



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:58 PM UTC

PDB ID : 9G8K / pdb_00009g8k
Title : Structure of K⁺-dependent Na⁺-PPase from *Thermotoga maritima* in complex with Ca²⁺ and Etidronate
Authors : Vidilaseris, K.; Liu, J.; Goldman, A.
Deposited on : 2024-07-23
Resolution : 3.15 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

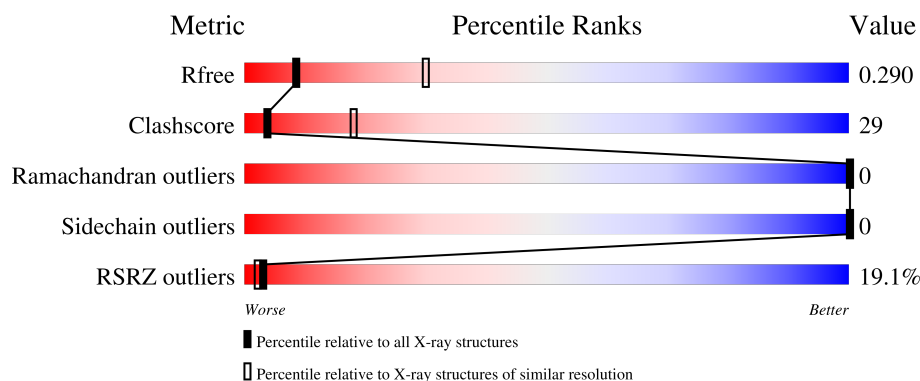
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.15 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}	180053	2361 (3.20-3.12)
Clashscore	190562	2486 (3.20-3.12)
Ramachandran outliers	187476	2405 (3.20-3.12)
Sidechain outliers	187428	2404 (3.20-3.12)
RSRZ outliers	180081	2361 (3.20-3.12)

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	735	17% 55% 41% 5%
1	B	735	19% 51% 43% 5%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 10320 atoms, of which 104 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.

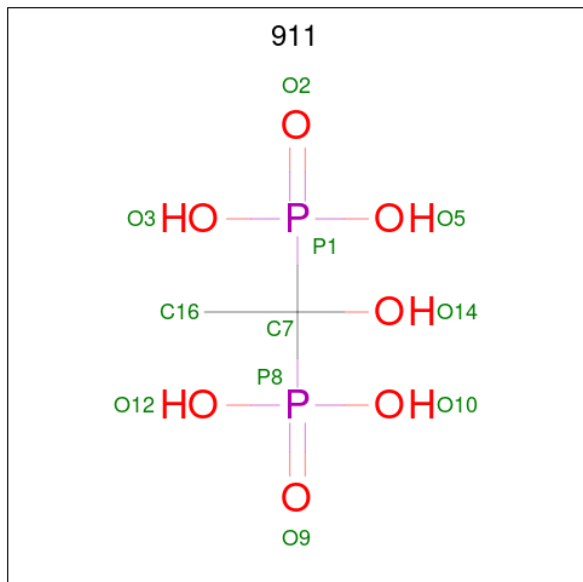
- Molecule 1 is a protein called K(+)-stimulated pyrophosphate-energized sodium pump.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	700	Total	C	N	O	S	0	0	0
			5087	3331	801	928	27			
1	B	698	Total	C	N	O	S	0	0	0
			5020	3289	785	922	24			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MET	-	initiating methionine	UNP Q9S5X0
A	-7	ARG	-	expression tag	UNP Q9S5X0
A	-6	GLY	-	expression tag	UNP Q9S5X0
A	-5	SER	-	expression tag	UNP Q9S5X0
A	-4	HIS	-	expression tag	UNP Q9S5X0
A	-3	HIS	-	expression tag	UNP Q9S5X0
A	-2	HIS	-	expression tag	UNP Q9S5X0
A	-1	HIS	-	expression tag	UNP Q9S5X0
A	0	HIS	-	expression tag	UNP Q9S5X0
A	1	HIS	-	expression tag	UNP Q9S5X0
A	353	LEU	VAL	engineered mutation	UNP Q9S5X0
A	395	GLY	SER	engineered mutation	UNP Q9S5X0
B	-8	MET	-	initiating methionine	UNP Q9S5X0
B	-7	ARG	-	expression tag	UNP Q9S5X0
B	-6	GLY	-	expression tag	UNP Q9S5X0
B	-5	SER	-	expression tag	UNP Q9S5X0
B	-4	HIS	-	expression tag	UNP Q9S5X0
B	-3	HIS	-	expression tag	UNP Q9S5X0
B	-2	HIS	-	expression tag	UNP Q9S5X0
B	-1	HIS	-	expression tag	UNP Q9S5X0
B	0	HIS	-	expression tag	UNP Q9S5X0
B	1	HIS	-	expression tag	UNP Q9S5X0
B	353	LEU	VAL	engineered mutation	UNP Q9S5X0
B	395	GLY	SER	engineered mutation	UNP Q9S5X0

- Molecule 2 is (1-hydroxyethane-1,1-diyl)bis(phosphonic acid) (CCD ID: 911) (formula: $C_2H_8O_7P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			17	2	6	7	2		
2	B	1	Total	C	H	O	P	0	0
			17	2	6	7	2		

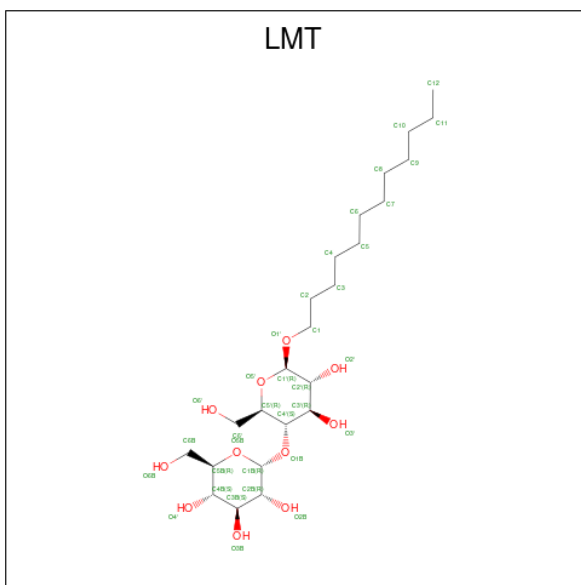
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	4	Total	Mg	0	0
			4	4		
3	B	5	Total	Mg	0	0
			5	5		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	B	1	Total	Ca	0	0
			1	1		

- Molecule 5 is DODECYL-BETA-D-MALTOSIDE (CCD ID: LMT) (formula: $C_{24}H_{46}O_{11}$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total 81	C 24	H 46	O 11	0	0
5	B	1	Total 81	C 24	H 46	O 11	0	0

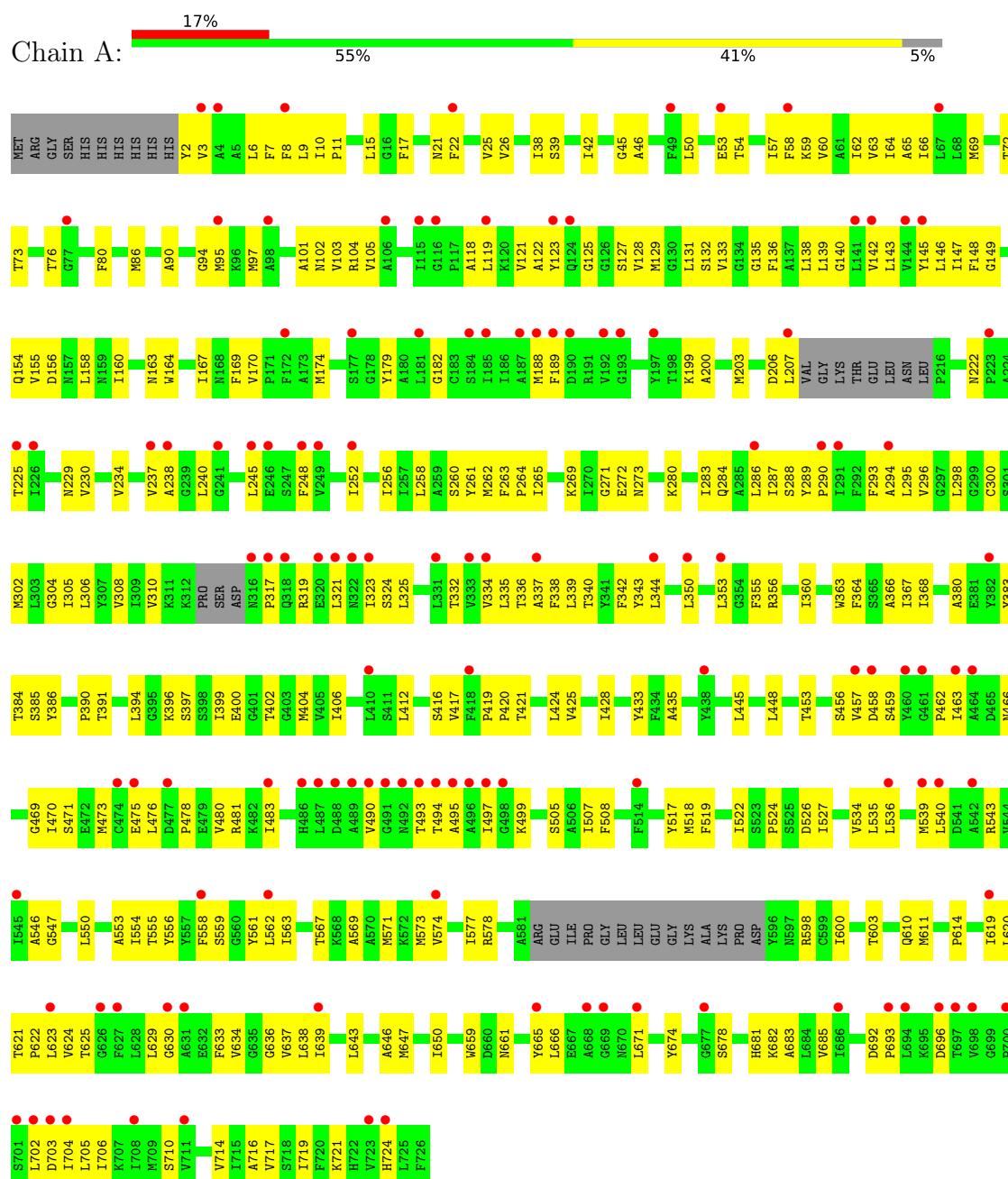
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	2	Total O 2 2	0	0
6	B	4	Total O 4 4	0	0

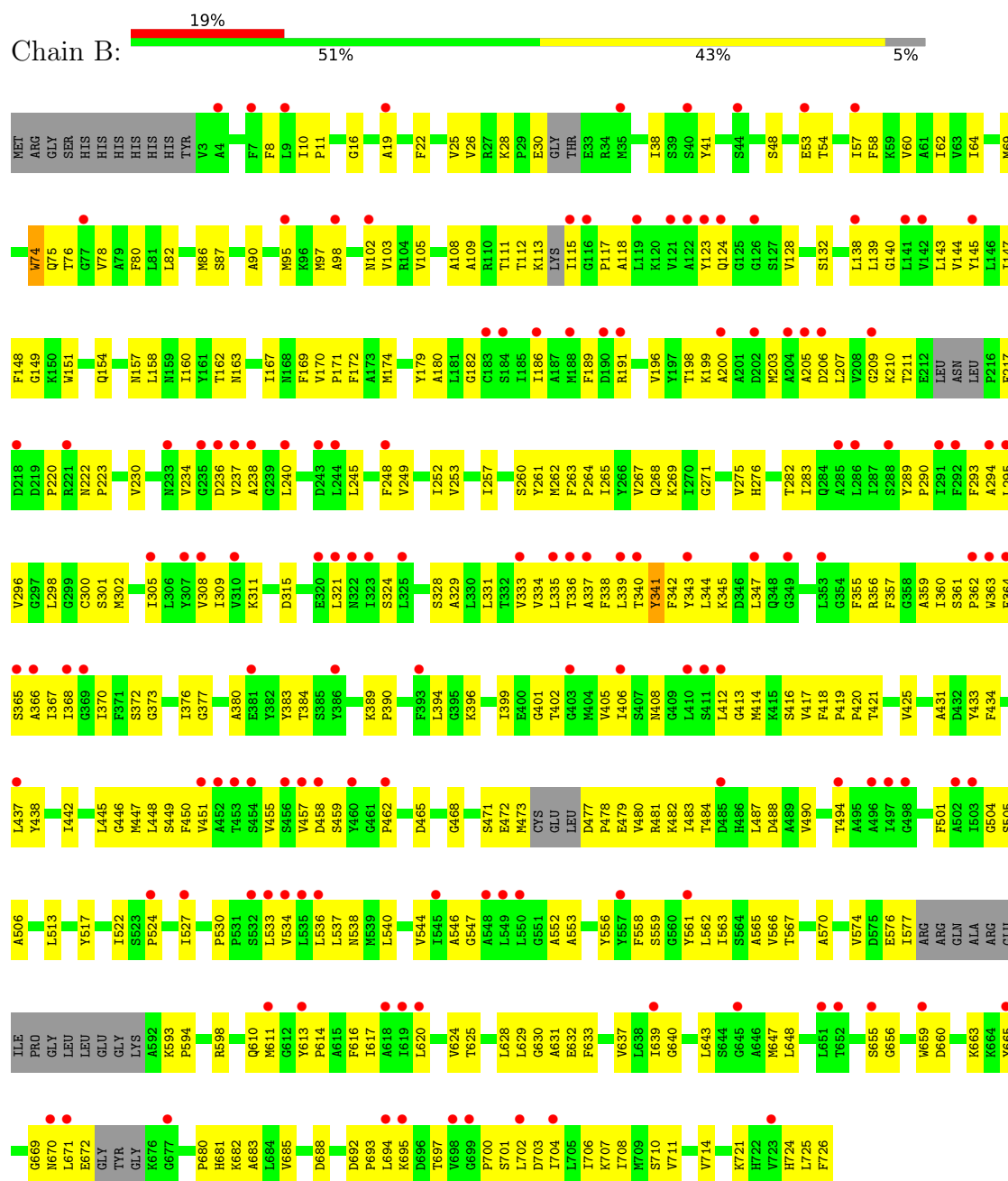
3 Residue-property plots [i](#)

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: K(+)-stimulated pyrophosphate-energized sodium pump



● Molecule 1: K(+)-stimulated pyrophosphate-energized sodium pump



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	83.74Å 111.66Å 105.20Å 90.00° 106.67° 90.00°	Depositor
Resolution (Å)	80.22 – 3.15 80.22 – 3.15	Depositor EDS
% Data completeness (in resolution range)	59.5 (80.22-3.15) 59.7 (80.22-3.15)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.56 (at 3.13Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.269 , 0.294 0.266 , 0.290	Depositor DCC
R_{free} test set	960 reflections (2.97%)	wwPDB-VP
Wilson B-factor (Å ²)	113.6	Xtriage
Anisotropy	0.057	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 142.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	10320	wwPDB-VP
Average B, all atoms (Å ²)	97.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.66% 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: MG, LMT, CA, 911

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	0.18	0/5192	0.44	4/7077 (0.1%)
1	B	0.19	0/5122	0.45	4/6987 (0.1%)
All	All	0.18	0/10314	0.44	8/14064 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	463	ILE	N-CA-C	-11.39	99.48	110.42
1	A	463	ILE	N-CA-CB	8.17	120.11	110.55
1	A	475	GLU	N-CA-C	-7.81	97.44	109.24
1	B	98	ALA	N-CA-C	7.60	119.64	111.36
1	B	74	TRP	N-CA-C	6.26	118.91	111.71
1	A	462	PRO	CB-CA-C	-5.85	102.20	111.04
1	B	26	VAL	N-CA-C	-5.78	104.72	110.62
1	B	341	TYR	N-CA-C	5.33	117.08	111.28

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	5087	0	5085	298	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5020	0	4976	303	0
2	A	11	6	3	0	0
2	B	11	6	4	0	0
3	A	4	0	0	0	0
3	B	5	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	B	70	92	92	2	0
6	A	2	0	0	0	0
6	B	4	0	0	0	0
All	All	10216	104	10160	585	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 29.

All (585) 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:207:LEU:HD22	1:A:574:VAL:CG2	1.69	1.23
1:A:207:LEU:CD2	1:A:574:VAL:HG21	1.81	1.10
1:A:546:ALA:HB1	1:B:425:VAL:HG13	1.28	1.08
1:A:573:MET:HE3	1:A:603:THR:HG21	1.35	1.05
1:B:22:PHE:HA	1:B:97:MET:SD	2.02	0.99
1:A:536:LEU:HD11	1:B:536:LEU:HD11	1.41	0.99
1:A:425:VAL:HG13	1:B:546:ALA:HB1	1.44	0.98
1:A:296:VAL:HG13	1:A:335:LEU:HD23	1.42	0.97
1:A:25:VAL:HG21	1:A:97:MET:HE1	1.48	0.95
1:B:157:ASN:OD1	1:B:158:LEU:N	2.00	0.95
1:B:237:VAL:HG23	1:B:462:PRO:HG2	1.50	0.93
1:B:262:MET:HA	1:B:265:ILE:HG12	1.52	0.92
1:A:97:MET:HE2	1:A:125:GLY:HA2	1.50	0.92
1:B:522:ILE:HD13	1:B:534:VAL:HG11	1.52	0.91
1:A:155:VAL:HG22	1:A:284:GLN:HG2	1.52	0.91
1:A:402:THR:HG22	1:A:683:ALA:HB2	1.51	0.90
1:A:308:VAL:HG21	1:A:324:SER:HB2	1.54	0.90
1:B:199:LYS:HG3	1:B:693:PRO:HA	1.51	0.89
1:B:138:LEU:HD13	1:B:295:LEU:HD23	1.53	0.89
1:B:198:THR:HG22	1:B:199:LYS:HE2	1.54	0.88
1:A:76:THR:HG21	1:A:174:MET:HG3	1.56	0.87
1:A:207:LEU:HD22	1:A:574:VAL:HG21	0.88	0.87
1:A:390:PRO:HB2	1:A:412:LEU:HD11	1.57	0.87

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:471:SER:HB2	1:B:481:ARG:HA	1.56	0.86
1:A:571:MET:HE2	1:A:571:MET:HA	1.58	0.86
1:A:163:ASN:OD1	1:A:164:TRP:N	2.07	0.85
1:B:87:SER:HB2	1:B:186:ILE:HG21	1.56	0.85
1:A:265:ILE:HG22	1:A:522:ILE:HG12	1.60	0.83
1:A:470:ILE:HA	1:A:473:MET:HG2	1.59	0.83
1:A:386:TYR:HA	1:A:391:THR:HB	1.59	0.83
1:A:399:ILE:HD11	1:A:671:LEU:HD21	1.60	0.82
1:A:448:LEU:HD11	1:A:505:SER:HB3	1.60	0.82
1:A:466:ASN:O	1:A:470:ILE:HG12	1.79	0.82
1:B:16:GLY:HA2	5:B:803:LMT:H123	1.61	0.82
1:B:665:TYR:CE1	1:B:670:ASN:HB3	2.16	0.80
1:A:133:VAL:HG13	1:A:245:LEU:HD12	1.63	0.80
1:A:102:ASN:OD1	1:A:103:VAL:N	2.14	0.80
1:A:262:MET:HA	1:A:265:ILE:HG12	1.64	0.80
1:B:663:LYS:HD2	1:B:685:VAL:HG12	1.63	0.79
1:A:25:VAL:HG21	1:A:97:MET:CE	2.12	0.79
1:A:8:PHE:HD1	1:A:142:VAL:HG11	1.46	0.79
1:B:76:THR:HG21	1:B:174:MET:HG3	1.64	0.79
1:B:86:MET:HE2	1:B:86:MET:HA	1.65	0.79
1:B:48:SER:HB2	1:B:598:ARG:NH2	1.98	0.79
1:B:308:VAL:HG21	1:B:324:SER:HB2	1.62	0.79
1:B:446:GLY:HA2	1:B:449:SER:OG	1.83	0.78
1:A:102:ASN:OD1	1:A:103:VAL:HG13	1.84	0.77
1:A:188:MET:HE1	1:A:619:ILE:HD11	1.67	0.77
1:A:73:THR:HG23	1:A:76:THR:HG23	1.68	0.76
1:A:39:SER:O	1:A:42:ILE:HG12	1.86	0.76
1:B:38:ILE:HA	1:B:41:TYR:CD2	2.22	0.75
1:A:95:MET:HE1	1:A:234:VAL:HA	1.66	0.75
1:A:340:THR:HG21	1:A:363:TRP:HB2	1.68	0.75
1:B:220:PRO:HB3	1:B:473:MET:HG2	1.69	0.75
1:A:90:ALA:HA	1:A:132:SER:OG	1.86	0.74
1:B:87:SER:CB	1:B:186:ILE:HG21	2.17	0.74
1:B:223:PRO:HG3	1:B:577:ILE:HD13	1.69	0.74
1:A:647:MET:HE3	1:B:552:ALA:HB3	1.69	0.74
1:B:25:VAL:HA	1:B:28:LYS:HG2	1.70	0.73
1:B:448:LEU:HD11	1:B:505:SER:HB3	1.69	0.73
1:B:558:PHE:O	1:B:562:LEU:HD23	1.88	0.73
1:B:459:SER:O	1:B:462:PRO:HD2	1.88	0.73
1:A:308:VAL:HG21	1:A:324:SER:CB	2.19	0.72
1:B:97:MET:HE2	1:B:128:VAL:HG21	1.71	0.72

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:262:MET:HA	1:B:265:ILE:CG1	2.20	0.72
1:B:199:LYS:HD2	1:B:692:ASP:HB3	1.72	0.71
1:A:53:GLU:O	1:A:57:ILE:HG23	1.91	0.71
1:A:263:PHE:HB2	1:A:283:ILE:HG13	1.71	0.71
1:A:97:MET:HE3	1:A:101:ALA:HB2	1.73	0.71
1:A:717:VAL:O	1:A:721:LYS:HB2	1.91	0.71
1:A:340:THR:HG22	1:A:360:ILE:HA	1.72	0.70
1:A:620:LEU:O	1:A:624:VAL:HG12	1.92	0.70
1:A:540:LEU:HG	1:B:437:LEU:HD11	1.74	0.70
1:A:428:ILE:HG12	1:A:508:PHE:HE1	1.56	0.69
1:B:373:GLY:HA2	1:B:447:MET:HE3	1.73	0.69
1:B:704:ILE:O	1:B:708:ILE:HG22	1.93	0.69
1:B:364:PHE:O	1:B:368:ILE:HG23	1.93	0.69
1:B:206:ASP:O	1:B:210:LYS:HG2	1.92	0.69
1:A:304:GLY:O	1:A:308:VAL:HG23	1.94	0.68
1:A:397:SER:O	1:A:400:GLU:HG2	1.94	0.68
1:A:402:THR:HA	1:A:683:ALA:HB1	1.75	0.68
1:A:666:LEU:HD22	1:A:681:HIS:HB2	1.73	0.68
1:A:573:MET:HE3	1:A:603:THR:CG2	2.19	0.68
1:B:147:ILE:O	1:B:151:TRP:HB3	1.94	0.68
1:B:53:GLU:O	1:B:57:ILE:HG23	1.94	0.68
1:A:25:VAL:HG21	1:A:97:MET:SD	2.34	0.68
1:A:139:LEU:O	1:A:143:LEU:HG	1.94	0.68
1:B:139:LEU:O	1:B:143:LEU:HG	1.92	0.68
1:A:355:PHE:CE1	1:A:435:ALA:HB1	2.28	0.68
1:B:522:ILE:CD1	1:B:534:VAL:HG11	2.23	0.68
1:B:293:PHE:CD1	1:B:336:THR:HG21	2.29	0.67
1:A:263:PHE:HB2	1:A:283:ILE:HG21	1.75	0.67
1:A:692:ASP:HB2	1:A:693:PRO:HD3	1.76	0.67
1:A:97:MET:HG2	1:A:128:VAL:CG2	2.25	0.67
1:A:97:MET:HG2	1:A:128:VAL:HG21	1.75	0.67
1:A:522:ILE:HG13	1:A:534:VAL:HG11	1.77	0.67
1:A:97:MET:HG2	1:A:128:VAL:CB	2.24	0.66
1:A:133:VAL:HG13	1:A:245:LEU:HB2	1.77	0.66
1:A:11:PRO:O	1:A:15:LEU:HG	1.94	0.66
1:A:21:ASN:O	1:A:25:VAL:HG13	1.96	0.66
1:A:265:ILE:CG2	1:A:522:ILE:HG12	2.26	0.66
1:B:163:ASN:HD22	1:B:167:ILE:HD13	1.61	0.66
1:A:189:PHE:HA	1:A:611:MET:HE1	1.78	0.66
1:A:258:LEU:O	1:A:262:MET:HG3	1.96	0.66
1:A:336:THR:HA	1:A:339:LEU:HB3	1.77	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:703:ASP:O	1:B:706:ILE:HG12	1.96	0.66
1:A:97:MET:HG2	1:A:128:VAL:HB	1.78	0.65
1:B:154:GLN:OE1	1:B:171:PRO:HB2	1.96	0.65
1:B:340:THR:HG22	1:B:360:ILE:HA	1.78	0.65
1:A:263:PHE:HB3	1:A:264:PRO:HD3	1.76	0.65
1:B:113:LYS:C	1:B:115:ILE:HG22	2.22	0.65
1:A:402:THR:HG22	1:A:683:ALA:CB	2.26	0.65
1:B:10:ILE:HG22	1:B:298:LEU:HD23	1.79	0.65
1:B:267:VAL:HG21	1:B:527:ILE:HG23	1.78	0.65
1:B:725:LEU:O	1:B:725:LEU:HD23	1.95	0.65
1:A:199:LYS:HE2	1:A:199:LYS:HA	1.79	0.65
1:A:286:LEU:HD13	1:A:353:LEU:HD21	1.79	0.64
1:A:678:SER:O	1:A:682:LYS:HG3	1.96	0.64
1:B:565:ALA:HA	1:B:610:GLN:OE1	1.97	0.64
1:A:149:GLY:O	1:A:155:VAL:HG12	1.97	0.64
1:A:480:VAL:O	1:A:483:ILE:HG12	1.97	0.64
1:A:261:TYR:O	1:A:265:ILE:HG23	1.98	0.64
1:A:65:ALA:O	1:A:69:MET:HG2	1.98	0.64
1:A:558:PHE:CG	1:A:705:LEU:HD12	2.33	0.64
1:B:236:ASP:HB2	1:B:462:PRO:HG3	1.81	0.63
1:A:207:LEU:CD2	1:A:574:VAL:CG2	2.58	0.63
1:A:666:LEU:CD2	1:A:681:HIS:HB2	2.28	0.63
1:A:293:PHE:CZ	1:A:366:ALA:HB1	2.33	0.63
1:B:112:THR:HG21	1:B:117:PRO:HB2	1.80	0.63
1:B:396:LYS:O	1:B:399:ILE:HG12	1.98	0.63
1:A:10:ILE:HG22	1:A:298:LEU:HD23	1.79	0.63
1:B:517:TYR:HB2	1:B:714:VAL:HG22	1.81	0.63
1:A:404:MET:HE1	1:B:567:THR:HB	1.81	0.62
1:B:124:GLN:CB	1:B:309:ILE:HD11	2.29	0.62
1:B:170:VAL:HG11	1:B:260:SER:HB3	1.79	0.62
1:B:530:PRO:HD2	1:B:533:LEU:HD13	1.80	0.62
1:A:262:MET:CE	1:A:353:LEU:HG	2.30	0.62
1:A:293:PHE:HB3	1:A:445:LEU:HD21	1.82	0.62
1:B:25:VAL:CG2	1:B:97:MET:HE1	2.29	0.62
1:A:163:ASN:HB3	1:A:167:ILE:HG12	1.82	0.62
1:B:558:PHE:CZ	1:B:701:SER:HB3	2.35	0.62
1:A:383:TYR:HE2	1:A:419:PRO:HG2	1.65	0.61
1:A:561:TYR:CE1	1:A:614:PRO:HD3	2.36	0.61
1:A:229:ASN:O	1:A:466:ASN:ND2	2.33	0.61
1:B:321:LEU:HD23	1:B:457:VAL:HG13	1.80	0.61
1:A:386:TYR:HD2	1:A:665:TYR:HD2	1.48	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:209:GLY:HA3	1:B:217:GLU:O	2.00	0.61
1:B:399:ILE:HA	1:B:680:PRO:HG3	1.82	0.61
1:A:517:TYR:HB2	1:A:714:VAL:HG22	1.82	0.60
1:A:558:PHE:CE2	1:A:562:LEU:HD11	2.37	0.60
1:A:340:THR:CB	1:A:363:TRP:HB2	2.31	0.60
1:A:25:VAL:CG2	1:A:97:MET:HE1	2.28	0.60
1:A:703:ASP:O	1:A:706:ILE:HG12	2.01	0.60
1:B:372:SER:O	1:B:376:ILE:HG23	2.02	0.60
1:A:26:VAL:HA	1:A:104:ARG:HH21	1.65	0.60
1:B:260:SER:O	1:B:264:PRO:HD3	2.01	0.60
1:A:360:ILE:HG23	1:A:364:PHE:CE2	2.36	0.59
1:A:553:ALA:HB1	1:B:418:PHE:HA	1.83	0.59
1:B:556:TYR:CD1	1:B:648:LEU:HD11	2.37	0.59
1:A:563:ILE:O	1:A:567:THR:HG23	2.02	0.59
1:B:390:PRO:HB2	1:B:412:LEU:HD11	1.84	0.59
1:B:471:SER:CB	1:B:481:ARG:HA	2.30	0.59
1:A:73:THR:CG2	1:A:76:THR:HG23	2.31	0.59
1:A:470:ILE:HA	1:A:473:MET:CG	2.30	0.59
1:B:57:ILE:HD12	1:B:186:ILE:HD13	1.84	0.59
1:A:340:THR:CG2	1:A:363:TRP:HB2	2.32	0.59
1:A:306:LEU:O	1:A:310:VAL:HG23	2.03	0.59
1:A:495:ALA:O	1:A:499:LYS:HG2	2.02	0.59
1:A:248:PHE:CE1	1:A:252:ILE:HD11	2.38	0.59
1:A:262:MET:HA	1:A:265:ILE:CG1	2.33	0.59
1:B:558:PHE:HZ	1:B:701:SER:HB3	1.68	0.59
1:A:269:LYS:NZ	1:A:273:ASN:HA	2.17	0.59
1:A:22:PHE:O	1:A:26:VAL:HG23	2.03	0.58
1:B:563:ILE:HD11	1:B:694:LEU:HD21	1.84	0.58
1:A:524:PRO:HA	1:A:527:ILE:HG12	1.84	0.58
1:B:338:PHE:HB3	1:B:342:PHE:CE2	2.38	0.58
1:B:367:ILE:HA	1:B:370:ILE:HD12	1.84	0.58
1:A:469:GLY:O	1:A:473:MET:HG2	2.04	0.58
1:A:222:ASN:O	1:A:225:THR:HB	2.04	0.58
1:B:248:PHE:CE1	1:B:252:ILE:HD11	2.38	0.58
1:B:298:LEU:HG	1:B:302:MET:HE2	1.83	0.58
1:B:487:LEU:O	1:B:490:VAL:HG22	2.03	0.58
1:A:263:PHE:CB	1:A:283:ILE:HG13	2.33	0.58
1:B:356:ARG:HG3	1:B:433:TYR:O	2.04	0.58
1:A:46:ALA:O	1:A:50:LEU:HG	2.03	0.58
1:A:356:ARG:HD2	1:A:433:TYR:O	2.04	0.58
1:B:97:MET:HE2	1:B:128:VAL:CG2	2.34	0.58

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112:THR:HB	1:B:117:PRO:HG2	1.86	0.58
1:B:465:ASP:HA	1:B:488:ASP:CG	2.29	0.58
1:A:133:VAL:HG13	1:A:245:LEU:CD1	2.31	0.57
1:A:416:SER:O	1:A:419:PRO:HD2	2.04	0.57
1:A:716:ALA:O	1:A:719:ILE:HG12	2.04	0.57
1:A:610:GLN:O	1:A:614:PRO:HD2	2.05	0.57
1:B:368:ILE:HD11	1:B:431:ALA:HB2	1.85	0.57
1:B:480:VAL:O	1:B:484:THR:HG23	2.05	0.57
1:B:563:ILE:O	1:B:567:THR:HG23	2.03	0.57
1:B:517:TYR:CA	1:B:714:VAL:HG22	2.35	0.57
1:A:167:ILE:HG13	1:A:169:PHE:HE2	1.69	0.57
1:B:478:PRO:HA	1:B:481:ARG:HG2	1.87	0.57
1:B:90:ALA:HA	1:B:132:SER:OG	2.04	0.57
1:A:386:TYR:CD2	1:A:665:TYR:HD2	2.23	0.57
1:B:57:ILE:HG22	1:B:189:PHE:CG	2.40	0.57
1:A:163:ASN:OD1	1:A:164:TRP:CD1	2.58	0.56
1:A:350:LEU:HD22	1:A:355:PHE:CE2	2.40	0.56
1:B:261:TYR:O	1:B:264:PRO:HD2	2.05	0.56
1:B:199:LYS:HB3	1:B:566:VAL:HG11	1.85	0.56
1:B:293:PHE:CE1	1:B:336:THR:HG21	2.40	0.56
1:B:300:CYS:SG	1:B:331:LEU:HD22	2.46	0.56
1:B:506:ALA:HB1	1:B:703:ASP:HB2	1.87	0.56
1:B:25:VAL:HG21	1:B:97:MET:CE	2.36	0.56
1:B:261:TYR:O	1:B:265:ILE:HG23	2.04	0.56
1:B:477:ASP:HB3	1:B:480:VAL:HB	1.87	0.56
1:B:240:LEU:HD23	1:B:458:ASP:HB3	1.87	0.56
1:A:17:PHE:CD2	1:A:131:LEU:HD13	2.41	0.56
1:A:147:ILE:HD12	1:A:147:ILE:H	1.69	0.56
1:A:350:LEU:HD22	1:A:355:PHE:CD2	2.41	0.56
1:B:38:ILE:HA	1:B:41:TYR:HD2	1.71	0.56
1:A:526:ASP:HB3	1:A:534:VAL:HG22	1.88	0.56
1:A:634:VAL:O	1:A:638:LEU:HG	2.05	0.56
1:B:19:ALA:HB1	5:B:803:LMT:H51	1.86	0.56
1:A:8:PHE:CD1	1:A:142:VAL:HG11	2.36	0.55
1:A:22:PHE:O	1:A:25:VAL:HG22	2.07	0.55
1:A:555:THR:HG23	1:A:702:LEU:HD22	1.88	0.55
1:A:50:LEU:HD11	1:A:95:MET:HG2	1.88	0.55
1:B:54:THR:HA	1:B:57:ILE:HG12	1.88	0.55
1:A:343:TYR:HB3	1:A:344:LEU:HD12	1.88	0.55
1:A:340:THR:HG21	1:A:363:TRP:CB	2.35	0.55
1:A:519:PHE:O	1:A:522:ILE:HD13	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:535:LEU:HB3	1:B:540:LEU:HD23	1.88	0.55
1:A:105:VAL:HG21	1:A:122:ALA:HB2	1.89	0.55
1:B:451:VAL:O	1:B:455:VAL:HG23	2.06	0.55
1:B:478:PRO:O	1:B:481:ARG:HG2	2.07	0.55
1:A:167:ILE:HG13	1:A:169:PHE:CE2	2.43	0.54
1:A:394:LEU:HD21	1:A:659:TRP:CD1	2.43	0.54
1:B:506:ALA:CB	1:B:703:ASP:HB2	2.37	0.54
1:A:629:LEU:HD22	1:A:633:PHE:CD2	2.43	0.54
1:A:248:PHE:HB2	1:A:448:LEU:HB3	1.89	0.54
1:B:112:THR:HB	1:B:117:PRO:CG	2.38	0.54
1:B:416:SER:O	1:B:419:PRO:HD2	2.06	0.54
1:B:681:HIS:O	1:B:685:VAL:HG13	2.07	0.53
1:A:296:VAL:CG1	1:A:335:LEU:HD23	2.27	0.53
1:A:390:PRO:HB2	1:A:412:LEU:CD1	2.34	0.53
1:A:535:LEU:HB3	1:B:540:LEU:CD2	2.38	0.53
1:A:260:SER:O	1:A:264:PRO:HD3	2.08	0.53
1:A:8:PHE:HD1	1:A:142:VAL:CG1	2.17	0.53
1:A:133:VAL:HG13	1:A:245:LEU:CG	2.39	0.53
1:A:148:PHE:HB3	1:A:154:GLN:NE2	2.23	0.53
1:A:340:THR:HB	1:A:360:ILE:HD12	1.91	0.53
1:A:428:ILE:HG12	1:A:508:PHE:CE1	2.43	0.53
1:A:383:TYR:CG	1:A:416:SER:HB2	2.44	0.53
1:B:145:TYR:HD1	1:B:172:PHE:CZ	2.27	0.53
1:A:271:GLY:O	1:A:272:GLU:HB2	2.09	0.52
1:B:48:SER:HB2	1:B:598:ARG:HH21	1.72	0.52
1:B:338:PHE:HB3	1:B:342:PHE:HE2	1.74	0.52
1:A:131:LEU:HD21	1:A:305:ILE:CD1	2.39	0.52
1:A:263:PHE:HD1	1:A:283:ILE:HG13	1.74	0.52
1:A:263:PHE:CD1	1:A:283:ILE:HG13	2.45	0.52
1:A:417:VAL:HA	1:A:650:ILE:HG21	1.92	0.52
1:B:97:MET:CE	1:B:128:VAL:HG21	2.40	0.52
1:B:334:VAL:O	1:B:337:ALA:HB3	2.10	0.52
1:B:364:PHE:HB3	1:B:434:PHE:CE2	2.44	0.52
1:A:133:VAL:HG13	1:A:245:LEU:CB	2.38	0.52
1:A:199:LYS:HD2	1:A:696:ASP:HB2	1.91	0.52
1:B:263:PHE:CB	1:B:283:ILE:HG13	2.40	0.52
1:B:370:ILE:HG12	1:B:446:GLY:O	2.08	0.52
1:B:340:THR:HG21	1:B:363:TRP:HB2	1.91	0.52
1:B:112:THR:CG2	1:B:117:PRO:HB2	2.39	0.52
1:B:296:VAL:CG1	1:B:335:LEU:HD22	2.39	0.52
1:B:480:VAL:HA	1:B:483:ILE:CD1	2.39	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:517:TYR:HB2	1:B:714:VAL:CG2	2.40	0.52
1:A:248:PHE:CZ	1:A:294:ALA:HB1	2.45	0.52
1:B:506:ALA:HA	1:B:707:LYS:HD3	1.92	0.52
1:B:296:VAL:HG11	1:B:336:THR:HG23	1.91	0.52
1:A:692:ASP:CB	1:A:693:PRO:HD3	2.40	0.51
1:B:336:THR:HA	1:B:339:LEU:HB3	1.92	0.51
1:B:471:SER:HB3	1:B:484:THR:OG1	2.11	0.51
1:B:561:TYR:CD1	1:B:614:PRO:HG3	2.44	0.51
1:A:123:TYR:OH	1:A:305:ILE:HG22	2.10	0.51
1:B:479:GLU:O	1:B:483:ILE:HG23	2.10	0.51
1:B:524:PRO:O	1:B:527:ILE:HG12	2.11	0.51
1:A:364:PHE:O	1:A:367:ILE:HG12	2.10	0.51
1:A:517:TYR:CA	1:A:714:VAL:HG22	2.40	0.51
1:B:112:THR:CB	1:B:117:PRO:HB2	2.40	0.51
1:A:478:PRO:HG3	1:A:481:ARG:HH11	1.75	0.51
1:A:38:ILE:O	1:A:42:ILE:HG23	2.11	0.51
1:A:133:VAL:HA	1:A:245:LEU:HD12	1.92	0.51
1:B:383:TYR:CE2	1:B:419:PRO:HG2	2.46	0.51
1:A:261:TYR:O	1:A:264:PRO:HD2	2.11	0.51
1:A:573:MET:O	1:A:577:ILE:HD13	2.11	0.51
1:B:396:LYS:HD2	1:B:671:LEU:CD2	2.40	0.51
1:B:402:THR:HA	1:B:683:ALA:HB1	1.92	0.51
1:A:127:SER:HA	1:A:456:SER:OG	2.11	0.51
1:B:624:VAL:HG13	1:B:625:THR:N	2.26	0.51
1:A:188:MET:HA	1:A:704:ILE:HG21	1.93	0.50
1:B:140:GLY:HA3	1:B:179:TYR:OH	2.11	0.50
1:B:697:THR:C	1:B:700:PRO:HD2	2.36	0.50
1:A:262:MET:HE2	1:A:353:LEU:HG	1.92	0.50
1:B:30:GLU:HG3	1:B:103:VAL:HG13	1.93	0.50
1:B:630:GLY:HA2	1:B:724:HIS:HB3	1.92	0.50
1:A:636:GLY:HA2	1:A:639:ILE:HD11	1.92	0.50
1:B:200:ALA:HA	1:B:570:ALA:HB2	1.93	0.50
1:B:447:MET:O	1:B:501:PHE:HZ	1.94	0.50
1:A:54:THR:HA	1:A:57:ILE:HG12	1.93	0.50
1:B:629:LEU:HD22	1:B:633:PHE:CD2	2.46	0.50
1:A:518:MET:HG3	1:B:540:LEU:HD13	1.93	0.50
1:B:74:TRP:CE2	1:B:75:GLN:NE2	2.80	0.50
1:A:269:LYS:O	1:A:269:LYS:HG3	2.11	0.50
1:B:109:ALA:HB1	1:B:483:ILE:HD12	1.94	0.50
1:B:682:LYS:O	1:B:685:VAL:HG22	2.11	0.50
1:A:200:ALA:HB2	1:A:569:ALA:HB3	1.93	0.50

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470:ILE:CA	1:A:473:MET:HG2	2.36	0.50
1:A:550:LEU:O	1:A:554:ILE:HG13	2.12	0.50
1:B:261:TYR:C	1:B:264:PRO:HD2	2.35	0.50
1:B:360:ILE:HG13	1:B:360:ILE:O	2.12	0.50
1:A:142:VAL:O	1:A:146:LEU:HG	2.12	0.50
1:A:6:LEU:HA	1:A:9:LEU:CD2	2.42	0.49
1:B:376:ILE:HG13	1:B:377:GLY:N	2.26	0.49
1:A:6:LEU:O	1:A:9:LEU:HG	2.13	0.49
1:A:158:LEU:HD13	1:A:283:ILE:CG2	2.43	0.49
1:A:302:MET:O	1:A:305:ILE:HG12	2.12	0.49
1:B:8:PHE:O	1:B:11:PRO:HD2	2.12	0.49
1:B:355:PHE:CE2	1:B:362:PRO:HD3	2.47	0.49
1:B:643:LEU:O	1:B:647:MET:HG2	2.12	0.49
1:B:682:LYS:HA	1:B:685:VAL:HG22	1.94	0.49
1:B:237:VAL:CG2	1:B:462:PRO:HG2	2.34	0.49
1:B:419:PRO:N	1:B:420:PRO:HD2	2.27	0.49
1:B:706:ILE:HG13	1:B:707:LYS:N	2.27	0.49
1:A:383:TYR:CE2	1:A:419:PRO:HG2	2.47	0.49
1:B:513:LEU:HD13	1:B:711:VAL:HG23	1.94	0.49
1:A:207:LEU:HD11	1:A:571:MET:HE1	1.94	0.49
1:B:148:PHE:O	1:B:154:GLN:HG2	2.12	0.49
1:B:296:VAL:HG13	1:B:335:LEU:HD22	1.94	0.49
1:B:710:SER:O	1:B:714:VAL:HG23	2.11	0.49
1:A:95:MET:CE	1:A:234:VAL:HA	2.40	0.49
1:A:269:LYS:HZ1	1:A:273:ASN:HA	1.76	0.49
1:B:145:TYR:O	1:B:149:GLY:HA3	2.13	0.49
1:A:133:VAL:CG1	1:A:245:LEU:HD12	2.40	0.49
1:B:109:ALA:HB1	1:B:483:ILE:CD1	2.43	0.49
1:B:230:VAL:O	1:B:234:VAL:HG23	2.13	0.49
1:A:263:PHE:HB2	1:A:283:ILE:CG1	2.42	0.49
1:A:490:VAL:O	1:A:494:THR:HG23	2.12	0.49
1:A:682:LYS:O	1:A:685:VAL:HG12	2.12	0.49
1:B:345:LYS:HA	1:B:359:ALA:HB2	1.94	0.49
1:B:25:VAL:HB	1:B:97:MET:HE1	1.95	0.48
1:A:289:TYR:HH	1:A:340:THR:HG1	1.59	0.48
1:B:671:LEU:HG	1:B:672:GLU:N	2.28	0.48
1:A:237:VAL:HG22	1:A:459:SER:HA	1.95	0.48
1:B:293:PHE:CZ	1:B:366:ALA:HB1	2.48	0.48
1:B:480:VAL:O	1:B:483:ILE:HG12	2.13	0.48
1:A:556:TYR:O	1:B:414:MET:HB3	2.14	0.48
1:B:628:LEU:HB3	1:B:629:LEU:HD12	1.95	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:480:VAL:HA	1:B:483:ILE:HD11	1.96	0.48
1:B:559:SER:HB3	1:B:702:LEU:HD21	1.95	0.48
1:B:660:ASP:HA	1:B:688:ASP:OD2	2.13	0.48
1:A:380:ALA:O	1:A:384:THR:HG22	2.13	0.48
1:A:470:ILE:HD13	1:A:473:MET:HE3	1.96	0.48
1:B:80:PHE:CE2	1:B:182:GLY:HA2	2.49	0.48
1:B:257:ILE:HG23	1:B:261:TYR:CE2	2.48	0.48
1:A:419:PRO:HD2	1:A:420:PRO:HD2	1.96	0.48
1:A:630:GLY:HA2	1:A:724:HIS:HB3	1.94	0.48
1:B:624:VAL:HG13	1:B:625:THR:H	1.78	0.48
1:A:543:ARG:NH1	1:A:629:LEU:O	2.47	0.48
1:B:438:TYR:O	1:B:442:ILE:HG12	2.14	0.48
1:A:507:ILE:HD13	1:A:646:ALA:HB1	1.95	0.47
1:A:517:TYR:HB2	1:A:714:VAL:CG2	2.44	0.47
1:A:578:ARG:NE	1:A:578:ARG:HA	2.28	0.47
1:B:167:ILE:HG22	1:B:169:PHE:CD2	2.49	0.47
1:B:167:ILE:HG22	1:B:169:PHE:HD2	1.79	0.47
1:B:205:ALA:HA	1:B:222:ASN:HD21	1.79	0.47
1:B:207:LEU:O	1:B:211:THR:N	2.46	0.47
1:B:482:LYS:HD3	1:B:482:LYS:HA	1.71	0.47
1:B:373:GLY:O	1:B:376:ILE:HG12	2.14	0.47
1:B:478:PRO:HA	1:B:481:ARG:NE	2.29	0.47
1:B:537:LEU:HD12	1:B:632:GLU:OE1	2.14	0.47
1:A:97:MET:CE	1:A:125:GLY:HA2	2.34	0.47
1:B:102:ASN:O	1:B:105:VAL:HG22	2.15	0.47
1:B:337:ALA:O	1:B:341:TYR:HB2	2.13	0.47
1:B:556:TYR:CE1	1:B:648:LEU:HD11	2.50	0.47
1:B:671:LEU:HG	1:B:672:GLU:H	1.79	0.47
1:A:60:VAL:O	1:A:64:ILE:HG12	2.14	0.47
1:A:95:MET:HE2	1:A:238:ALA:HB2	1.97	0.47
1:B:468:GLY:O	1:B:472:GLU:HG2	2.13	0.47
1:A:230:VAL:O	1:A:234:VAL:HG23	2.15	0.47
1:A:240:LEU:HD23	1:A:458:ASP:HB3	1.96	0.47
1:A:248:PHE:CZ	1:A:252:ILE:HD11	2.50	0.47
1:B:517:TYR:CB	1:B:714:VAL:HG22	2.43	0.47
1:B:614:PRO:HA	1:B:617:ILE:HD12	1.96	0.47
1:B:109:ALA:HA	1:B:118:ALA:HB2	1.96	0.47
1:B:445:LEU:O	1:B:449:SER:N	2.48	0.47
1:B:639:ILE:HG13	1:B:640:GLY:N	2.29	0.47
1:B:237:VAL:HG23	1:B:462:PRO:CG	2.34	0.46
1:B:364:PHE:HA	1:B:367:ILE:HG12	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:366:ALA:O	1:B:370:ILE:HG13	2.15	0.46
1:A:547:GLY:O	1:A:637:VAL:HA	2.15	0.46
1:B:22:PHE:CA	1:B:97:MET:SD	2.92	0.46
1:B:60:VAL:O	1:B:64:ILE:HG12	2.15	0.46
1:B:97:MET:HG2	1:B:128:VAL:HB	1.98	0.46
1:B:616:PHE:O	1:B:620:LEU:HB2	2.15	0.46
1:B:702:LEU:O	1:B:706:ILE:HG23	2.15	0.46
1:A:302:MET:HA	1:A:305:ILE:HG12	1.96	0.46
1:B:293:PHE:CE2	1:B:366:ALA:HB1	2.50	0.46
1:B:357:PHE:HE2	1:B:434:PHE:CE1	2.33	0.46
1:A:59:LYS:O	1:A:63:VAL:HG23	2.16	0.46
1:A:705:LEU:C	1:A:705:LEU:HD23	2.41	0.46
1:A:160:ILE:HD12	1:A:160:ILE:H	1.80	0.46
1:A:360:ILE:HG13	1:A:360:ILE:O	2.14	0.46
1:A:536:LEU:HD12	1:B:538:ASN:CG	2.41	0.46
1:B:69:MET:HE2	1:B:78:VAL:HG23	1.96	0.46
1:B:355:PHE:CD2	1:B:361:SER:HB3	2.51	0.46
1:A:321:LEU:HD13	1:A:457:VAL:HG13	1.97	0.46
1:A:517:TYR:CB	1:A:714:VAL:HG22	2.46	0.46
1:A:539:MET:HG2	1:B:639:ILE:HG21	1.98	0.46
1:A:248:PHE:CE1	1:A:294:ALA:HB1	2.51	0.46
1:A:256:ILE:HG23	1:A:287:ILE:HG23	1.98	0.46
1:A:643:LEU:O	1:A:647:MET:HG2	2.16	0.46
1:B:196:VAL:HA	1:B:566:VAL:HG22	1.97	0.46
1:B:282:THR:HG23	1:B:347:LEU:HD23	1.98	0.46
1:B:459:SER:C	1:B:462:PRO:HD2	2.40	0.46
1:B:490:VAL:O	1:B:494:THR:HG23	2.15	0.46
1:A:140:GLY:HA3	1:A:179:TYR:OH	2.16	0.46
1:A:364:PHE:O	1:A:368:ILE:HG12	2.16	0.46
1:B:373:GLY:CA	1:B:447:MET:HE3	2.44	0.45
1:A:424:LEU:O	1:A:428:ILE:HG13	2.16	0.45
1:B:376:ILE:CD1	1:B:504:GLY:HA3	2.46	0.45
1:B:396:LYS:HD2	1:B:671:LEU:HD23	1.99	0.45
1:B:111:THR:HG23	1:B:112:THR:HG23	1.97	0.45
1:B:418:PHE:HB3	1:B:419:PRO:HD3	1.98	0.45
1:B:725:LEU:HD23	1:B:725:LEU:C	2.41	0.45
1:A:340:THR:CG2	1:A:360:ILE:HD12	2.46	0.45
1:A:396:LYS:O	1:A:399:ILE:HG12	2.16	0.45
1:A:10:ILE:HG23	1:A:302:MET:CE	2.47	0.45
1:B:401:GLY:O	1:B:405:VAL:HG23	2.17	0.45
1:A:633:PHE:O	1:A:637:VAL:HG23	2.16	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:97:MET:SD	1:B:128:VAL:HG21	2.57	0.45
1:B:289:TYR:N	1:B:290:PRO:HD2	2.31	0.45
1:B:373:GLY:HA2	1:B:376:ILE:HG12	1.99	0.45
1:B:402:THR:HG23	1:B:683:ALA:HA	1.99	0.45
1:B:405:VAL:HG12	1:B:659:TRP:HE1	1.82	0.45
1:A:471:SER:OG	1:A:476:LEU:HD23	2.17	0.45
1:B:22:PHE:HA	1:B:97:MET:CE	2.47	0.45
1:B:199:LYS:HA	1:B:199:LYS:HD3	1.72	0.45
1:A:419:PRO:N	1:A:420:PRO:HD2	2.31	0.45
1:B:669:GLY:O	1:B:670:ASN:C	2.59	0.45
1:A:105:VAL:HG13	1:A:118:ALA:HB1	1.99	0.45
1:A:286:LEU:CD1	1:A:353:LEU:HD21	2.46	0.45
1:A:262:MET:HE1	1:A:353:LEU:HG	2.00	0.44
1:B:95:MET:HE1	1:B:234:VAL:HG22	1.99	0.44
1:B:97:MET:HG2	1:B:128:VAL:CB	2.47	0.44
1:A:419:PRO:CD	1:A:420:PRO:HD2	2.47	0.44
1:B:631:ALA:HB2	1:B:721:LYS:HA	2.00	0.44
1:A:262:MET:HA	1:A:265:ILE:CD1	2.47	0.44
1:B:343:TYR:HB3	1:B:344:LEU:HD12	1.99	0.44
1:B:547:GLY:O	1:B:637:VAL:HA	2.18	0.44
1:B:54:THR:HA	1:B:57:ILE:CD1	2.47	0.44
1:B:69:MET:HG2	1:B:74:TRP:HA	2.00	0.44
1:A:86:MET:SD	1:A:136:PHE:HD1	2.40	0.44
1:B:25:VAL:CG2	1:B:97:MET:CE	2.94	0.44
1:B:180:ALA:HB2	1:B:253:VAL:HG21	1.99	0.44
1:B:262:MET:HA	1:B:265:ILE:CD1	2.47	0.44
1:A:421:THR:HG21	1:B:553:ALA:HB2	1.99	0.44
1:B:149:GLY:HA2	1:B:154:GLN:HB2	1.98	0.44
1:B:367:ILE:HG13	1:B:368:ILE:N	2.33	0.44
1:B:421:THR:O	1:B:425:VAL:HG23	2.18	0.44
1:A:261:TYR:C	1:A:264:PRO:HD2	2.42	0.44
1:A:289:TYR:N	1:A:290:PRO:HD2	2.33	0.44
1:A:406:ILE:HA	1:A:659:TRP:HZ2	1.83	0.44
1:B:203:MET:HE1	1:B:567:THR:HG22	2.00	0.44
1:A:156:ASP:O	1:A:280:LYS:HD2	2.18	0.44
1:B:628:LEU:CB	1:B:629:LEU:HD12	2.47	0.44
1:A:145:TYR:OH	1:A:288:SER:HB3	2.18	0.43
1:B:267:VAL:CG2	1:B:527:ILE:HG23	2.47	0.43
1:A:15:LEU:HD11	1:A:139:LEU:HD22	2.00	0.43
1:B:361:SER:HB3	1:B:362:PRO:HD3	2.01	0.43
1:A:385:SER:HA	1:A:661:ASN:OD1	2.18	0.43

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:559:SER:O	1:A:563:ILE:HG13	2.19	0.43
1:B:413:GLY:O	1:B:417:VAL:HG23	2.18	0.43
1:A:578:ARG:HA	1:A:578:ARG:HE	1.84	0.43
1:A:300:CYS:SG	1:A:332:THR:HA	2.58	0.43
1:A:539:MET:HE2	1:B:639:ILE:HD12	1.98	0.43
1:A:558:PHE:CE1	1:A:614:PRO:HB2	2.54	0.43
1:A:661:ASN:N	1:A:661:ASN:HD22	2.17	0.43
1:A:2:TYR:CD2	1:A:3:VAL:HG23	2.53	0.43
1:A:131:LEU:CD2	1:A:302:MET:HG2	2.47	0.43
1:B:656:GLY:HA3	1:B:695:LYS:HB3	2.00	0.43
1:A:11:PRO:HG3	1:A:138:LEU:CB	2.48	0.43
1:A:319:ARG:O	1:A:323:ILE:HG12	2.19	0.43
1:B:54:THR:O	1:B:57:ILE:HG12	2.18	0.43
1:B:380:ALA:O	1:B:384:THR:HG22	2.19	0.43
1:B:628:LEU:O	1:B:726:PHE:HB2	2.18	0.43
1:A:170:VAL:HG11	1:A:260:SER:HB3	2.01	0.43
1:A:517:TYR:HA	1:A:714:VAL:HG22	2.01	0.43
1:B:57:ILE:HD12	1:B:186:ILE:CD1	2.49	0.43
1:B:112:THR:HB	1:B:117:PRO:HB2	2.01	0.43
1:B:538:ASN:O	1:B:544:VAL:HG21	2.19	0.43
1:B:613:TYR:HB3	1:B:614:PRO:HD3	1.99	0.43
1:B:115:ILE:O	1:B:117:PRO:HD2	2.19	0.43
1:B:108:ALA:HA	1:B:111:THR:HG22	2.00	0.42
1:A:419:PRO:HB2	1:A:420:PRO:HD3	2.01	0.42
1:A:469:GLY:O	1:A:473:MET:N	2.51	0.42
1:B:64:ILE:HG21	1:B:80:PHE:CE2	2.54	0.42
1:B:311:LYS:HA	1:B:311:LYS:HD3	1.72	0.42
1:B:329:ALA:O	1:B:333:VAL:HG23	2.19	0.42
1:A:6:LEU:HA	1:A:9:LEU:HD23	2.01	0.42
1:A:710:SER:O	1:A:714:VAL:HG23	2.19	0.42
1:B:160:ILE:HD12	1:B:160:ILE:H	1.84	0.42
1:B:237:VAL:HG22	1:B:459:SER:HA	2.02	0.42
1:B:257:ILE:HG23	1:B:261:TYR:CD2	2.54	0.42
1:B:269:LYS:HG2	1:B:271:GLY:O	2.18	0.42
1:B:365:SER:O	1:B:368:ILE:HG12	2.20	0.42
1:A:148:PHE:HB3	1:A:154:GLN:HE22	1.84	0.42
1:A:400:GLU:HG3	1:A:404:MET:CB	2.48	0.42
1:B:25:VAL:HA	1:B:28:LYS:CG	2.46	0.42
1:B:162:THR:HA	1:B:167:ILE:O	2.19	0.42
1:B:655:SER:HB3	1:B:659:TRP:CZ3	2.54	0.42
1:A:558:PHE:O	1:A:562:LEU:HG	2.19	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:621:THR:O	1:A:625:THR:HG23	2.20	0.42
1:A:573:MET:CE	1:A:603:THR:HG21	2.27	0.42
1:B:268:GLN:O	1:B:275:VAL:HG12	2.19	0.42
1:B:189:PHE:HA	1:B:611:MET:CE	2.50	0.42
1:B:261:TYR:O	1:B:265:ILE:HG12	2.20	0.42
1:A:131:LEU:HD21	1:A:305:ILE:HD11	2.01	0.42
1:A:623:LEU:HD12	1:A:623:LEU:N	2.34	0.42
1:B:82:LEU:HD23	1:B:144:VAL:HG23	2.02	0.42
1:B:199:LYS:HG3	1:B:693:PRO:CA	2.35	0.42
1:A:58:PHE:O	1:A:62:ILE:HG13	2.20	0.42
1:A:104:ARG:HB2	1:A:121:VAL:HG11	2.01	0.42
1:B:123:TYR:CE2	1:B:305:ILE:HG23	2.54	0.42
1:B:123:TYR:OH	1:B:305:ILE:HG12	2.20	0.42
1:B:480:VAL:HA	1:B:483:ILE:HG12	2.02	0.42
1:A:598:ARG:HA	1:A:598:ARG:HD2	1.75	0.41
1:B:138:LEU:HD21	1:B:294:ALA:HB3	2.02	0.41
1:B:301:SER:HA	1:B:328:SER:OG	2.20	0.41
1:A:160:ILE:HG21	1:A:524:PRO:HG3	2.02	0.41
1:A:558:PHE:CD2	1:A:705:LEU:HD12	2.54	0.41
1:A:558:PHE:CD1	1:A:705:LEU:HD12	2.55	0.41
1:B:111:THR:CG2	1:B:112:THR:HG23	2.50	0.41
1:B:394:LEU:HD13	1:B:408:ASN:HB3	2.02	0.41
1:A:147:ILE:HD12	1:A:147:ILE:N	2.34	0.41
1:B:205:ALA:HA	1:B:222:ASN:ND2	2.34	0.41
1:B:365:SER:HA	1:B:368:ILE:HG12	2.02	0.41
1:A:72:THR:HA	1:A:163:ASN:ND2	2.36	0.41
1:A:80:PHE:CE1	1:A:182:GLY:HA2	2.55	0.41
1:B:593:LYS:N	1:B:594:PRO:HD2	2.35	0.41
1:A:103:VAL:HG12	1:A:470:ILE:HG21	2.02	0.41
1:B:370:ILE:HG23	1:B:450:PHE:HE1	1.85	0.41
1:A:158:LEU:HD21	1:A:287:ILE:CD1	2.50	0.41
1:A:62:ILE:O	1:A:66:ILE:HG12	2.21	0.41
1:A:69:MET:HE2	1:A:69:MET:HB3	1.89	0.41
1:A:94:GLY:HA3	1:A:129:MET:SD	2.61	0.41
1:A:338:PHE:HD1	1:A:342:PHE:CD2	2.38	0.41
1:A:671:LEU:HG	1:A:674:TYR:HD2	1.85	0.41
1:B:25:VAL:CB	1:B:97:MET:HE1	2.51	0.41
1:B:160:ILE:HG21	1:B:524:PRO:HG3	2.01	0.41
1:A:45:GLY:HA3	1:A:600:ILE:HD12	2.02	0.41
1:A:50:LEU:HD11	1:A:95:MET:CG	2.50	0.41
1:A:493:THR:O	1:A:497:ILE:HG13	2.21	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:571:MET:HA	1:A:571:MET:CE	2.39	0.41
1:B:157:ASN:HD21	1:B:171:PRO:HG3	1.86	0.41
1:B:517:TYR:HA	1:B:714:VAL:HG22	2.02	0.41
1:B:576:GLU:O	1:B:577:ILE:HB	2.21	0.41
1:A:7:PHE:HB3	1:A:295:LEU:HD13	2.03	0.41
1:A:203:MET:O	1:A:206:ASP:OD1	2.39	0.41
1:A:624:VAL:HG13	1:A:625:THR:N	2.36	0.41
1:B:25:VAL:HG21	1:B:97:MET:HE3	2.02	0.41
1:A:11:PRO:HB3	1:A:135:GLY:O	2.21	0.40
1:A:133:VAL:CA	1:A:245:LEU:HD12	2.50	0.40
1:A:199:LYS:HE2	1:A:199:LYS:CA	2.49	0.40
1:A:419:PRO:HB2	1:A:420:PRO:CD	2.51	0.40
1:B:95:MET:HE1	1:B:234:VAL:CG2	2.51	0.40
1:B:191:ARG:NH2	1:B:240:LEU:HB2	2.36	0.40
1:B:245:LEU:O	1:B:249:VAL:HG23	2.21	0.40
1:B:95:MET:CG	1:B:238:ALA:HB2	2.52	0.40
1:B:115:ILE:HD11	1:B:315:ASP:OD1	2.21	0.40
1:B:267:VAL:HG12	1:B:276:HIS:HA	2.01	0.40
1:A:119:LEU:HD22	1:A:317:PRO:HB3	2.03	0.40
1:A:539:MET:HG2	1:B:639:ILE:HD13	2.03	0.40
1:B:207:LEU:HD23	1:B:574:VAL:HG21	2.02	0.40
1:A:621:THR:HB	1:A:622:PRO:HD3	2.03	0.40
1:B:58:PHE:O	1:B:62:ILE:HG13	2.22	0.40
1:B:389:LYS:N	1:B:390:PRO:HD2	2.36	0.40
1:A:293:PHE:CE2	1:A:336:THR:HG21	2.55	0.40
1:A:325:LEU:HD23	1:A:453:THR:CG2	2.52	0.40
1:A:334:VAL:O	1:A:337:ALA:HB3	2.22	0.40
1:B:262:MET:CA	1:B:265:ILE:HG12	2.35	0.40
1:B:406:ILE:HA	1:B:659:TRP:HZ2	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	692/735 (94%)	677 (98%)	15 (2%)	0	100	100
1	B	684/735 (93%)	667 (98%)	17 (2%)	0	100	100
All	All	1376/1470 (94%)	1344 (98%)	32 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	509/575 (88%)	509 (100%)	0	100	100
1	B	498/575 (87%)	498 (100%)	0	100	100
All	All	1007/1150 (88%)	1007 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	124	GLN
1	B	163	ASN
1	B	273	ASN
1	B	606	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 11 are monoatomic - leaving 4 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	911	A	801	3,4	10,10,10	0.88	0	17,18,18	0.67	0
5	LMT	B	803	-	36,36,36	0.99	0	47,47,47	1.55	8 (17%)
5	LMT	B	802	-	36,36,36	1.00	0	47,47,47	1.43	11 (23%)
2	911	B	801	3,4	10,10,10	0.87	0	17,18,18	0.65	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	911	A	801	3,4	-	8/18/18/18	-
5	LMT	B	803	-	-	9/21/61/61	0/2/2/2
5	LMT	B	802	-	-	6/21/61/61	0/2/2/2
2	911	B	801	3,4	-	8/18/18/18	-

There are no bond length outliers.

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	803	LMT	O5B-C1B-C2B	3.46	117.48	110.37
5	B	803	LMT	C4B-C3B-C2B	3.44	116.87	110.83
5	B	803	LMT	C6'-C5'-C4'	-3.41	103.78	113.38
5	B	803	LMT	C3B-C4B-C5B	3.20	116.04	110.23
5	B	803	LMT	O1B-C1B-C2B	-2.86	101.06	108.09

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	802	LMT	O5B-C5B-C4B	2.81	114.77	109.70
5	B	802	LMT	C1B-O1B-C4'	-2.72	111.53	117.98
5	B	802	LMT	C1B-C2B-C3B	2.70	115.69	110.01
5	B	802	LMT	C4B-C3B-C2B	2.56	115.33	110.83
5	B	802	LMT	C6B-C5B-C4B	-2.51	106.85	113.02
5	B	803	LMT	O2B-C2B-C3B	-2.50	104.49	110.38
5	B	803	LMT	C2'-C3'-C4'	2.47	115.28	109.68
5	B	802	LMT	C2'-C3'-C4'	2.33	114.96	109.68
5	B	802	LMT	C1'-O5'-C5'	-2.25	109.33	113.72
5	B	803	LMT	O5'-C5'-C6'	2.22	111.94	106.44
5	B	802	LMT	C3'-C4'-C5'	2.22	115.85	110.93
5	B	802	LMT	C1B-O5B-C5B	-2.21	109.40	113.72
5	B	802	LMT	O1'-C1'-C2'	-2.21	104.91	108.27
5	B	802	LMT	O2B-C2B-C3B	-2.02	105.60	110.38

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	802	LMT	C2'-C1'-O1'-C1
5	B	802	LMT	O5'-C1'-O1'-C1
5	B	803	LMT	C2-C1-O1'-C1'
5	B	803	LMT	C5-C6-C7-C8
5	B	803	LMT	C3-C4-C5-C6
5	B	803	LMT	C7-C8-C9-C10
5	B	802	LMT	C3-C4-C5-C6
2	A	801	911	C16-C7-P8-O10
2	B	801	911	C16-C7-P8-O10
5	B	802	LMT	O1'-C1-C2-C3
5	B	803	LMT	C9-C10-C11-C12
2	A	801	911	O14-C7-P8-O9
2	B	801	911	O14-C7-P8-O9
5	B	802	LMT	C6-C7-C8-C9
2	A	801	911	P1-C7-P8-O9
2	B	801	911	P1-C7-P8-O9
2	A	801	911	P1-C7-P8-O12
2	A	801	911	O14-C7-P8-O10
2	A	801	911	O14-C7-P8-O12
2	A	801	911	C16-C7-P8-O12
2	B	801	911	P1-C7-P8-O12
2	B	801	911	O14-C7-P8-O10
2	B	801	911	O14-C7-P8-O12

Continued on next page...

Continued from previous page...

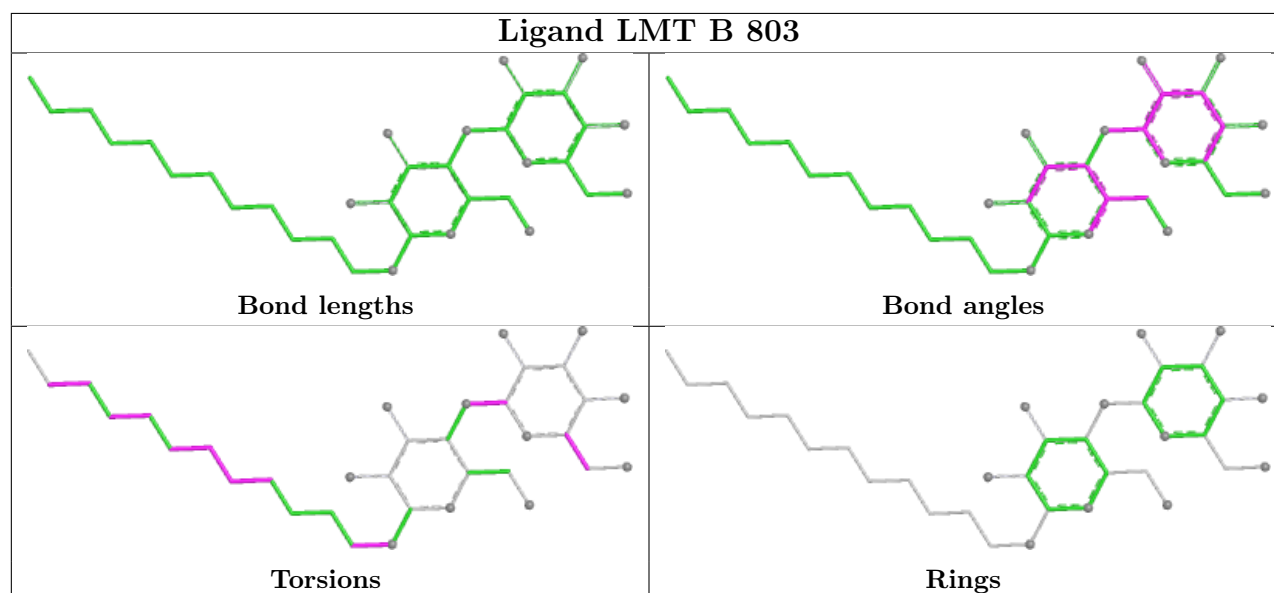
Mol	Chain	Res	Type	Atoms
2	B	801	911	C16-C7-P8-O12
5	B	803	LMT	C4B-C5B-C6B-O6B
5	B	803	LMT	C4-C5-C6-C7
5	B	802	LMT	C9-C10-C11-C12
5	B	803	LMT	O5B-C1B-O1B-C4'
5	B	803	LMT	O5B-C5B-C6B-O6B
2	A	801	911	C16-C7-P8-O9
2	B	801	911	C16-C7-P8-O9

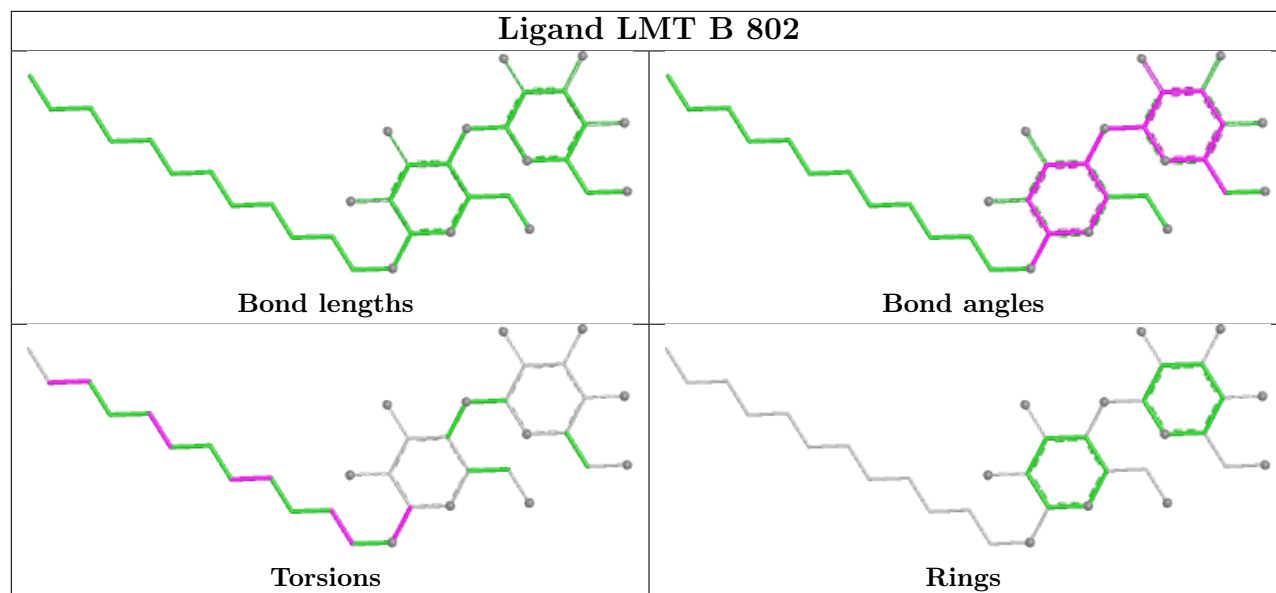
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	803	LMT	2	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	700/735 (95%)	1.01	126 (18%)	3 2	33, 94, 145, 198	0
1	B	698/735 (94%)	1.14	141 (20%)	3 2	36, 94, 152, 199	0
All	All	1398/1470 (95%)	1.07	267 (19%)	3 2	33, 94, 148, 199	0

All (267) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	494	THR	12.4
1	A	141	LEU	11.3
1	A	490	VAL	11.2
1	B	123	TYR	10.8
1	B	233	ASN	10.6
1	A	491	GLY	10.4
1	A	489	ALA	10.0
1	A	318	GLN	9.6
1	A	495	ALA	9.4
1	A	458	ASP	8.7
1	B	291	ILE	8.1
1	B	322	ASN	7.9
1	B	494	THR	7.7
1	B	248	PHE	7.7
1	A	460	TYR	7.6
1	B	40	SER	7.2
1	B	498	GLY	7.1
1	B	453	THR	7.0
1	B	497	ILE	6.9
1	A	188	MET	6.7
1	A	493	THR	6.5
1	A	123	TYR	6.5
1	B	410	LEU	6.4
1	B	321	LEU	6.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	308	VAL	6.4
1	A	286	LEU	6.3
1	B	411	SER	6.3
1	B	237	VAL	6.3
1	B	145	TYR	6.2
1	A	457	VAL	6.2
1	B	343	TYR	6.1
1	B	4	ALA	6.0
1	A	177	SER	5.9
1	B	457	VAL	5.8
1	B	694	LEU	5.7
1	B	141	LEU	5.7
1	A	704	ILE	5.5
1	A	475	GLU	5.3
1	B	325	LEU	5.3
1	B	240	LEU	5.2
1	A	497	ILE	5.2
1	B	292	PHE	5.2
1	B	323	ILE	5.2
1	A	487	LEU	5.1
1	A	190	ASP	5.1
1	A	119	LEU	4.9
1	B	456	SER	4.9
1	B	406	ILE	4.9
1	B	652	THR	4.8
1	B	655	SER	4.7
1	A	189	PHE	4.7
1	B	138	LEU	4.7
1	A	317	PRO	4.6
1	B	236	ASP	4.6
1	B	188	MET	4.5
1	A	124	GLN	4.4
1	A	249	VAL	4.4
1	B	353	LEU	4.3
1	A	290	PRO	4.2
1	B	454	SER	4.2
1	A	323	ILE	4.2
1	B	186	ILE	4.2
1	A	172	PHE	4.1
1	B	119	LEU	4.1
1	B	142	VAL	4.0
1	B	95	MET	4.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	418	PHE	4.0
1	A	703	ASP	4.0
1	A	542	ALA	4.0
1	A	536	LEU	4.0
1	B	288	SER	4.0
1	B	235	GLY	3.9
1	A	463	ILE	3.9
1	B	44	SER	3.9
1	B	305	ILE	3.9
1	B	191	ARG	3.8
1	B	294	ALA	3.8
1	B	310	VAL	3.8
1	B	365	SER	3.8
1	B	533	LEU	3.8
1	A	321	LEU	3.7
1	B	295	LEU	3.7
1	B	337	ALA	3.7
1	A	492	ASN	3.7
1	B	53	GLU	3.7
1	A	184	SER	3.7
1	B	613	TYR	3.7
1	B	35	MET	3.7
1	A	708	ILE	3.7
1	B	412	LEU	3.6
1	A	187	ALA	3.6
1	A	316	ASN	3.6
1	A	700	PRO	3.6
1	B	460	TYR	3.6
1	A	701	SER	3.6
1	A	461	GLY	3.5
1	B	339	LEU	3.5
1	B	458	ASP	3.5
1	A	320	GLU	3.5
1	B	557	TYR	3.4
1	B	699	GLY	3.4
1	A	410	LEU	3.4
1	B	205	ALA	3.4
1	A	77	GLY	3.4
1	A	626	GLY	3.4
1	B	122	ALA	3.4
1	B	190	ASP	3.3
1	B	651	LEU	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	286	LEU	3.3
1	A	498	GLY	3.3
1	A	677	GLY	3.3
1	B	670	ASN	3.3
1	A	58	PHE	3.3
1	A	144	VAL	3.2
1	B	336	THR	3.2
1	A	630	GLY	3.2
1	A	8	PHE	3.2
1	A	3	VAL	3.2
1	A	639	ILE	3.2
1	B	244	LEU	3.1
1	A	181	LEU	3.1
1	B	116	GLY	3.1
1	B	285	ALA	3.1
1	A	353	LEU	3.1
1	B	77	GLY	3.1
1	B	386	TYR	3.1
1	A	116	GLY	3.0
1	B	366	ALA	3.0
1	A	344	LEU	3.0
1	B	702	LEU	3.0
1	B	502	ALA	3.0
1	A	698	VAL	3.0
1	A	514	PHE	2.9
1	A	671	LEU	2.9
1	B	362	PRO	2.9
1	A	145	TYR	2.9
1	A	197	TYR	2.9
1	B	218	ASP	2.9
1	A	53	GLU	2.9
1	B	98	ALA	2.9
1	B	665	TYR	2.9
1	A	488	ASP	2.9
1	B	243	ASP	2.9
1	B	452	ALA	2.9
1	B	349	GLY	2.8
1	B	307	TYR	2.8
1	A	4	ALA	2.8
1	B	238	ALA	2.8
1	A	483	ILE	2.8
1	A	668	ALA	2.8

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	496	ALA	2.8
1	A	694	LEU	2.8
1	A	382	TYR	2.8
1	A	291	ILE	2.8
1	B	639	ILE	2.8
1	A	438	TYR	2.7
1	A	246	GLU	2.7
1	B	364	PHE	2.7
1	B	618	ALA	2.7
1	B	536	LEU	2.7
1	B	393	PHE	2.7
1	B	451	VAL	2.7
1	B	124	GLN	2.7
1	A	562	LEU	2.7
1	A	115	ILE	2.6
1	A	693	PRO	2.6
1	A	669	GLY	2.6
1	A	337	ALA	2.6
1	A	540	LEU	2.6
1	B	535	LEU	2.6
1	B	183	CYS	2.6
1	A	238	ALA	2.6
1	A	294	ALA	2.6
1	B	532	SER	2.6
1	B	202	ASP	2.6
1	B	209	GLY	2.6
1	A	486	HIS	2.6
1	A	322	ASN	2.6
1	B	206	ASP	2.6
1	A	574	VAL	2.6
1	B	204	ALA	2.6
1	B	527	ILE	2.5
1	B	619	ILE	2.5
1	A	623	LEU	2.5
1	B	347	LEU	2.5
1	A	333	VAL	2.5
1	B	9	LEU	2.5
1	B	561	TYR	2.5
1	B	7	PHE	2.5
1	A	241	GLY	2.5
1	A	142	VAL	2.5
1	A	334	VAL	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	503	ILE	2.5
1	B	126	GLY	2.5
1	B	548	ALA	2.4
1	A	619	ILE	2.4
1	B	221	ARG	2.4
1	A	245	LEU	2.4
1	B	437	LEU	2.4
1	B	620	LEU	2.4
1	A	723	VAL	2.4
1	A	185	ILE	2.4
1	A	686	ILE	2.4
1	A	95	MET	2.4
1	A	237	VAL	2.4
1	B	723	VAL	2.4
1	A	98	ALA	2.4
1	A	226	ILE	2.4
1	B	368	ILE	2.4
1	A	248	PHE	2.4
1	B	340	THR	2.4
1	A	193	GLY	2.4
1	A	477	ASP	2.3
1	B	333	VAL	2.3
1	B	698	VAL	2.3
1	B	659	TRP	2.3
1	A	724	HIS	2.3
1	A	22	PHE	2.3
1	A	225	THR	2.3
1	A	49	PHE	2.3
1	A	558	PHE	2.3
1	B	545	ILE	2.3
1	A	697	THR	2.3
1	B	320	GLU	2.2
1	B	549	LEU	2.2
1	B	381	GLU	2.2
1	A	496	ALA	2.2
1	B	363	TRP	2.2
1	A	192	VAL	2.2
1	A	539	MET	2.2
1	A	631	ALA	2.2
1	B	534	VAL	2.2
1	A	464	ALA	2.2
1	B	200	ALA	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	403	GLY	2.2
1	B	524	PRO	2.2
1	A	252	ILE	2.2
1	B	335	LEU	2.2
1	B	550	LEU	2.2
1	B	369	GLY	2.2
1	B	485	ASP	2.2
1	B	671	LEU	2.1
1	B	19	ALA	2.1
1	A	702	LEU	2.1
1	A	665	TYR	2.1
1	B	677	GLY	2.1
1	A	627	PHE	2.1
1	A	207	LEU	2.1
1	B	115	ILE	2.1
1	B	184	SER	2.1
1	A	696	ASP	2.1
1	A	106	ALA	2.1
1	B	645	GLY	2.1
1	A	711	VAL	2.0
1	B	121	VAL	2.0
1	A	67	LEU	2.0
1	A	331	LEU	2.0
1	A	545	ILE	2.0
1	B	704	ILE	2.0
1	B	611	MET	2.0
1	B	462	PRO	2.0
1	B	695	LYS	2.0
1	A	350	LEU	2.0
1	B	102	ASN	2.0
1	A	474	CYS	2.0
1	A	223	PRO	2.0
1	B	57	ILE	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands

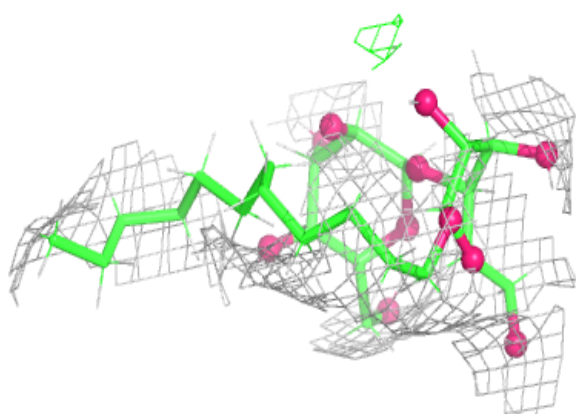
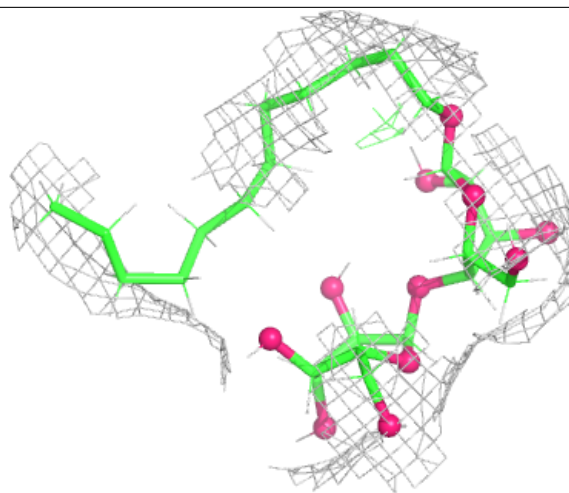
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	A	804	1/1	0.53	0.20	98,98,98,98	0
5	LMT	B	803	35/35	0.53	0.11	90,155,189,199	0
3	MG	A	805	1/1	0.64	0.13	102,102,102,102	0
5	LMT	B	802	35/35	0.66	0.12	89,133,180,195	0
3	MG	B	808	1/1	0.67	0.27	88,88,88,88	0
3	MG	B	806	1/1	0.76	0.22	101,101,101,101	0
2	911	A	801	11/11	0.80	0.08	104,134,157,165	0
3	MG	B	807	1/1	0.84	0.17	110,110,110,110	0
3	MG	A	802	1/1	0.84	0.20	85,85,85,85	0
3	MG	B	805	1/1	0.85	0.23	92,92,92,92	0
3	MG	A	803	1/1	0.85	0.15	91,91,91,91	0
2	911	B	801	11/11	0.86	0.07	120,147,163,166	0
3	MG	B	804	1/1	0.89	0.22	88,88,88,88	0
4	CA	B	809	1/1	0.93	0.19	98,98,98,98	0
4	CA	A	806	1/1	0.95	0.09	89,89,89,89	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.

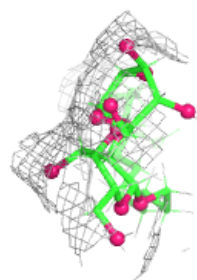
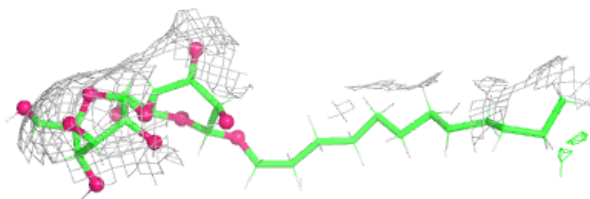
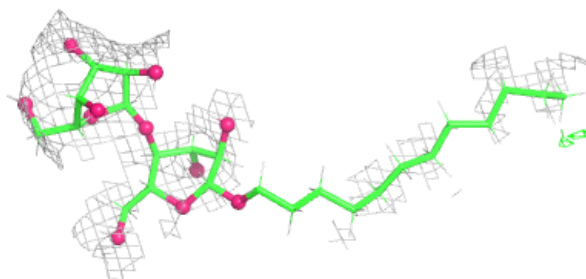
Electron density around LMT B 803:

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



Electron density around LMT B 802:

$2mF_o-DF_c$ (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.