HZ	1:B:311:MSE:HE1	1.69	0.55
1:A:550:ASN:ND2	1:A:552:ALA:H	2.02	0.55
1:A:184:VAL:HG13	1:A:205:GLN:NE2	2.22	0.55
1:B:102:GLN:HG2	1:B:121:TYR:CD1	2.42	0.55
1:B:539:ARG:HH11	1:B:539:ARG:CB	2.18	0.55
1:B:11:GLU:HG3	1:B:177:TYR:CB	2.37	0.55
1:A:104:VAL:HA	3:A:754:HOH:O	2.07	0.54
1:B:183:TRP:CD1	1:B:183:TRP:N	2.75	0.54
1:B:244:PRO:CB	1:B:593:PHE:CE1	2.81	0.54
1:A:9:THR:O	1:A:10:ARG:HG3	2.06	0.54
1:A:75:ILE:N	1:A:75:ILE:HD13	2.22	0.54
1:B:469:TYR:N	1:B:533:TYR:OH	2.40	0.54
1:A:140:TRP:CD2	1:A:379:ALA:O	2.61	0.54
1:A:598:GLN:O	1:A:599:GLN:HB2	2.08	0.54
1:B:9:THR:HA	1:B:178:THR:HG22	1.90	0.54
1:B:183:TRP:CD1	1:B:208:ALA:HB1	2.41	0.54
1:B:381:ASN:ND2	3:B:680:HOH:O	2.40	0.54
1:B:467:ARG:CG	1:B:467:ARG:NH1	2.63	0.54
1:B:470:GLY:O	1:B:475:SER:CA	2.49	0.54
1:A:8:PRO:CD	1:A:9:THR:H	2.14	0.54
1:A:532:MSE:HG3	1:A:533:TYR:H	1.73	0.53
1:A:100:ASN:HD22	1:A:129:ARG:HH12	1.55	0.53
1:B:14:LYS:CA	1:B:71:ARG:HH21	2.21	0.53
1:A:249:LEU:CD2	1:A:268:ARG:HE	2.22	0.53
1:B:143:ILE:O	1:B:143:ILE:CG2	2.43	0.53
1:B:239:PRO:O	3:B:701:HOH:O	2.19	0.53
1:A:207:VAL:HG11	1:A:210:GLY:O	2.07	0.53
1:A:407:MSE:HE3	1:A:440:PRO:HB2	1.90	0.53
1:B:14:LYS:HA	1:B:71:ARG:HH21	1.73	0.53
1:B:330:HIS:C	1:B:331:TYR:CD2	2.82	0.53
1:B:15:LEU:CD1	1:B:173:SER:CB	2.87	0.53
1:B:91:VAL:O	1:B:110:GLY:HA2	2.09	0.53
1:B:597:PRO:HB3	1:B:600:GLY:O	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:357:PHE:O	1:A:374:LEU:CD2	2.54	0.53
1:B:198:ASN:O	1:B:199:HIS:CB	2.56	0.53
1:A:73:VAL:O	1:A:127:SER:HA	2.08	0.53
1:A:238:ASN:HD22	1:A:238:ASN:C	2.11	0.53
1:B:407:MSE:HE2	1:B:442:THR:CB	2.37	0.53
1:B:539:ARG:HH11	1:B:539:ARG:HB2	1.74	0.53
1:B:253:CYS:SG	1:B:264:ILE:HG23	2.50	0.52
1:A:33:ARG:HB3	1:A:36:GLU:HG3	1.91	0.52
1:A:598:GLN:O	1:A:599:GLN:CB	2.57	0.52
1:B:410:ILE:HD13	1:B:442:THR:O	2.10	0.52
1:B:538:ASP:O	1:B:599:GLN:HG3	2.09	0.52
1:A:191:THR:HG21	1:A:271:ILE:CA	2.38	0.52
1:A:311:MSE:HE1	1:A:336:GLU:O	2.08	0.52
1:B:75:ILE:HB	1:B:124:ALA:HA	1.91	0.52
1:B:359:LEU:HD22	1:B:374:LEU:HD13	1.91	0.52
1:B:523:GLU:OE1	1:B:579:SER:HB3	2.10	0.52
1:B:361:LEU:CD1	2:B:604:Z77:CAZ	2.87	0.52
1:A:33:ARG:HA	1:A:35:TRP:CH2	2.44	0.52
1:A:314:ASP:O	1:A:318:MSE:HG3	2.10	0.52
1:A:509:THR:OG1	1:A:526:GLN:HB2	2.09	0.52
1:B:244:PRO:HG2	1:B:593:PHE:CE1	2.42	0.52
1:A:212:VAL:HA	1:A:255:THR:O	2.10	0.52
1:B:167:TYR:HB2	1:B:304:LYS:HG3	1.91	0.52
1:B:35:TRP:NE1	1:B:98:TRP:CD1	2.77	0.52
1:B:142:THR:CG2	1:B:144:PRO:O	2.53	0.52
1:A:14:LYS:HD2	1:A:176:LEU:HD22	1.92	0.52
1:A:24:ASP:OD1	3:A:826:HOH:O	2.19	0.52
1:B:271:ILE:HD12	1:B:271:ILE:H	1.74	0.52
1:A:184:VAL:HG13	1:A:205:GLN:HE22	1.75	0.51
1:B:376:SER:O	1:B:381:ASN:HB3	2.11	0.51
1:A:456:ILE:HG23	1:A:459:LEU:HD12	1.92	0.51
1:A:436:ASP:CG	1:A:438:THR:HG22	2.31	0.51
1:B:284:ASN:O	1:B:286:LYS:HG3	2.11	0.51
1:A:293:PHE:HE1	1:A:570:ILE:HG13	1.75	0.51
1:B:152:GLU:CG	1:B:153:ASN:N	2.67	0.51
1:A:93:HIS:HE1	1:A:166:ASN:OD1	1.94	0.51
1:B:426:ALA:HB3	1:B:427:PRO:HD3	1.92	0.51
1:A:140:TRP:HB3	1:A:379:ALA:O	2.10	0.51
1:B:388:HIS:CD2	1:B:424:TYR:OH	2.64	0.51
1:B:83:ARG:NH1	1:B:183:TRP:CH2	2.78	0.51
1:A:83:ARG:HH21	1:A:117:ASP:HB2	1.75	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:566:ASN:HD21	1:A:568:LYS:HG3	1.76	0.50
1:B:274:VAL:HG12	1:B:440:PRO:CD	2.40	0.50
1:B:390:GLN:HA	1:B:393:LYS:HG3	1.92	0.50
1:B:539:ARG:HB2	1:B:539:ARG:NH1	2.26	0.50
1:A:456:ILE:HG22	1:A:460:PHE:HE2	1.76	0.50
1:B:10:ARG:CZ	1:B:10:ARG:CB	2.87	0.50
1:A:8:PRO:HG3	1:A:264:ILE:H	1.76	0.50
1:B:216:LEU:HD12	1:B:252:LEU:HB2	1.93	0.50
1:A:230:THR:HG22	1:A:231:SER:OG	2.12	0.50
1:B:15:LEU:CD1	1:B:173:SER:CA	2.88	0.50
1:B:396:ILE:HG12	1:B:408:TRP:CE2	2.46	0.50
1:A:16:ASP:HB2	1:A:71:ARG:NH2	2.26	0.50
1:A:100:ASN:ND2	1:A:129:ARG:NH1	2.58	0.50
1:B:194:ALA:CB	1:B:199:HIS:CD2	2.94	0.50
1:B:248:TYR:CD2	1:B:249:LEU:N	2.79	0.50
1:B:433:ARG:NH1	1:B:461:ASP:OD1	2.44	0.50
1:A:8:PRO:HA	1:B:77:LYS:HZ1	1.77	0.50
1:A:472:TYR:CZ	2:A:604:Z77:HAPA	2.47	0.50
1:A:596:LYS:HE3	3:A:764:HOH:O	2.12	0.50
1:B:73:VAL:O	1:B:73:VAL:HG13	2.12	0.50
1:B:597:PRO:CB	1:B:600:GLY:O	2.59	0.50
1:A:302:ARG:CZ	1:A:302:ARG:HB3	2.41	0.50
1:B:11:GLU:N	1:B:11:GLU:OE2	2.45	0.50
1:B:377:GLU:OE1	1:B:377:GLU:HA	2.11	0.50
1:A:193:VAL:HG13	1:A:273:SER:HB3	1.93	0.50
1:A:203:ASP:OD1	1:A:233:THR:CB	2.60	0.50
1:B:194:ALA:CB	1:B:199:HIS:HD2	2.25	0.50
1:A:385:GLN:HB2	1:A:424:TYR:CE1	2.46	0.49
1:B:105:MSE:CE	1:B:115:GLU:CA	2.74	0.49
1:A:92:THR:HA	1:A:110:GLY:HA2	1.94	0.49
1:A:328:THR:HB	1:A:333:TYR:CD2	2.47	0.49
1:A:445:ASN:ND2	1:A:467:ARG:HH12	2.10	0.49
1:B:205:GLN:HG3	1:B:205:GLN:O	2.12	0.49
1:A:357:PHE:O	1:A:374:LEU:HD11	2.12	0.49
1:B:38:ALA:HA	1:B:70:GLN:OE1	2.13	0.49
1:B:89:ASP:HB2	1:B:172:ARG:HB3	1.95	0.49
1:B:187:ILE:HG22	1:B:188:THR:N	2.26	0.49
1:B:250:TYR:CD2	1:B:271:ILE:CD1	2.95	0.49
1:A:8:PRO:HA	1:B:77:LYS:NZ	2.27	0.49
1:B:102:GLN:HG2	1:B:121:TYR:CD2	2.47	0.49
1:B:384:THR:O	1:B:388:HIS:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:447:MSE:HA	1:B:467:ARG:NH2	2.27	0.49
1:A:13:LYS:O	1:A:174:VAL:O	2.31	0.49
1:A:506:GLY:N	1:A:529:TRP:CZ3	2.80	0.49
1:B:135:ASN:ND2	1:B:137:GLU:H	2.10	0.49
1:A:75:ILE:HB	1:A:124:ALA:HA	1.93	0.49
1:A:249:LEU:HD22	1:A:268:ARG:HE	1.78	0.49
1:B:52:ASN:H	1:B:52:ASN:HD22	1.59	0.49
1:B:105:MSE:HE3	1:B:115:GLU:N	2.26	0.49
1:B:456:ILE:HD13	1:B:456:ILE:O	2.12	0.49
1:A:456:ILE:HG22	1:A:456:ILE:O	2.11	0.49
1:B:210:GLY:HA2	1:B:257:LYS:O	2.13	0.49
1:B:330:HIS:N	1:B:330:HIS:CD2	2.81	0.49
1:B:94:TYR:HA	3:B:716:HOH:O	2.13	0.48
1:B:194:ALA:N	1:B:199:HIS:CD2	2.80	0.48
1:A:279:GLU:OE2	1:A:493:GLN:HG3	2.14	0.48
1:B:86:LEU:HD12	1:B:175:MSE:O	2.12	0.48
1:B:311:MSE:HE1	1:B:336:GLU:HB3	1.95	0.48
1:B:471:TRP:CZ2	1:B:508:ASP:HB2	2.47	0.48
1:A:35:TRP:HD1	1:A:101:ASN:HA	1.77	0.48
1:A:123:ILE:HG22	1:A:126:LYS:HB2	1.95	0.48
1:B:361:LEU:CD1	2:B:604:Z77:N3	2.76	0.48
1:A:49:GLY:HA2	1:A:305:GLY:HA3	1.94	0.48
1:A:188:THR:HB	1:A:204:TRP:CE3	2.48	0.48
1:A:566:ASN:HD21	1:A:568:LYS:HB2	1.77	0.48
1:B:200:ALA:CB	1:B:236:VAL:HG22	2.42	0.48
1:A:68:TRP:HE3	1:A:131:THR:HG22	1.78	0.48
1:A:200:ALA:HA	1:A:235:GLN:O	2.13	0.48
1:B:282:LEU:HD23	1:B:286:LYS:N	2.29	0.48
1:B:507:VAL:HG21	1:B:526:GLN:HA	1.96	0.48
1:A:200:ALA:HB1	1:A:234:LEU:CD2	2.42	0.48
1:A:445:ASN:HD21	1:A:467:ARG:HH22	1.60	0.48
1:B:117:ASP:OD1	1:B:119:THR:OG1	2.27	0.48
1:A:19:TRP:CD1	1:A:47:VAL:HG13	2.48	0.48
1:A:220:ASP:O	1:A:221:GLN:HB2	2.12	0.48
1:B:212:VAL:HG13	1:B:230:THR:CB	2.43	0.48
1:B:214:VAL:CG1	1:B:252:LEU:HD11	2.43	0.48
1:B:549:TRP:HD1	1:B:568:LYS:HD2	1.78	0.48
1:A:83:ARG:HB2	1:A:179:THR:O	2.14	0.48
1:A:163:ASP:OD1	1:A:562:ARG:HD2	2.13	0.48
1:B:40:GLN:CG	3:B:682:HOH:O	2.62	0.48
1:B:193:VAL:CG1	1:B:285:HIS:NE2	2.75	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:494:GLU:OE1	3:A:717:HOH:O	2.20	0.48
1:B:40:GLN:HG3	3:B:682:HOH:O	2.14	0.48
1:B:519:ASP:OD2	1:B:519:ASP:N	2.42	0.48
1:B:102:GLN:HG2	1:B:121:TYR:CE1	2.49	0.47
1:B:272:ARG:HA	1:B:284:ASN:ND2	2.17	0.47
1:B:341:ALA:CB	1:B:346:ILE:HG22	2.43	0.47
1:A:123:ILE:HG21	1:A:126:LYS:HG3	1.95	0.47
1:B:397:ALA:O	1:B:400:LYS:HE2	2.14	0.47
1:A:291:THR:HG21	1:A:591:MSE:HE1	1.95	0.47
1:A:455:THR:C	1:A:456:ILE:HD13	2.34	0.47
1:B:370:LYS:HA	1:B:371:PRO:HD2	1.72	0.47
1:A:52:ASN:ND2	1:A:52:ASN:N	2.61	0.47
1:A:549:TRP:CA	3:A:832:HOH:O	2.62	0.47
1:B:158:GLN:HB2	3:B:678:HOH:O	2.14	0.47
1:A:139:ASN:N	1:A:142:THR:HG22	2.23	0.47
1:A:272:ARG:CA	1:A:284:ASN:HD21	2.24	0.47
1:B:293:PHE:N	1:B:293:PHE:CD2	2.81	0.47
1:B:546:GLU:OE1	1:B:587:ARG:HD3	2.14	0.47
1:A:73:VAL:CG2	1:A:74:PHE:N	2.77	0.47
1:A:426:ALA:HB3	1:A:427:PRO:HD3	1.97	0.47
1:A:446:VAL:O	1:A:449:CYS:O	2.32	0.47
1:A:48:PRO:HD2	3:A:683:HOH:O	2.15	0.47
1:A:202:VAL:HG12	1:A:234:LEU:HD11	1.97	0.47
1:B:192:HIS:HB2	1:B:199:HIS:CE1	2.50	0.47
1:B:277:LYS:HB3	1:B:282:LEU:CD1	2.44	0.47
1:B:324:ASN:OD1	1:B:325:SER:HB3	2.14	0.47
1:A:191:THR:CG2	1:A:271:ILE:HG23	2.45	0.47
1:A:328:THR:C	1:A:329:SER:O	2.46	0.47
1:A:566:ASN:HD21	1:A:568:LYS:CB	2.27	0.47
1:A:43:ARG:NH2	3:A:703:HOH:O	2.40	0.46
1:B:5:VAL:HG12	1:B:6:GLU:N	2.28	0.46
1:B:10:ARG:NH2	1:B:79:TRP:CD1	2.82	0.46
1:B:83:ARG:HH21	1:B:117:ASP:CB	2.19	0.46
1:B:167:TYR:HB2	1:B:304:LYS:CD	2.45	0.46
1:B:250:TYR:CE2	1:B:271:ILE:HD13	2.50	0.46
1:B:292:GLY:HA3	1:B:325:SER:O	2.13	0.46
1:A:532:MSE:HG3	1:A:533:TYR:N	2.30	0.46
1:B:75:ILE:CD1	1:B:176:LEU:HD21	2.44	0.46
1:B:142:THR:HG22	1:B:145:PRO:HA	1.96	0.46
2:B:604:Z77:SAF	2:B:604:Z77:CAJ	3.03	0.46
1:A:19:TRP:CE3	1:A:71:ARG:HB3	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:GLN:HG2	1:A:121:TYR:CD1	2.51	0.46
1:A:241:LEU:HD23	1:A:271:ILE:HG22	1.97	0.46
1:A:273:SER:H	1:A:284:ASN:ND2	2.14	0.46
1:B:35:TRP:CD1	1:B:98:TRP:CD1	3.04	0.46
1:B:167:TYR:CB	1:B:304:LYS:HG3	2.45	0.46
1:B:532:MSE:CG	1:B:533:TYR:N	2.77	0.46
1:A:73:VAL:HG12	1:A:128:VAL:HG22	1.97	0.46
1:A:504:GLU:HG2	1:A:549:TRP:CE3	2.50	0.46
1:B:205:GLN:C	1:B:205:GLN:HE21	2.19	0.46
1:B:212:VAL:CG1	1:B:230:THR:HA	2.44	0.46
1:B:14:LYS:CG	1:B:175:MSE:HA	2.41	0.46
1:B:465:LEU:HB3	1:B:467:ARG:NH1	2.31	0.46
1:B:477:ASP:OD1	1:B:480:THR:HG23	2.14	0.46
1:A:223:VAL:HG12	1:A:223:VAL:O	2.16	0.46
1:A:477:ASP:OD1	1:A:480:THR:CG2	2.61	0.46
1:B:198:ASN:HA	1:B:239:PRO:HD3	1.98	0.46
1:B:203:ASP:CG	1:B:233:THR:OG1	2.54	0.46
1:A:119:THR:CB	1:A:120:PRO:HD3	2.42	0.46
1:A:361:LEU:HD22	2:A:604:Z77:HANA	1.98	0.46
1:B:35:TRP:CD1	1:B:98:TRP:CG	3.03	0.46
1:B:135:ASN:HD21	1:B:137:GLU:HB2	1.81	0.46
1:B:144:PRO:O	1:B:144:PRO:CD	2.63	0.46
1:B:238:ASN:O	1:B:238:ASN:OD1	2.30	0.46
1:B:482:GLU:HG3	1:B:536:VAL:CG2	2.45	0.46
1:B:486:GLU:HG3	1:B:536:VAL:HG13	1.96	0.46
1:B:560:ILE:HG22	1:B:560:ILE:O	2.16	0.46
1:A:194:ALA:C	1:A:196:ASP:N	2.67	0.46
1:B:322:GLY:HA3	1:B:588:TRP:HB3	1.98	0.46
1:A:73:VAL:CG2	1:A:74:PHE:H	2.25	0.46
1:B:43:ARG:NH1	1:B:55:PHE:CD1	2.84	0.46
1:B:250:TYR:CD2	1:B:271:ILE:HD11	2.51	0.46
1:A:100:ASN:O	1:A:101:ASN:CB	2.62	0.46
1:A:123:ILE:CG2	1:A:126:LYS:HG3	2.46	0.46
1:A:238:ASN:N	3:A:789:HOH:O	2.48	0.46
1:B:254:VAL:N	1:B:265:TYR:O	2.49	0.46
1:B:350:ASP:OD2	1:B:395:LEU:HD11	2.15	0.46
1:B:460:PHE:O	1:B:498:GLN:NE2	2.49	0.46
1:A:264:ILE:O	1:A:264:ILE:HG22	2.15	0.45
1:B:70:GLN:HA	1:B:130:ILE:O	2.15	0.45
1:A:18:LEU:HD23	1:A:18:LEU:HA	1.75	0.45
1:A:114:PHE:N	1:A:114:PHE:CD2	2.84	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:141:GLN:HG3	1:A:383:GLU:HB3	1.97	0.45
1:B:469:TYR:O	1:B:473:VAL:O	2.35	0.45
1:A:83:ARG:HD2	1:A:183:TRP:NE1	2.31	0.45
1:B:8:PRO:HG3	1:B:264:ILE:H	1.81	0.45
1:B:96:LYS:HD2	1:B:106:GLU:OE2	2.15	0.45
1:B:191:THR:HG21	1:B:271:ILE:CG2	2.46	0.45
1:A:14:LYS:C	1:A:16:ASP:N	2.69	0.45
1:A:100:ASN:O	1:A:101:ASN:HB2	2.16	0.45
1:A:381:ASN:C	1:A:381:ASN:OD1	2.54	0.45
1:A:447:MSE:HA	1:A:467:ARG:NH1	2.31	0.45
1:A:585:GLN:CG	3:A:636:HOH:O	2.43	0.45
1:B:76:PRO:HG2	1:B:79:TRP:CZ2	2.52	0.45
1:B:94:TYR:HA	1:B:107:HIS:O	2.15	0.45
1:B:207:VAL:HG13	1:B:208:ALA:O	2.12	0.45
1:A:215:GLU:CD	1:A:217:ARG:HH22	2.20	0.45
1:B:15:LEU:CG	1:B:48:PRO:HD3	2.42	0.45
1:B:139:ASN:HA	1:B:146:GLY:O	2.17	0.45
1:B:190:VAL:O	1:B:201:SER:HA	2.17	0.45
1:B:193:VAL:HG12	1:B:273:SER:CB	2.45	0.45
1:B:507:VAL:C	1:B:568:LYS:HG2	2.37	0.45
1:A:198:ASN:OD1	1:A:237:VAL:C	2.55	0.45
1:A:420:GLY:HA2	1:A:423:GLU:HB3	1.98	0.45
1:B:238:ASN:HA	1:B:239:PRO:HD3	1.62	0.45
1:B:288:PHE:O	1:B:544:VAL:HG22	2.16	0.45
1:B:566:ASN:HD21	1:B:568:LYS:CB	2.28	0.45
1:B:375:TYR:HA	1:B:380:VAL:O	2.17	0.45
1:B:412:ASN:HA	1:B:444:VAL:HB	1.98	0.45
1:B:470:GLY:O	1:B:476:GLY:N	2.49	0.45
1:B:502:ILE:HD13	1:B:537:PHE:CE1	2.51	0.45
1:B:538:ASP:O	1:B:599:GLN:CG	2.65	0.45
1:A:205:GLN:HE21	1:A:212:VAL:HG11	1.81	0.45
1:B:215:GLU:OE1	1:B:217:ARG:NH2	2.49	0.45
1:A:187:ILE:HD13	1:A:254:VAL:HG21	1.98	0.45
1:A:438:THR:HG23	1:A:439:ARG:HG3	1.98	0.45
1:B:94:TYR:C	1:B:94:TYR:CD2	2.90	0.45
1:B:385:GLN:NE2	1:B:424:TYR:O	2.50	0.45
1:B:23:LEU:N	3:B:633:HOH:O	2.05	0.45
1:B:268:ARG:H	1:B:268:ARG:HG2	1.50	0.45
1:A:311:MSE:HE2	1:A:340:TRP:HB2	1.95	0.44
1:B:205:GLN:HE22	1:B:207:VAL:HG23	1.74	0.44
1:B:472:TYR:CZ	2:B:604:Z77:HAPA	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:TRP:N	1:A:183:TRP:CD1	2.85	0.44
1:B:546:GLU:OE2	1:B:587:ARG:NH1	2.49	0.44
1:A:12:ILE:O	1:A:14:LYS:HG3	2.17	0.44
1:A:199:HIS:H	1:A:239:PRO:HG3	1.82	0.44
1:B:250:TYR:CE2	1:B:271:ILE:CD1	3.00	0.44
1:B:272:ARG:HH22	1:B:439:ARG:HG2	1.82	0.44
1:A:36:GLU:HA	1:A:129:ARG:NH2	2.26	0.44
1:A:163:ASP:HA	2:A:604:Z77:OAS	2.16	0.44
1:B:247:GLY:O	1:B:249:LEU:CD1	2.64	0.44
1:B:69:TYR:CE2	1:B:134:VAL:HG21	2.52	0.44
1:B:193:VAL:CA	1:B:199:HIS:CD2	3.01	0.44
1:B:267:LEU:O	1:B:269:VAL:HG23	2.16	0.44
1:A:39:LEU:N	1:A:70:GLN:OE1	2.41	0.44
1:B:52:ASN:HD21	1:B:168:ALA:H	1.66	0.44
1:A:249:LEU:CD1	1:A:249:LEU:N	2.80	0.44
1:A:388:HIS:HD2	1:A:424:TYR:OH	2.00	0.44
1:A:587:ARG:O	1:A:591:MSE:HG3	2.18	0.44
1:B:75:ILE:HG13	1:B:122:VAL:CG2	2.48	0.44
1:B:201:SER:O	1:B:234:LEU:HA	2.18	0.44
1:B:219:ALA:HB2	1:B:248:TYR:CZ	2.53	0.44
1:A:7:THR:HB	1:A:264:ILE:HG22	2.00	0.44
1:B:6:GLU:HG2	1:B:10:ARG:HA	1.99	0.44
1:B:167:TYR:HB2	1:B:304:LYS:CG	2.47	0.44
1:B:598:GLN:NE2	1:B:600:GLY:HA3	2.32	0.44
1:A:16:ASP:CG	1:B:13:LYS:HZ2	2.21	0.44
1:A:78:GLY:HA3	1:B:78:GLY:HA3	2.00	0.44
1:A:192:HIS:CE1	1:A:202:VAL:HG13	2.53	0.44
1:A:475:SER:HB3	1:A:520:MSE:SE	2.67	0.44
1:A:482:GLU:HG3	1:A:532:MSE:HE1	1.99	0.44
1:A:436:ASP:HA	1:A:437:PRO:HD2	1.81	0.43
1:A:447:MSE:CE	1:A:468:TYR:H	2.31	0.43
1:B:328:THR:HB	1:B:333:TYR:CD2	2.52	0.43
1:A:8:PRO:HG2	1:A:263:ASP:OD1	2.18	0.43
1:B:193:VAL:CG1	1:B:273:SER:HB3	2.46	0.43
1:B:216:LEU:HB3	1:B:225:ALA:CB	2.27	0.43
1:B:361:LEU:HD11	2:B:604:Z77:CAY	2.48	0.43
1:B:473:VAL:O	1:B:474:GLN:HB2	2.18	0.43
1:B:187:ILE:CG2	1:B:188:THR:N	2.81	0.43
1:B:290:PHE:HB2	1:B:545:GLY:CA	2.47	0.43
1:B:486:GLU:OE1	1:B:539:ARG:NH1	2.51	0.43
1:B:587:ARG:O	1:B:591:MSE:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:162:HIS:CD2	1:B:164:PHE:CE2	3.06	0.43
1:B:272:ARG:CA	1:B:284:ASN:HD21	2.19	0.43
1:A:422:ARG:HA	1:A:456:ILE:CD1	2.48	0.43
1:B:401:ASN:HB2	3:B:704:HOH:O	2.18	0.43
1:B:441:ILE:HD12	1:B:460:PHE:HD1	1.84	0.43
1:B:105:MSE:HE3	1:B:115:GLU:C	2.39	0.43
1:B:286:LYS:HA	1:B:287:PRO:HD3	1.79	0.43
1:B:315:HIS:CE1	3:B:668:HOH:O	2.65	0.43
1:A:15:LEU:HD12	1:A:173:SER:HB3	0.83	0.43
1:A:54:GLN:O	1:B:313:HIS:HA	2.18	0.43
1:A:66:ASN:N	1:A:66:ASN:HD22	2.15	0.43
1:A:87:ARG:HD2	1:A:115:GLU:OE1	2.18	0.43
1:A:139:ASN:N	1:A:142:THR:CG2	2.70	0.43
1:A:566:ASN:HD22	1:A:566:ASN:C	2.21	0.43
1:A:13:LYS:C	1:A:15:LEU:H	2.21	0.43
1:A:550:ASN:ND2	1:A:551:PHE:N	2.66	0.43
1:B:12:ILE:HG22	1:B:12:ILE:O	2.18	0.43
1:B:212:VAL:HG23	1:B:214:VAL:HG23	2.01	0.43
1:B:467:ARG:CD	1:B:469:TYR:CE1	3.00	0.43
1:B:567:LYS:HA	1:B:567:LYS:HD2	1.83	0.43
1:A:102:GLN:HE21	1:A:102:GLN:HA	1.84	0.43
1:A:380:VAL:HG13	1:A:384:THR:HG21	2.00	0.43
1:B:191:THR:CG2	1:B:271:ILE:HA	2.33	0.43
1:B:441:ILE:HD12	1:B:460:PHE:CD1	2.54	0.43
1:A:102:GLN:HA	1:A:102:GLN:NE2	2.34	0.43
1:A:106:GLU:N	3:A:763:HOH:O	2.41	0.43
1:A:107:HIS:HD2	3:A:866:HOH:O	2.01	0.43
1:B:218:ASP:CG	1:B:222:GLN:HG3	2.39	0.43
1:B:422:ARG:NH2	1:B:458:ASP:OD2	2.52	0.43
1:B:369:ASN:N	1:B:369:ASN:HD22	2.16	0.42
1:B:75:ILE:HG13	1:B:122:VAL:HG22	2.01	0.42
1:B:374:LEU:O	1:B:380:VAL:HB	2.19	0.42
2:B:604:Z77:HAC	2:B:604:Z77:HAB	1.71	0.42
1:A:238:ASN:C	1:A:238:ASN:ND2	2.72	0.42
1:B:102:GLN:HG2	1:B:121:TYR:CZ	2.55	0.42
1:B:490:LEU:O	1:B:494:GLU:HG2	2.20	0.42
1:A:94:TYR:CE1	1:A:106:GLU:HG2	2.55	0.42
1:B:4:PRO:HD3	1:B:87:ARG:NH1	2.33	0.42
1:B:488:GLU:O	1:B:488:GLU:HG3	2.20	0.42
2:B:604:Z77:HN1	2:B:604:Z77:HAP	1.53	0.42
1:A:123:ILE:O	1:A:123:ILE:CG2	2.63	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:150:THR:HG22	1:A:156:LYS:HG2	2.02	0.42
1:A:395:LEU:HD12	1:A:395:LEU:O	2.19	0.42
1:B:304:LYS:HE3	1:B:304:LYS:HB3	1.65	0.42
1:B:351:GLU:HG3	1:B:352:THR:N	2.35	0.42
1:B:2:LEU:HD23	1:B:2:LEU:HA	1.93	0.42
1:B:198:ASN:HD21	1:B:236:VAL:HG12	1.85	0.42
1:A:566:ASN:HD21	1:A:568:LYS:CG	2.32	0.42
1:B:239:PRO:N	3:B:701:HOH:O	2.52	0.42
1:A:518:THR:O	1:A:525:TYR:CD1	2.65	0.42
1:B:14:LYS:C	1:B:16:ASP:N	2.73	0.42
1:B:95:GLY:HA2	1:B:133:CYS:O	2.18	0.42
1:A:68:TRP:HE3	1:A:131:THR:CG2	2.33	0.42
1:A:599:GLN:HB2	1:A:599:GLN:HE21	1.43	0.42
1:B:14:LYS:CB	1:B:174:VAL:CG2	2.91	0.42
1:B:356:GLY:C	1:B:358:ASN:H	2.23	0.42
1:B:494:GLU:O	1:B:497:HIS:CD2	2.73	0.42
1:B:508:ASP:HB3	1:B:521:TRP:CZ3	2.55	0.42
1:B:538:ASP:O	1:B:599:GLN:HA	2.20	0.42
1:A:464:CYS:HA	1:A:501:ILE:O	2.20	0.41
1:B:89:ASP:O	1:B:90:ALA:HB2	2.20	0.41
1:B:102:GLN:O	1:B:104:VAL:HG13	2.20	0.41
1:B:186:ASP:CB	1:B:206:VAL:HB	2.48	0.41
1:B:402:HIS:HA	1:B:403:PRO:HD2	1.74	0.41
1:A:84:ILE:O	1:A:118:VAL:HG22	2.20	0.41
1:A:295:ARG:O	1:A:333:TYR:OH	2.37	0.41
1:A:381:ASN:O	1:A:384:THR:N	2.54	0.41
1:B:239:PRO:CA	3:B:701:HOH:O	2.68	0.41
1:B:243:GLN:HB3	1:B:244:PRO:HD2	2.01	0.41
1:B:248:TYR:C	1:B:249:LEU:HD12	2.40	0.41
1:B:449:CYS:HB3	1:B:454:ASP:HB2	2.01	0.41
1:B:504:GLU:HG2	1:B:549:TRP:CE3	2.56	0.41
1:A:368:GLY:HA2	1:A:369:ASN:HA	1.70	0.41
1:B:52:ASN:O	3:B:627:HOH:O	2.21	0.41
1:B:467:ARG:HD2	1:B:469:TYR:HE1	1.81	0.41
1:A:147:MSE:CE	1:A:161:PHE:HZ	2.06	0.41
1:A:255:THR:HA	1:A:263:ASP:O	2.19	0.41
1:B:328:THR:O	1:B:329:SER:C	2.59	0.41
1:A:15:LEU:O	1:A:16:ASP:C	2.57	0.41
1:A:102:GLN:HG2	1:A:121:TYR:CG	2.56	0.41
1:A:264:ILE:HD13	1:A:264:ILE:HA	1.92	0.41
1:B:43:ARG:HD2	1:B:55:PHE:CE1	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:220:ASP:O	1:B:221:GLN:HB2	2.20	0.41
1:B:282:LEU:HD23	1:B:285:HIS:C	2.41	0.41
1:B:141:GLN:CG	1:B:383:GLU:HB3	2.46	0.41
1:B:410:ILE:N	1:B:410:ILE:HD13	2.36	0.41
1:A:318:MSE:HE2	1:A:318:MSE:HB3	1.96	0.41
1:A:538:ASP:O	1:A:599:GLN:HG3	2.21	0.41
1:B:0:HIS:CD2	1:B:0:HIS:N	2.88	0.41
1:B:238:ASN:O	1:B:238:ASN:ND2	2.53	0.41
1:B:493:GLN:HG3	1:B:542:ALA:HB2	2.03	0.41
1:B:549:TRP:CE3	1:B:549:TRP:HA	2.49	0.41
1:A:23:LEU:HD13	1:A:63:TYR:CD1	2.56	0.41
1:A:65:GLY:C	1:A:66:ASN:HD22	2.24	0.41
1:B:501:ILE:HG12	1:B:545:GLY:HA3	2.01	0.41
1:A:550:ASN:HD22	1:A:552:ALA:N	2.07	0.41
2:A:604:Z77:HAC	2:A:604:Z77:HAB	1.73	0.41
1:B:12:ILE:CG2	1:B:14:LYS:HD2	2.44	0.41
1:B:183:TRP:N	1:B:208:ALA:HB3	2.33	0.41
1:B:215:GLU:CD	1:B:217:ARG:HH22	2.22	0.41
1:A:529:TRP:O	1:A:532:MSE:HG3	2.21	0.41
1:B:38:ALA:O	1:B:39:LEU:C	2.56	0.41
1:A:46:ALA:H	1:A:54:GLN:NE2	2.07	0.40
1:A:93:HIS:O	1:A:109:GLY:O	2.38	0.40
1:B:137:GLU:O	1:B:138:LEU:HD23	2.22	0.40
1:B:224:VAL:O	1:B:224:VAL:CG2	2.69	0.40
1:B:242:TRP:CZ2	1:B:345:GLY:HA2	2.55	0.40
1:B:272:ARG:NH2	1:B:439:ARG:NE	2.69	0.40
1:B:361:LEU:HA	1:B:362:GLY:HA3	1.91	0.40
1:B:550:ASN:HD22	1:B:552:ALA:H	1.68	0.40
1:A:33:ARG:HD2	1:A:36:GLU:OE2	2.21	0.40
1:A:76:PRO:HA	1:B:10:ARG:HD2	2.03	0.40
1:A:197:CYS:O	1:A:238:ASN:ND2	2.55	0.40
1:B:5:VAL:CG1	1:B:6:GLU:N	2.84	0.40
1:A:92:THR:HG1	1:A:171:HIS:CE1	2.39	0.40
1:A:388:HIS:CD2	1:A:424:TYR:OH	2.74	0.40
1:B:421:ALA:O	1:B:425:PHE:HD2	2.04	0.40
1:B:447:MSE:CE	1:B:469:TYR:CE2	3.05	0.40
1:A:328:THR:HA	1:A:333:TYR:CZ	2.55	0.40
1:B:105:MSE:CE	1:B:114:PHE:O	2.69	0.40
1:B:192:HIS:O	1:B:199:HIS:HB3	2.21	0.40
1:B:239:PRO:C	3:B:701:HOH:O	2.59	0.40
1:A:75:ILE:HG12	1:A:126:LYS:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:PRO:HG2	1:A:79:TRP:CZ2	2.56	0.40
1:A:215:GLU:HG3	1:A:217:ARG:NH1	2.25	0.40
1:B:102:GLN:HG2	1:B:121:TYR:CE2	2.55	0.40
1:B:274:VAL:HG11	1:B:406:VAL:O	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:366:GLU:OE2	1:B:474:GLN:N[2_555]	2.05	0.15

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	601/605 (99%)	579 (96%)	20 (3%)	2 (0%)	41	46
1	B	601/605 (99%)	556 (92%)	42 (7%)	3 (0%)	29	29
All	All	1202/1210 (99%)	1135 (94%)	62 (5%)	5 (0%)	34	37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	8	PRO
1	A	239	PRO
1	B	143	ILE
1	B	370	LYS
1	B	144	PRO

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	509/500 (102%)	450 (88%)	59 (12%)	5	3
1	B	509/500 (102%)	436 (86%)	73 (14%)	3	2
All	All	1018/1000 (102%)	886 (87%)	132 (13%)	4	2

All (132) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	ARG
1	A	5	VAL
1	A	7	THR
1	A	12	ILE
1	A	15	LEU
1	A	42	SER
1	A	43	ARG
1	A	47	VAL
1	A	52	ASN
1	A	66	ASN
1	A	71	ARG
1	A	75	ILE
1	A	102	GLN
1	A	122	VAL
1	A	123	ILE
1	A	148	VAL
1	A	163	ASP
1	A	173	SER
1	A	176	LEU
1	A	178	THR
1	A	179	THR
1	A	193	VAL
1	A	198	ASN
1	A	201	SER
1	A	204	TRP
1	A	218	ASP
1	A	220	ASP

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Mol	Chain	Res	Type
1	A	226	THR
1	A	233	THR
1	A	234	LEU
1	A	235	GLN
1	A	238	ASN
1	A	255	THR
1	A	258	SER
1	A	264	ILE
1	A	272	ARG
1	A	274	VAL
1	A	298	ASP
1	A	302	ARG
1	A	329	SER
1	A	359	LEU
1	A	360	SER
1	A	378	GLU
1	A	383	GLU
1	A	419	GLN
1	A	441	ILE
1	A	473	VAL
1	A	480	THR
1	A	494	GLU
1	A	513	LEU
1	A	518	THR
1	A	532	MSE
1	A	544	VAL
1	A	550	ASN
1	A	566	ASN
1	A	575	ARG
1	A	583	LEU
1	A	585	GLN
1	A	599	GLN
1	B	0	HIS
1	B	3	ARG
1	B	6	GLU
1	B	12	ILE
1	B	15	LEU
1	B	16	ASP
1	B	40	GLN
1	B	41	GLU
1	B	47	VAL
1	B	61	ARG

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Mol	Chain	Res	Type
1	B	71	ARG
1	B	94	TYR
1	B	119	THR
1	B	122	VAL
1	B	130	ILE
1	B	142	THR
1	B	148	VAL
1	B	149	ILE
1	B	152	GLU
1	B	157	LYS
1	B	159	SER
1	B	174	VAL
1	B	175	MSE
1	B	178	THR
1	B	179	THR
1	B	183	TRP
1	B	185	ASP
1	B	197	CYS
1	B	198	ASN
1	B	199	HIS
1	B	201	SER
1	B	202	VAL
1	B	203	ASP
1	B	205	GLN
1	B	209	ASN
1	B	212	VAL
1	B	218	ASP
1	B	220	ASP
1	B	222	GLN
1	B	226	THR
1	B	228	GLN
1	B	237	VAL
1	B	238	ASN
1	B	241	LEU
1	B	268	ARG
1	B	272	ARG
1	B	302	ARG
1	B	330	HIS
1	B	346	ILE
1	B	359	LEU
1	B	383	GLU
1	B	392	ILE

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Mol	Chain	Res	Type
1	B	410	ILE
1	B	450	ASP
1	B	454	ASP
1	B	456	ILE
1	B	467	ARG
1	B	473	VAL
1	B	478	LEU
1	B	480	THR
1	B	488	GLU
1	B	494	GLU
1	B	513	LEU
1	B	518	THR
1	B	532	MSE
1	B	535	ARG
1	B	550	ASN
1	B	566	ASN
1	B	567	LYS
1	B	583	LEU
1	B	591	MSE
1	B	598	GLN
1	B	599	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (42) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	52	ASN
1	A	54	GLN
1	A	66	ASN
1	A	93	HIS
1	A	100	ASN
1	A	101	ASN
1	A	102	GLN
1	A	107	HIS
1	A	135	ASN
1	A	192	HIS
1	A	235	GLN
1	A	238	ASN
1	A	243	GLN
1	A	284	ASN
1	A	313	HIS
1	A	330	HIS
1	A	388	HIS

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Mol	Chain	Res	Type
1	A	401	ASN
1	A	445	ASN
1	A	550	ASN
1	A	566	ASN
1	A	585	GLN
1	A	599	GLN
1	B	52	ASN
1	B	54	GLN
1	B	93	HIS
1	B	135	ASN
1	B	198	ASN
1	B	205	GLN
1	B	209	ASN
1	B	243	GLN
1	B	284	ASN
1	B	313	HIS
1	B	330	HIS
1	B	369	ASN
1	B	388	HIS
1	B	401	ASN
1	B	445	ASN
1	B	474	GLN
1	B	550	ASN
1	B	566	ASN
1	B	599	GLN

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

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	Z77	A	604	-	31,31,31	1.80	8 (25%)	40,43,43	1.88	8 (20%)
2	Z77	B	604	-	31,31,31	1.70	7 (22%)	40,43,43	1.50	9 (22%)

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	Z77	A	604	-	-	2/17/17/17	0/3/3/3
2	Z77	B	604	-	-	3/17/17/17	0/3/3/3

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	604	Z77	CAP-CAY	4.31	1.55	1.51
2	A	604	Z77	CAM-CAY	4.29	1.41	1.34
2	A	604	Z77	CAZ-N3	4.04	1.41	1.35
2	B	604	Z77	CAT-SAF	3.95	1.74	1.67
2	B	604	Z77	CAW-N1	-3.90	1.33	1.41
2	B	604	Z77	CAM-CAY	3.82	1.40	1.34
2	B	604	Z77	CAZ-N3	3.30	1.40	1.35
2	A	604	Z77	CAT-SAF	3.12	1.72	1.67
2	B	604	Z77	CAP-CAY	2.95	1.54	1.51
2	A	604	Z77	CAW-N1	-2.86	1.35	1.41
2	A	604	Z77	CAZ-CAY	-2.63	1.39	1.45
2	A	604	Z77	CAP-N2	2.44	1.48	1.45
2	B	604	Z77	CAP-N2	2.19	1.48	1.45
2	B	604	Z77	CBA-CAM	-2.17	1.39	1.43
2	A	604	Z77	CAC-CAV	2.13	1.55	1.51

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	604	Z77	N1-CAT-N2	6.30	122.98	115.11
2	A	604	Z77	SAF-CAT-N2	-5.84	116.20	124.42
2	B	604	Z77	CBB-N3-CAZ	-3.65	120.16	124.80
2	A	604	Z77	OAD-CAZ-CAY	-3.43	119.86	124.96
2	B	604	Z77	CAP-N2-CAO	3.28	121.51	117.36
2	A	604	Z77	CAA-OAS-CAX	-3.25	110.47	117.51
2	A	604	Z77	CAY-CAZ-N3	3.02	119.58	115.08
2	B	604	Z77	CAY-CAZ-N3	2.99	119.54	115.08
2	B	604	Z77	CAP-CAY-CAM	-2.96	115.18	121.66
2	B	604	Z77	CAP-N2-CAT	-2.88	117.64	122.53
2	A	604	Z77	CBB-N3-CAZ	-2.87	121.15	124.80
2	B	604	Z77	CBA-CAK-CAU	-2.81	120.36	123.02
2	B	604	Z77	OAD-CAZ-N3	-2.52	117.09	121.67
2	A	604	Z77	CBA-CAK-CAU	-2.50	120.65	123.02
2	A	604	Z77	CAO-N2-CAT	-2.41	117.27	121.92
2	B	604	Z77	SAF-CAT-N2	-2.30	121.18	124.42
2	B	604	Z77	CBA-CBB-N3	2.08	120.47	118.69

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	604	Z77	CAI-CAX-OAS-CAA
2	B	604	Z77	CAJ-CAX-OAS-CAA
2	A	604	Z77	CAJ-CAX-OAS-CAA
2	A	604	Z77	CAI-CAX-OAS-CAA
2	B	604	Z77	N2-CAP-CAY-CAM

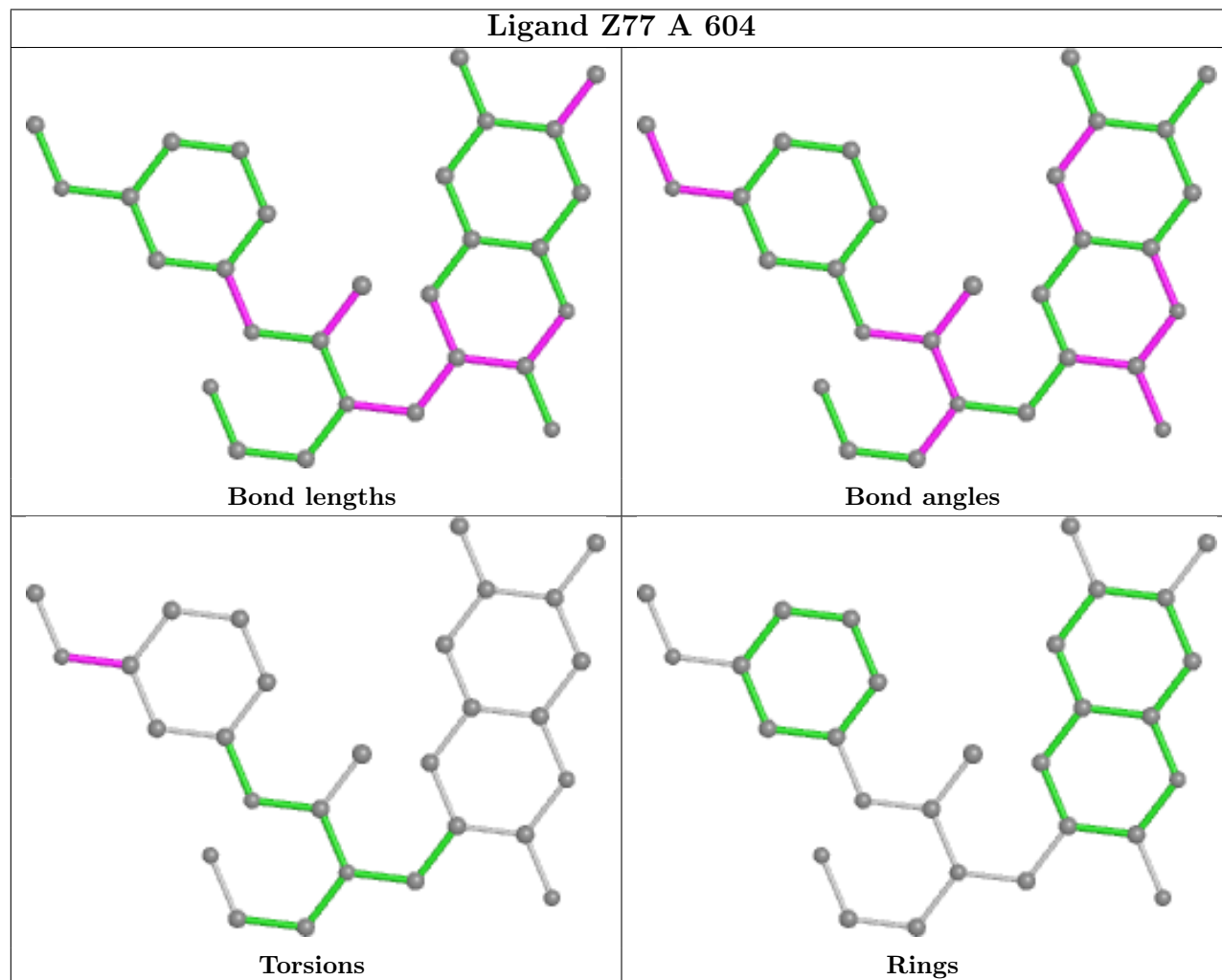
There are no ring outliers.

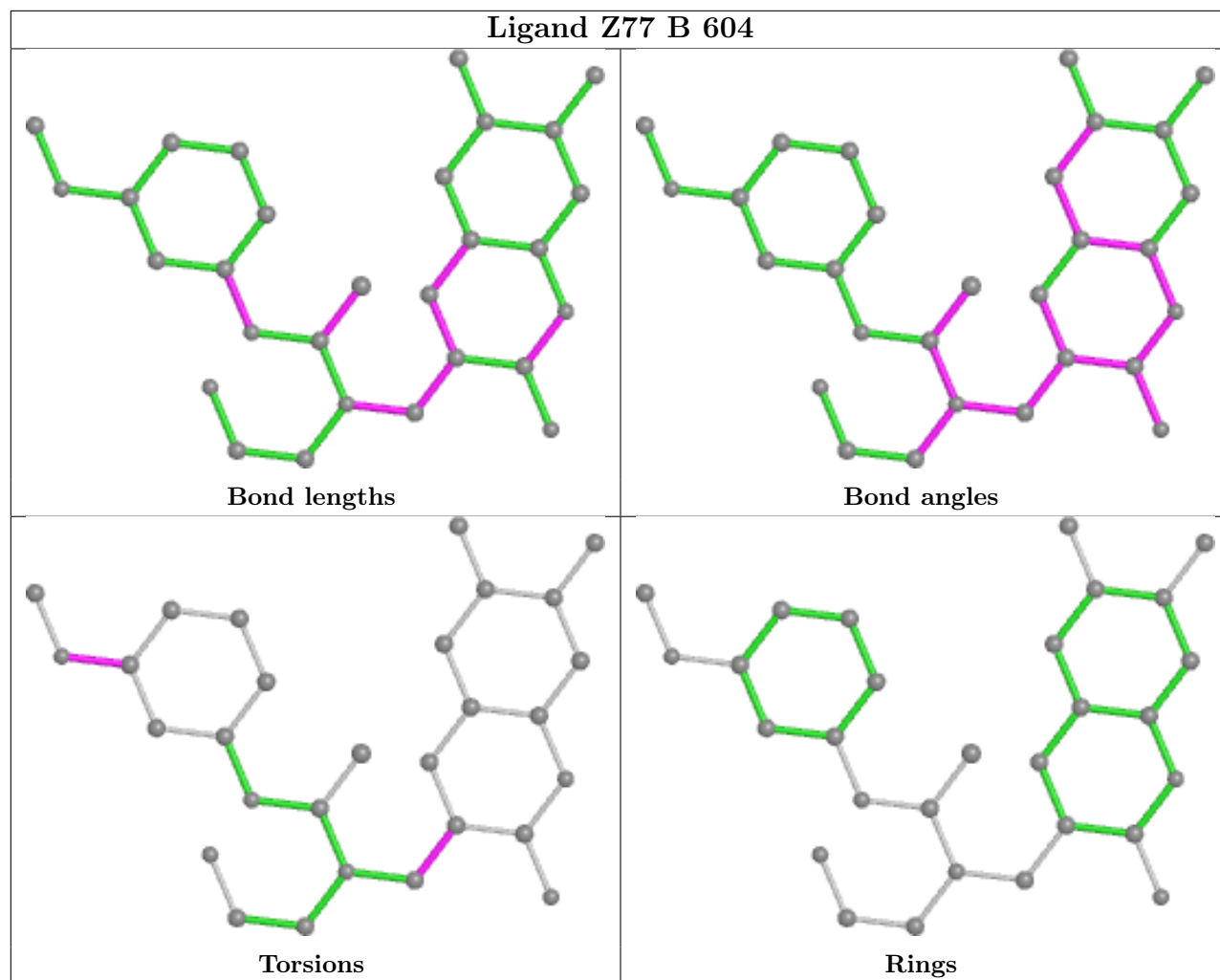
2 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	604	Z77	6	0
2	B	604	Z77	10	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	590/605 (97%)	0.29	33 (5%) 24 26	21, 47, 105, 138	0
1	B	590/605 (97%)	0.77	75 (12%) 3 3	29, 85, 166, 230	0
All	All	1180/1210 (97%)	0.53	108 (9%) 9 9	21, 66, 142, 230	0

All (108) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	545	GLY	8.6
1	B	204	TRP	7.9
1	B	231	SER	7.4
1	B	208	ALA	7.1
1	B	209	ASN	6.9
1	A	208	ALA	6.6
1	B	212	VAL	6.4
1	A	199	HIS	5.9
1	B	239	PRO	5.7
1	B	289	TYR	5.2
1	B	207	VAL	5.0
1	B	206	VAL	4.9
1	B	240	HIS	4.9
1	A	230	THR	4.9
1	B	463	LEU	4.7
1	B	230	THR	4.6
1	B	537	PHE	4.6
1	B	501	ILE	4.5
1	B	274	VAL	4.4
1	B	601	GLY	4.3
1	A	207	VAL	4.2
1	B	283	ILE	4.1
1	A	209	ASN	4.1
1	A	8	PRO	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	288	PHE	4.0
1	B	600	GLY	4.0
1	A	231	SER	4.0
1	B	425	PHE	3.9
1	B	598	GLN	3.9
1	A	252	LEU	3.9
1	B	182	THR	3.8
1	B	282	LEU	3.8
1	B	242	TRP	3.8
1	A	214	VAL	3.7
1	B	241	LEU	3.6
1	B	281	PHE	3.6
1	B	225	ALA	3.5
1	B	379	ALA	3.5
1	A	264	ILE	3.5
1	B	250	TYR	3.4
1	B	290	PHE	3.3
1	B	236	VAL	3.3
1	B	77	LYS	3.2
1	A	80	ALA	3.1
1	B	292	GLY	3.1
1	B	380	VAL	3.0
1	B	500	ILE	3.0
1	A	363	ILE	3.0
1	A	98	TRP	3.0
1	B	16	ASP	3.0
1	A	256	ALA	3.0
1	B	191	THR	2.9
1	B	243	GLN	2.9
1	A	235	GLN	2.9
1	B	211	ASP	2.9
1	B	199	HIS	2.9
1	B	544	VAL	2.9
1	A	79	TRP	2.8
1	B	257	LYS	2.8
1	B	536	VAL	2.8
1	A	16	ASP	2.7
1	A	260	THR	2.7
1	B	424	TYR	2.7
1	B	261	GLU	2.6
1	B	489	LEU	2.6
1	B	259	GLN	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	271	ILE	2.6
1	B	255	THR	2.5
1	B	214	VAL	2.5
1	B	256	ALA	2.5
1	B	196	ASP	2.5
1	A	216	LEU	2.5
1	B	229	GLY	2.5
1	A	253	CYS	2.5
1	A	257	LYS	2.5
1	B	222	GLN	2.5
1	B	357	PHE	2.4
1	B	246	GLU	2.4
1	B	535	ARG	2.4
1	A	510	LEU	2.4
1	B	224	VAL	2.4
1	B	549	TRP	2.3
1	B	152	GLU	2.3
1	A	379	ALA	2.3
1	A	470	GLY	2.3
1	A	211	ASP	2.3
1	A	84	ILE	2.3
1	A	35	TRP	2.2
1	B	469	TYR	2.2
1	B	253	CYS	2.2
1	B	277	LYS	2.2
1	A	362	GLY	2.2
1	B	368	GLY	2.2
1	A	511	ALA	2.2
1	A	47	VAL	2.1
1	B	510	LEU	2.1
1	B	531	ASP	2.1
1	A	15	LEU	2.1
1	B	216	LEU	2.1
1	B	386	GLN	2.1
1	B	588	TRP	2.1
1	B	369	ASN	2.1
1	A	183	TRP	2.1
1	B	223	VAL	2.0
1	B	410	ILE	2.0
1	B	205	GLN	2.0
1	A	601	GLY	2.0
1	B	387	ALA	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](#)

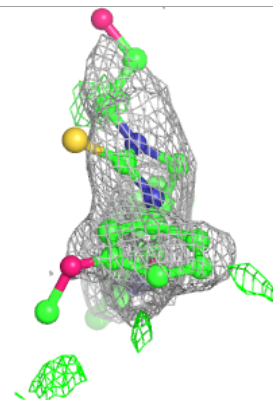
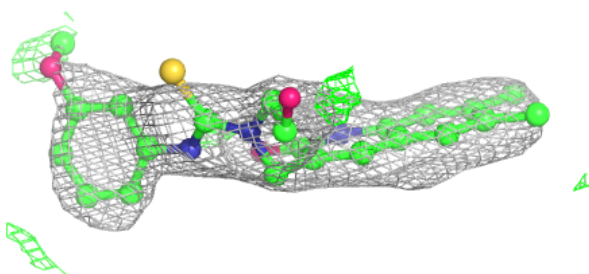
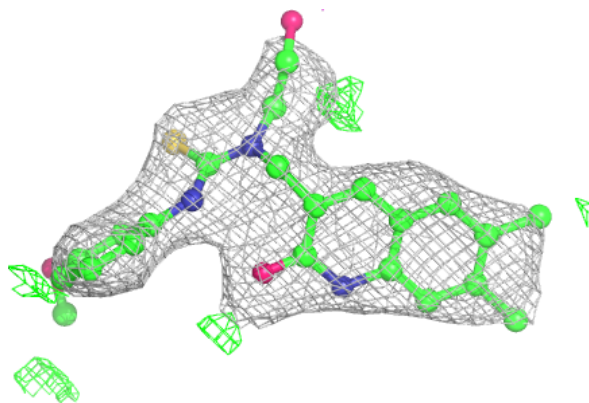
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	Z77	B	604	29/29	0.85	0.21	63,75,94,123	5
2	Z77	A	604	29/29	0.91	0.17	48,65,106,111	2

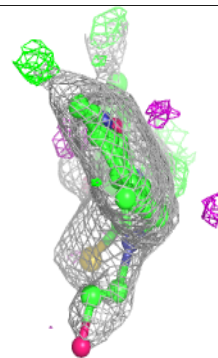
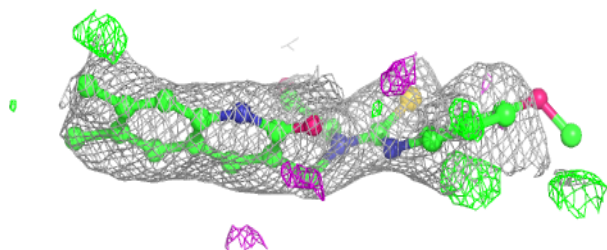
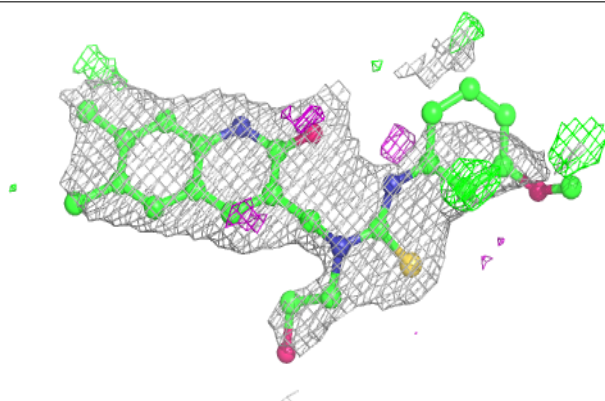
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around Z77 B 604:

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

**Electron density around Z77 A 604:**

$2mF_o-DF_c$ (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.