



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:42 PM UTC

PDB ID : 3TLM / pdb_00003tln
Title : Crystal Structure of Endoplasmic Reticulum Ca²⁺-ATPase (SERCA) From Bovine Muscle
Authors : Sacchetto, R.; Bertipaglia, I.; Giannetti, S.; Cendron, L.; Mascarello, F.; Damiani, E.; Carafoli, E.; Zanotti, G.
Deposited on : 2011-08-30
Resolution : 2.95 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

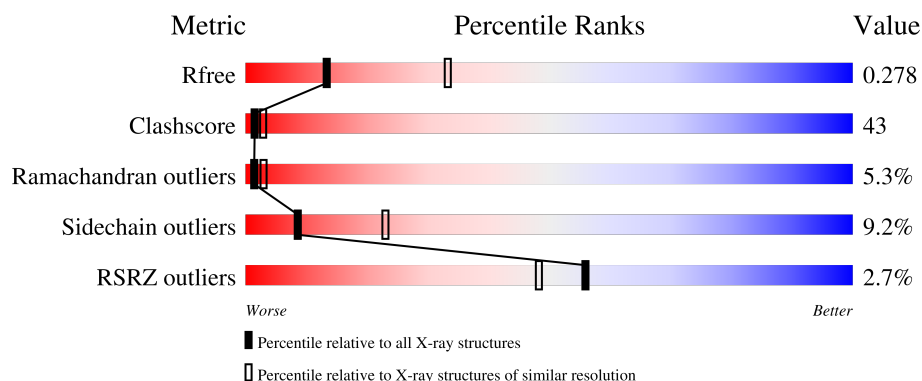
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

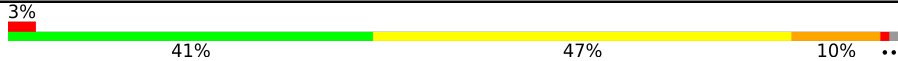
The reported resolution of this entry is 2.95 Å.

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	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	992	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7687 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 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	987	Total	C	N	O	S	0	0	0
			7619	4850	1278	1437	54			

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Ca	0	0
			2	2		

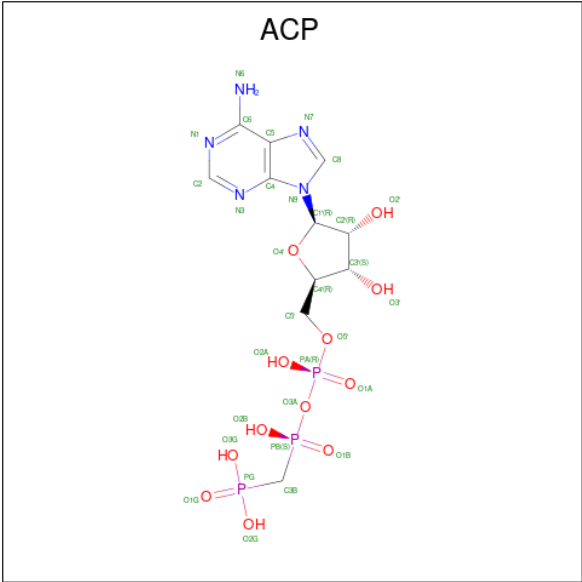
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		

- Molecule 4 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	K	0	0
			1	1		

- Molecule 5 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (CCD ID: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			31	11	5	12	3		

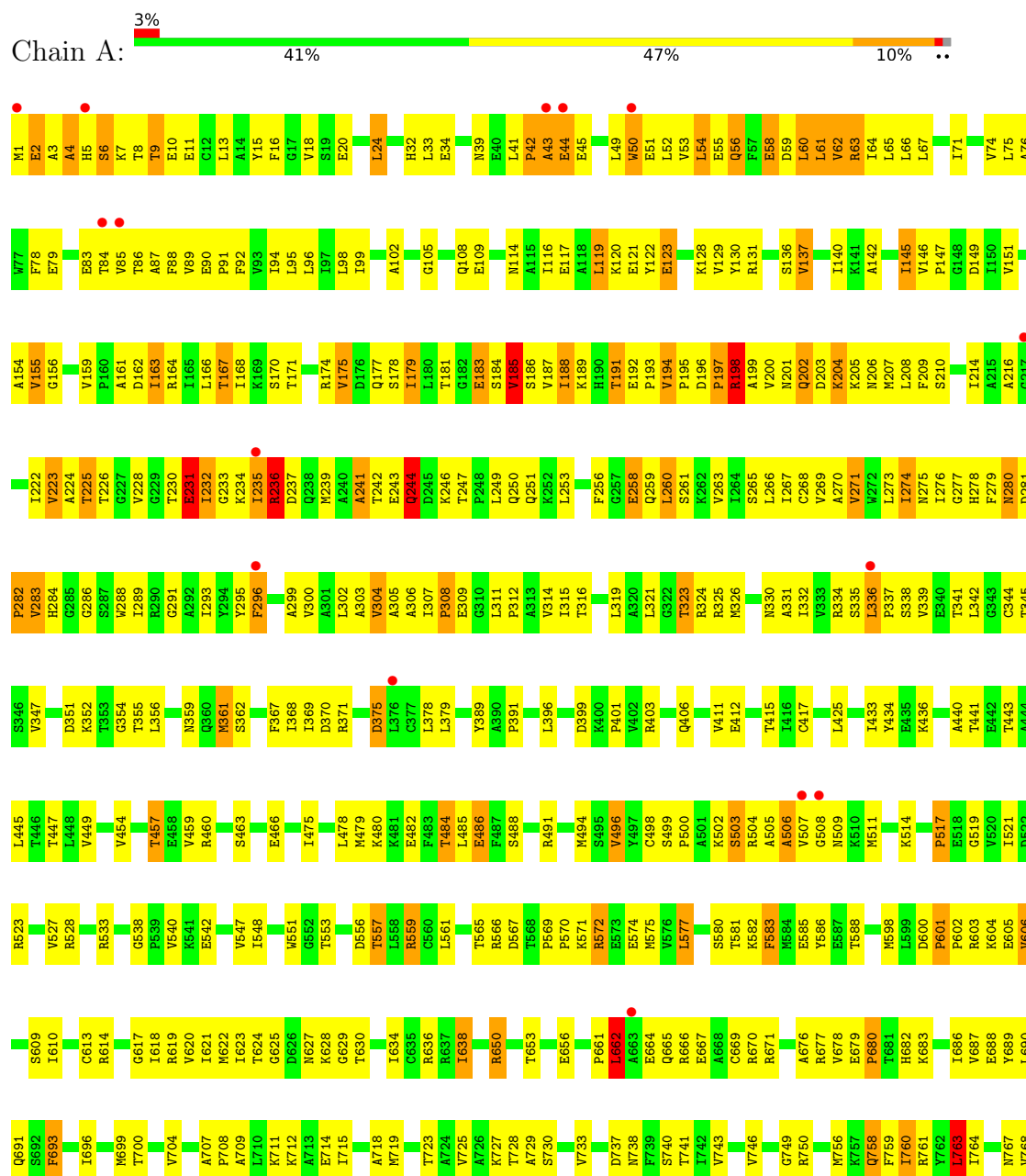
- Molecule 6 is water.

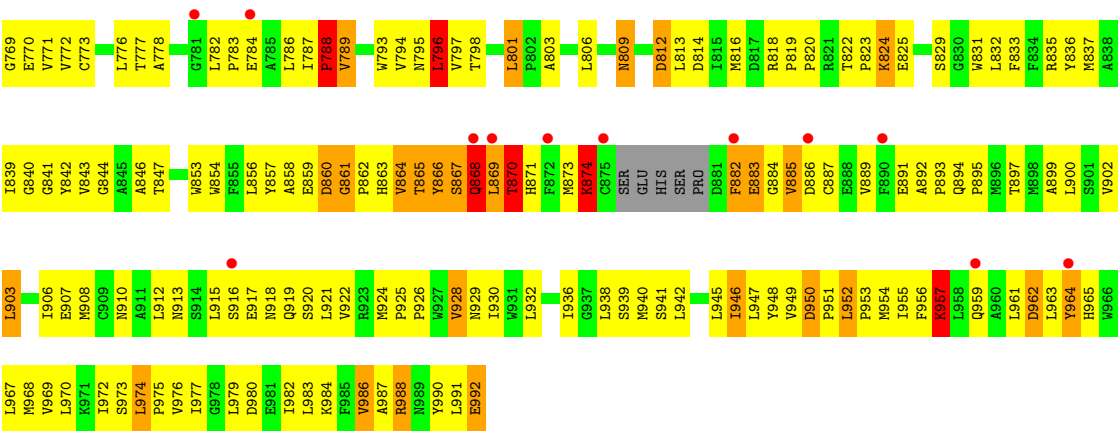
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	33	Total	O	0	0
			33	33		

3 Residue-property plots

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

- Molecule 1: Sarcoplasmic/endoplasmic reticulum calcium ATPase 1





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	156.58Å 75.26Å 151.80Å 90.00° 108.30° 90.00°	Depositor
Resolution (Å)	41.99 – 2.95 41.99 – 2.95	Depositor EDS
% Data completeness (in resolution range)	99.6 (41.99-2.95) 99.6 (41.99-2.95)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.95Å)	Xtriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.205 , 0.277 0.206 , 0.278	Depositor DCC
R_{free} test set	1790 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	68.3	Xtriage
Anisotropy	0.581	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 71.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7687	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, ACP, MG, CA

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	0.45	0/7757	0.99	35/10523 (0.3%)

There are no bond length outliers.

All (35) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	56	GLN	N-CA-C	-9.78	101.37	113.20
1	A	5	HIS	N-CA-C	-9.66	102.30	114.56
1	A	924	MET	CA-C-N	8.71	129.35	120.38
1	A	924	MET	C-N-CA	8.71	129.35	120.38
1	A	847	THR	N-CA-C	-8.23	103.69	114.31
1	A	882	PHE	N-CA-C	-8.12	102.93	112.92
1	A	191	THR	N-CA-C	7.84	119.61	111.14
1	A	63	ARG	N-CA-C	-7.83	102.74	111.28
1	A	163	ILE	N-CA-C	7.72	119.24	108.12
1	A	600	ASP	CA-C-N	7.51	128.12	120.38
1	A	600	ASP	C-N-CA	7.51	128.12	120.38
1	A	957	LYS	N-CA-C	7.04	117.57	108.34
1	A	846	ALA	N-CA-C	-6.98	101.98	113.50
1	A	928	VAL	N-CA-C	-6.89	102.21	111.44
1	A	869	LEU	N-CA-C	-6.59	103.81	112.24
1	A	296	PHE	N-CA-C	-6.28	104.54	111.82
1	A	42	PRO	N-CA-C	-6.17	106.44	114.03
1	A	601	PRO	N-CA-C	6.11	118.15	110.70
1	A	606	VAL	N-CA-C	6.06	116.18	110.30
1	A	583	PHE	N-CA-C	6.04	117.86	111.28
1	A	4	ALA	N-CA-C	5.75	116.98	107.73
1	A	874	LYS	N-CA-C	-5.74	107.52	114.75
1	A	693	PHE	N-CA-C	-5.71	104.51	113.02
1	A	13	LEU	N-CA-C	-5.65	105.21	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	868	GLN	N-CA-C	-5.64	105.98	112.86
1	A	885	VAL	N-CA-C	-5.52	107.60	112.90
1	A	361	MET	N-CA-C	5.50	119.07	110.32
1	A	159	VAL	CA-C-N	5.24	125.04	119.28
1	A	159	VAL	C-N-CA	5.24	125.04	119.28
1	A	559	ARG	N-CA-C	-5.22	100.72	109.24
1	A	577	LEU	N-CA-C	5.20	120.27	113.30
1	A	194	VAL	CA-C-N	5.18	126.32	119.84
1	A	194	VAL	C-N-CA	5.18	126.32	119.84
1	A	368	ILE	N-CA-C	-5.09	102.32	108.53
1	A	604	LYS	N-CA-C	5.03	116.76	111.28

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7619	0	7732	665	0
2	A	2	0	0	0	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	31	0	14	7	0
6	A	33	0	0	6	0
All	All	7687	0	7746	667	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 43.

All (667) 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:662:LEU:H	1:A:662:LEU:HD22	1.20	1.04
1:A:964:TYR:H	1:A:967:LEU:HD12	1.22	1.01
1:A:49:LEU:HB3	1:A:52:LEU:HB2	1.42	1.00

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:145:ILE:HD13	1:A:223:VAL:HG21	1.44	0.98
1:A:602:PRO:HB3	1:A:638:ILE:HD11	1.44	0.97
1:A:822:THR:HG22	1:A:824:LYS:H	1.31	0.95
1:A:336:LEU:H	1:A:336:LEU:HD12	1.35	0.92
1:A:809:ASN:ND2	1:A:929:ASN:HD22	1.71	0.89
1:A:463:SER:HB3	1:A:466:GLU:HG3	1.55	0.88
1:A:769:GLY:HA3	1:A:843:VAL:HG13	1.58	0.84
1:A:627:ASN:HD22	1:A:630:THR:H	1.23	0.84
1:A:95:LEU:O	1:A:99:ILE:HG12	1.78	0.83
1:A:311:LEU:O	1:A:314:VAL:HG12	1.77	0.83
1:A:280:ASN:HD22	1:A:281:ASP:N	1.76	0.83
1:A:145:ILE:CD1	1:A:223:VAL:HG21	2.09	0.83
1:A:679:GLU:HB3	1:A:680:PRO:HD2	1.60	0.83
1:A:814:ASP:H	1:A:818:ARG:NH2	1.78	0.81
1:A:837:MET:HE2	1:A:837:MET:HA	1.62	0.80
1:A:862:PRO:HD3	1:A:889:VAL:HG11	1.61	0.80
1:A:983:LEU:O	1:A:986:VAL:HG12	1.82	0.80
1:A:179:ILE:HD13	1:A:179:ILE:O	1.82	0.79
1:A:352:LYS:HG3	1:A:622:MET:HE2	1.63	0.79
1:A:162:ASP:OD2	1:A:230:THR:HA	1.81	0.79
1:A:24:LEU:HD22	1:A:149:ASP:HB3	1.63	0.79
1:A:862:PRO:HG3	1:A:889:VAL:HG21	1.64	0.79
1:A:196:ASP:HB3	1:A:198:ARG:NH2	1.97	0.79
1:A:155:VAL:HG12	1:A:216:ALA:HA	1.62	0.79
1:A:197:PRO:HD2	1:A:198:ARG:NH1	1.99	0.78
1:A:511:MET:HE2	1:A:569:PRO:HB3	1.66	0.77
1:A:306:ALA:HA	1:A:767:ASN:ND2	1.99	0.77
1:A:874:LYS:HB2	1:A:874:LYS:HZ2	1.49	0.77
1:A:49:LEU:HB3	1:A:52:LEU:CB	2.14	0.77
1:A:897:THR:OG1	1:A:957:LYS:HB3	1.84	0.76
1:A:53:VAL:HG23	1:A:54:LEU:HD12	1.66	0.76
1:A:688:GLU:HG3	1:A:712:LYS:HE2	1.68	0.76
1:A:151:VAL:HG11	1:A:163:ILE:HD13	1.68	0.76
1:A:334:ARG:CB	1:A:334:ARG:HH11	1.99	0.76
1:A:796:LEU:HD22	1:A:796:LEU:O	1.87	0.75
1:A:602:PRO:CB	1:A:638:ILE:HD11	2.16	0.74
1:A:687:VAL:O	1:A:691:GLN:HG3	1.87	0.74
1:A:920:SER:OG	1:A:922:VAL:HG12	1.87	0.74
1:A:250:GLN:HG2	1:A:315:ILE:HD12	1.68	0.74
1:A:610:ILE:HD12	1:A:620:VAL:HG11	1.70	0.74
1:A:161:ALA:HA	1:A:210:SER:HB2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:ARG:HE	1:A:198:ARG:C	1.95	0.74
1:A:797:VAL:HG13	1:A:939:SER:HB3	1.69	0.73
1:A:230:THR:C	1:A:232:ILE:H	1.97	0.73
1:A:119:LEU:HD21	1:A:330:ASN:HA	1.70	0.73
1:A:863:HIS:O	1:A:865:THR:N	2.21	0.73
1:A:839:ILE:CD1	1:A:979:LEU:HD22	2.19	0.72
1:A:246:LYS:HG3	1:A:251:GLN:HG2	1.71	0.72
1:A:302:LEU:HD11	1:A:771:VAL:HG22	1.71	0.72
1:A:412:GLU:OE1	1:A:528:ARG:HD2	1.89	0.72
1:A:336:LEU:H	1:A:336:LEU:CD1	2.03	0.72
1:A:174:ARG:HH21	1:A:186:SER:HB2	1.56	0.71
1:A:188:ILE:HD13	1:A:189:LYS:H	1.54	0.71
1:A:282:PRO:HG2	1:A:283:VAL:H	1.55	0.71
1:A:707:ALA:HB3	1:A:708:PRO:HD3	1.72	0.71
1:A:65:LEU:HG	1:A:304:VAL:HG13	1.73	0.71
1:A:275:ASN:O	1:A:277:GLY:N	2.23	0.71
1:A:184:SER:O	1:A:185:VAL:HG13	1.90	0.71
1:A:839:ILE:HD13	1:A:979:LEU:HD22	1.74	0.70
1:A:865:THR:HG22	1:A:866:TYR:CD2	2.27	0.70
1:A:308:PRO:HG3	1:A:763:LEU:HD12	1.71	0.70
1:A:494:MET:HE2	6:A:999:HOH:O	1.90	0.70
1:A:979:LEU:C	1:A:979:LEU:HD23	2.16	0.70
1:A:233:GLY:O	1:A:236:ARG:HB2	1.92	0.69
1:A:843:VAL:HA	1:A:906:ILE:HD13	1.73	0.69
1:A:650:ARG:HH11	1:A:650:ARG:HB2	1.57	0.69
1:A:403:ARG:HD3	1:A:406:GLN:HG3	1.74	0.69
1:A:207:MET:O	1:A:208:LEU:HD23	1.92	0.68
1:A:326:MET:HE2	1:A:326:MET:HA	1.74	0.68
1:A:650:ARG:HH11	1:A:650:ARG:CB	2.07	0.68
1:A:662:LEU:HD22	1:A:662:LEU:N	2.04	0.68
1:A:893:PRO:HB2	1:A:957:LYS:HG3	1.76	0.68
1:A:769:GLY:HA2	1:A:772:VAL:HB	1.75	0.67
1:A:583:PHE:HA	1:A:586:TYR:HD2	1.59	0.67
1:A:667:GLU:HG3	1:A:671:ARG:HH12	1.60	0.67
1:A:670:ARG:NH1	1:A:670:ARG:HB3	2.10	0.67
1:A:24:LEU:HD13	1:A:149:ASP:HA	1.77	0.67
1:A:833:PHE:O	1:A:837:MET:HG2	1.95	0.67
1:A:71:ILE:HD11	1:A:300:VAL:HG11	1.75	0.67
1:A:334:ARG:HB3	1:A:334:ARG:NH1	2.09	0.67
1:A:662:LEU:H	1:A:662:LEU:CD2	2.01	0.67
1:A:688:GLU:CG	1:A:712:LYS:HE2	2.25	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:843:VAL:HG23	1:A:906:ILE:HG21	1.76	0.66
1:A:306:ALA:HA	1:A:767:ASN:HD22	1.61	0.66
1:A:312:PRO:O	1:A:315:ILE:HG12	1.95	0.66
1:A:519:GLY:O	1:A:523:ARG:HG3	1.96	0.66
1:A:670:ARG:HB3	1:A:670:ARG:HH11	1.60	0.66
1:A:347:VAL:HG22	1:A:619:ARG:HB3	1.78	0.66
1:A:571:LYS:O	1:A:574:GLU:HG2	1.96	0.66
1:A:899:ALA:O	1:A:902:VAL:HG12	1.96	0.66
1:A:8:THR:HG22	1:A:193:PRO:HG3	1.76	0.66
1:A:151:VAL:HG11	1:A:163:ILE:CD1	2.25	0.66
1:A:686:ILE:O	1:A:690:LEU:HD13	1.95	0.66
1:A:321:LEU:HG	1:A:325:ARG:HH21	1.62	0.65
1:A:824:LYS:HZ3	1:A:824:LYS:HA	1.62	0.65
1:A:1:MET:HG2	1:A:225:THR:HA	1.79	0.65
1:A:614:ARG:HH11	1:A:614:ARG:HG2	1.60	0.65
1:A:334:ARG:HH11	1:A:334:ARG:HB3	1.61	0.65
1:A:787:ILE:HB	1:A:788:PRO:HD2	1.79	0.65
1:A:883:GLU:O	1:A:885:VAL:HG23	1.97	0.65
1:A:964:TYR:N	1:A:967:LEU:HD12	2.03	0.65
1:A:198:ARG:N	1:A:198:ARG:NE	2.45	0.65
1:A:445:LEU:HD11	1:A:598:MET:HE2	1.79	0.65
1:A:486:GLU:HA	6:A:999:HOH:O	1.98	0.64
1:A:62:VAL:O	1:A:66:LEU:HG	1.97	0.64
1:A:917:GLU:HG2	1:A:918:ASN:OD1	1.96	0.64
1:A:71:ILE:O	1:A:75:LEU:HG	1.96	0.64
1:A:60:LEU:HG	1:A:61:LEU:H	1.62	0.64
1:A:379:LEU:CD1	1:A:547:VAL:HG21	2.28	0.64
1:A:60:LEU:H	1:A:60:LEU:HD23	1.61	0.64
1:A:210:SER:O	1:A:232:ILE:HG21	1.97	0.64
1:A:665:GLN:NE2	1:A:689:TYR:OH	2.31	0.64
1:A:670:ARG:HD2	1:A:693:PHE:CE1	2.33	0.64
1:A:854:TRP:HA	1:A:858:ALA:CB	2.28	0.64
1:A:247:THR:O	1:A:251:GLN:HG3	1.98	0.64
1:A:361:MET:HE3	1:A:440:ALA:HB3	1.79	0.64
1:A:244:GLN:H	1:A:244:GLN:HE21	1.46	0.64
1:A:908:MET:HE3	1:A:936:ILE:HA	1.80	0.63
1:A:925:PRO:O	1:A:928:VAL:HG13	1.97	0.63
1:A:175:VAL:O	1:A:187:VAL:HG12	1.97	0.63
1:A:941:SER:O	1:A:945:LEU:HD13	1.98	0.63
1:A:145:ILE:HD12	1:A:146:VAL:N	2.13	0.63
1:A:42:PRO:O	1:A:44:GLU:N	2.32	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:196:ASP:HB3	1:A:198:ARG:HH22	1.63	0.63
1:A:768:VAL:O	1:A:772:VAL:HG23	1.99	0.63
1:A:391:PRO:HD2	1:A:434:TYR:CE2	2.34	0.63
1:A:155:VAL:HA	1:A:214:ILE:HG22	1.80	0.63
1:A:950:ASP:C	1:A:953:PRO:HD2	2.23	0.63
1:A:55:GLU:HA	1:A:55:GLU:OE1	1.98	0.62
1:A:796:LEU:HD13	1:A:797:VAL:HG23	1.79	0.62
1:A:619:ARG:NH2	1:A:670:ARG:HA	2.14	0.62
1:A:661:PRO:HG2	1:A:664:GLU:HG3	1.82	0.62
1:A:59:ASP:CG	1:A:312:PRO:HB3	2.25	0.62
1:A:130:TYR:CZ	1:A:137:VAL:HG13	2.34	0.62
1:A:908:MET:HG3	1:A:940:MET:HE1	1.82	0.62
1:A:236:ARG:HH21	1:A:237:ASP:HA	1.64	0.62
1:A:908:MET:CE	1:A:936:ILE:HA	2.29	0.62
1:A:342:LEU:HD21	1:A:715:ILE:HG21	1.81	0.62
1:A:184:SER:C	1:A:185:VAL:HG22	2.25	0.62
1:A:769:GLY:HA3	1:A:843:VAL:CG1	2.29	0.62
1:A:786:LEU:HD23	1:A:900:LEU:HD13	1.82	0.61
1:A:436:LYS:HB3	1:A:443:THR:HG21	1.83	0.61
1:A:973:SER:O	1:A:976:VAL:HG12	1.99	0.61
1:A:244:GLN:HE21	1:A:244:GLN:N	1.99	0.61
1:A:280:ASN:HD22	1:A:280:ASN:C	2.07	0.61
1:A:794:VAL:HG13	1:A:900:LEU:HD11	1.82	0.61
1:A:956:PHE:O	1:A:957:LYS:NZ	2.21	0.61
1:A:171:THR:HG21	1:A:577:LEU:HD23	1.83	0.61
1:A:723:THR:O	1:A:727:LYS:HG3	2.00	0.61
1:A:276:ILE:HA	1:A:279:PHE:CG	2.36	0.60
1:A:575:MET:HG2	1:A:586:TYR:CE1	2.36	0.60
1:A:583:PHE:HA	1:A:586:TYR:CD2	2.36	0.60
1:A:770:GLU:O	1:A:773:CYS:HB3	2.01	0.60
1:A:843:VAL:HG23	1:A:906:ILE:CG2	2.30	0.60
1:A:903:LEU:O	1:A:906:ILE:HG22	2.02	0.60
1:A:918:ASN:HD22	1:A:987:ALA:HB3	1.66	0.60
1:A:281:ASP:CB	1:A:282:PRO:HD2	2.32	0.60
1:A:336:LEU:HD12	1:A:336:LEU:N	2.13	0.60
1:A:39:ASN:HB2	1:A:226:THR:HB	1.84	0.60
1:A:174:ARG:NH2	1:A:186:SER:HB2	2.16	0.60
1:A:181:THR:OG1	1:A:183:GLU:HG2	2.02	0.60
1:A:824:LYS:HA	1:A:824:LYS:NZ	2.17	0.60
1:A:7:LYS:HB3	1:A:11:GLU:HB2	1.84	0.59
1:A:623:ILE:HG21	1:A:683:LYS:HG2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:603:ARG:HB2	1:A:606:VAL:HG23	1.85	0.59
1:A:315:ILE:HG13	1:A:316:THR:N	2.17	0.59
1:A:628:LYS:HD3	1:A:653:THR:HG22	1.84	0.59
1:A:166:LEU:HD21	1:A:222:ILE:HG22	1.84	0.59
1:A:361:MET:HE3	1:A:440:ALA:CB	2.33	0.59
1:A:714:GLU:O	1:A:715:ILE:HD13	2.03	0.59
1:A:362:SER:HA	6:A:1029:HOH:O	2.02	0.59
1:A:670:ARG:HD2	1:A:693:PHE:CZ	2.37	0.59
1:A:230:THR:HB	1:A:232:ILE:HG23	1.83	0.59
1:A:375:ASP:OD2	1:A:375:ASP:N	2.33	0.59
1:A:268:CYS:HB3	1:A:299:ALA:HB1	1.85	0.59
1:A:856:LEU:O	1:A:858:ALA:N	2.35	0.59
1:A:53:VAL:O	1:A:55:GLU:N	2.34	0.59
1:A:336:LEU:N	1:A:337:PRO:HD2	2.18	0.59
1:A:862:PRO:CG	1:A:889:VAL:HG21	2.33	0.59
5:A:1001:ACP:H8	5:A:1001:ACP:H3'	1.85	0.58
1:A:865:THR:HG22	1:A:866:TYR:HD2	1.65	0.58
1:A:946:ILE:HG13	1:A:956:PHE:CE2	2.38	0.58
1:A:874:LYS:HZ2	1:A:882:PHE:HB3	1.68	0.58
1:A:65:LEU:CD1	1:A:304:VAL:HG13	2.34	0.58
1:A:991:LEU:HD22	1:A:992:GLU:OE1	2.04	0.58
1:A:197:PRO:HD2	1:A:198:ARG:HH12	1.68	0.58
1:A:314:VAL:HG22	1:A:756:MET:HE1	1.86	0.58
1:A:4:ALA:HB1	1:A:6:SER:OG	2.04	0.58
1:A:738:ASN:OD1	1:A:740:SER:HB2	2.02	0.58
1:A:667:GLU:HG3	1:A:671:ARG:NH1	2.19	0.58
1:A:241:ALA:HB1	1:A:243:GLU:OE2	2.03	0.57
1:A:787:ILE:HB	1:A:788:PRO:CD	2.34	0.57
1:A:355:THR:CG2	1:A:700:THR:HG22	2.34	0.57
1:A:916:SER:OG	1:A:919:GLN:HB2	2.04	0.57
1:A:831:TRP:CH2	1:A:987:ALA:HB2	2.39	0.57
1:A:156:GLY:HA2	1:A:725:VAL:HG23	1.85	0.57
1:A:177:GLN:HE22	1:A:189:LYS:NZ	2.02	0.57
1:A:279:PHE:O	1:A:291:GLY:HA3	2.04	0.57
1:A:63:ARG:HA	1:A:66:LEU:HD12	1.87	0.57
1:A:445:LEU:O	1:A:449:VAL:HG23	2.04	0.57
1:A:743:VAL:O	1:A:746:VAL:HG12	2.04	0.57
1:A:829:SER:H	1:A:832:LEU:HD12	1.70	0.57
1:A:351:ASP:OD2	5:A:1001:ACP:O3G	2.23	0.57
1:A:511:MET:HE3	1:A:566:ARG:HD3	1.87	0.57
1:A:556:ASP:O	1:A:557:THR:C	2.48	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:991:LEU:O	1:A:991:LEU:HD23	2.05	0.56
1:A:854:TRP:CE3	1:A:895:PRO:HB3	2.40	0.56
1:A:957:LYS:NZ	1:A:957:LYS:HA	2.20	0.56
1:A:65:LEU:CG	1:A:304:VAL:HG13	2.35	0.56
1:A:120:LYS:C	1:A:122:TYR:H	2.13	0.56
1:A:250:GLN:CG	1:A:315:ILE:HD12	2.35	0.56
1:A:864:VAL:HG21	1:A:868:GLN:HA	1.85	0.56
1:A:339:VAL:HG12	1:A:749:GLY:HA2	1.86	0.56
1:A:894:GLN:N	1:A:895:PRO:HD2	2.20	0.56
1:A:625:GLY:O	1:A:677:ARG:HD3	2.05	0.56
1:A:743:VAL:HA	1:A:746:VAL:HG12	1.88	0.56
1:A:938:LEU:C	1:A:938:LEU:HD13	2.31	0.56
1:A:411:VAL:HA	1:A:454:VAL:HG11	1.88	0.56
1:A:463:SER:HB3	1:A:466:GLU:CG	2.32	0.56
1:A:67:LEU:C	1:A:67:LEU:HD23	2.31	0.56
1:A:96:LEU:HD23	1:A:796:LEU:HD21	1.86	0.56
1:A:570:PRO:HG2	1:A:575:MET:SD	2.46	0.56
1:A:758:GLN:HE22	1:A:917:GLU:HB2	1.71	0.56
1:A:835:ARG:HH22	1:A:984:LYS:CG	2.20	0.55
1:A:293:ILE:HA	1:A:296:PHE:HD1	1.71	0.55
1:A:504:ARG:C	1:A:506:ALA:H	2.14	0.55
1:A:759:PHE:O	1:A:763:LEU:HB2	2.06	0.55
1:A:196:ASP:CB	1:A:198:ARG:HH22	2.18	0.55
1:A:273:LEU:HD12	1:A:274:ILE:N	2.21	0.55
1:A:342:LEU:HA	1:A:345:THR:OG1	2.06	0.55
1:A:415:THR:HA	1:A:475:ILE:HG21	1.89	0.55
1:A:511:MET:CE	1:A:569:PRO:HB3	2.35	0.55
1:A:236:ARG:O	1:A:239:MET:HG2	2.06	0.55
1:A:129:VAL:HG21	1:A:140:ILE:HD13	1.88	0.55
1:A:174:ARG:HE	1:A:186:SER:CB	2.19	0.55
1:A:177:GLN:NE2	1:A:189:LYS:NZ	2.55	0.55
1:A:853:TRP:CZ2	1:A:968:MET:HE3	2.42	0.55
1:A:950:ASP:O	1:A:953:PRO:HD2	2.07	0.55
1:A:273:LEU:C	1:A:275:ASN:H	2.15	0.55
1:A:281:ASP:HB3	1:A:282:PRO:HD2	1.89	0.55
1:A:768:VAL:HG21	1:A:837:MET:HE1	1.89	0.54
1:A:224:ALA:C	1:A:225:THR:HG22	2.32	0.54
1:A:323:THR:HG22	1:A:324:ARG:N	2.21	0.54
1:A:39:ASN:CG	1:A:226:THR:HB	2.33	0.54
1:A:56:GLN:HG3	1:A:102:ALA:HA	1.89	0.54
1:A:613:CYS:HB3	1:A:618:ILE:HB	1.90	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:915:LEU:HD11	1:A:926:PRO:HA	1.90	0.54
1:A:142:ALA:O	1:A:145:ILE:HG23	2.07	0.54
1:A:33:LEU:C	1:A:33:LEU:HD23	2.33	0.54
1:A:230:THR:C	1:A:232:ILE:N	2.66	0.54
1:A:342:LEU:CD2	1:A:715:ILE:HG21	2.38	0.54
1:A:867:SER:O	1:A:870:THR:N	2.38	0.54
1:A:119:LEU:HD12	1:A:332:ILE:CG1	2.37	0.54
1:A:279:PHE:HA	1:A:291:GLY:HA3	1.89	0.54
1:A:837:MET:HE2	1:A:837:MET:CA	2.34	0.54
1:A:117:GLU:O	1:A:121:GLU:HG2	2.07	0.54
1:A:234:LYS:C	1:A:236:ARG:H	2.16	0.54
1:A:389:TYR:HA	1:A:447:THR:HG21	1.90	0.53
1:A:614:ARG:HG2	1:A:614:ARG:NH1	2.24	0.53
1:A:128:LYS:HE2	6:A:1002:HOH:O	2.08	0.53
1:A:910:ASN:O	1:A:913:ASN:HB2	2.09	0.53
1:A:979:LEU:HD23	1:A:979:LEU:O	2.09	0.53
1:A:42:PRO:C	1:A:44:GLU:N	2.66	0.53
1:A:478:LEU:HD22	1:A:478:LEU:O	2.08	0.53
1:A:268:CYS:O	1:A:271:VAL:HG12	2.09	0.53
1:A:759:PHE:HD1	1:A:760:ILE:HD12	1.72	0.53
1:A:803:ALA:O	1:A:806:LEU:HB2	2.08	0.53
1:A:908:MET:HE3	1:A:936:ILE:HG23	1.89	0.53
1:A:480:LYS:HB3	1:A:499:SER:OG	2.08	0.53
1:A:345:THR:O	1:A:618:ILE:HD12	2.09	0.53
1:A:669:CYS:HB3	1:A:690:LEU:CD1	2.39	0.53
1:A:809:ASN:HD22	1:A:929:ASN:HD22	1.53	0.53
1:A:839:ILE:HD11	1:A:979:LEU:HD22	1.91	0.53
1:A:3:ALA:O	1:A:4:ALA:HB2	2.09	0.52
1:A:9:THR:OG1	1:A:10:GLU:N	2.39	0.52
1:A:39:ASN:CB	1:A:226:THR:HB	2.39	0.52
1:A:355:THR:HG23	1:A:700:THR:HG22	1.91	0.52
1:A:963:LEU:O	1:A:965:HIS:N	2.41	0.52
1:A:196:ASP:CA	1:A:198:ARG:HH22	2.22	0.52
1:A:288:TRP:NE1	1:A:289:ILE:HG13	2.25	0.52
1:A:342:LEU:O	1:A:746:VAL:HG23	2.08	0.52
1:A:653:THR:HG23	1:A:656:GLU:OE1	2.09	0.52
1:A:86:THR:HG23	1:A:789:VAL:HG21	1.91	0.52
1:A:147:PRO:HG3	1:A:226:THR:HG23	1.90	0.52
1:A:156:GLY:HA2	1:A:725:VAL:CG2	2.39	0.52
1:A:666:ARG:HG2	1:A:689:TYR:CD2	2.44	0.52
1:A:874:LYS:NZ	1:A:882:PHE:HD2	2.07	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:902:VAL:HA	1:A:969:VAL:HG13	1.92	0.52
1:A:259:GLN:O	1:A:263:VAL:HG23	2.10	0.52
1:A:949:VAL:C	1:A:951:PRO:HD2	2.35	0.52
1:A:64:ILE:HG21	1:A:307:ILE:CD1	2.39	0.52
1:A:258:GLU:HA	1:A:261:SER:OG	2.10	0.52
1:A:379:LEU:HD12	1:A:547:VAL:HG21	1.90	0.52
1:A:11:GLU:O	1:A:15:TYR:HB2	2.10	0.52
1:A:484:THR:HB	1:A:496:VAL:HG23	1.92	0.52
1:A:278:HIS:O	1:A:281:ASP:HB2	2.10	0.52
1:A:575:MET:HG2	1:A:586:TYR:CD1	2.45	0.52
1:A:679:GLU:CB	1:A:680:PRO:HD2	2.37	0.51
1:A:793:TRP:O	1:A:794:VAL:C	2.53	0.51
1:A:334:ARG:HD2	1:A:733:VAL:HG23	1.91	0.51
1:A:559:ARG:NH2	5:A:1001:ACP:O1B	2.42	0.51
1:A:835:ARG:HH22	1:A:984:LYS:HG2	1.75	0.51
1:A:864:VAL:HG12	1:A:869:LEU:HG	1.92	0.51
1:A:232:ILE:HG13	1:A:232:ILE:O	2.08	0.51
1:A:281:ASP:O	1:A:286:GLY:HA2	2.11	0.51
1:A:39:ASN:CG	1:A:39:ASN:O	2.52	0.51
1:A:51:GLU:HA	1:A:54:LEU:HD13	1.91	0.51
1:A:59:ASP:OD1	1:A:60:LEU:HD23	2.11	0.51
1:A:371:ARG:HD2	1:A:378:LEU:HD23	1.93	0.51
1:A:854:TRP:HA	1:A:858:ALA:HB3	1.91	0.51
1:A:874:LYS:HZ2	1:A:882:PHE:HD2	1.58	0.51
1:A:912:LEU:HD22	1:A:926:PRO:HG3	1.92	0.51
1:A:50:TRP:O	1:A:53:VAL:HG22	2.09	0.51
1:A:968:MET:O	1:A:972:ILE:HG12	2.11	0.51
1:A:230:THR:O	1:A:232:ILE:N	2.44	0.51
1:A:284:HIS:C	1:A:286:GLY:H	2.18	0.51
1:A:767:ASN:HA	1:A:770:GLU:HB2	1.92	0.51
1:A:874:LYS:HB2	1:A:874:LYS:NZ	2.21	0.51
1:A:794:VAL:HG13	1:A:900:LEU:CD1	2.40	0.51
1:A:43:ALA:O	1:A:45:GLU:N	2.41	0.51
1:A:61:LEU:O	1:A:63:ARG:N	2.38	0.51
1:A:174:ARG:NH2	1:A:186:SER:O	2.44	0.51
1:A:177:GLN:HE22	1:A:189:LYS:HZ3	1.58	0.51
1:A:203:ASP:O	1:A:205:LYS:HG3	2.11	0.51
1:A:627:ASN:ND2	1:A:629:GLY:N	2.59	0.51
1:A:854:TRP:O	1:A:858:ALA:HB3	2.11	0.51
1:A:979:LEU:O	1:A:982:ILE:HB	2.11	0.51
1:A:679:GLU:HB3	1:A:680:PRO:CD	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:777:THR:HG23	1:A:778:ALA:N	2.26	0.50
1:A:883:GLU:HG3	1:A:885:VAL:HG23	1.94	0.50
1:A:605:GLU:HB2	1:A:740:SER:OG	2.11	0.50
1:A:627:ASN:ND2	1:A:629:GLY:H	2.08	0.50
1:A:580:SER:HA	1:A:583:PHE:CD2	2.47	0.50
1:A:624:THR:O	1:A:678:VAL:HG22	2.11	0.50
1:A:203:ASP:O	1:A:205:LYS:N	2.44	0.50
1:A:261:SER:O	1:A:265:SER:HB2	2.12	0.50
1:A:809:ASN:ND2	1:A:929:ASN:ND2	2.51	0.50
1:A:947:LEU:HD23	1:A:948:TYR:CE2	2.46	0.50
1:A:1:MET:HG2	1:A:226:THR:H	1.76	0.50
1:A:62:VAL:HG22	1:A:98:LEU:HD22	1.93	0.50
1:A:131:ARG:HG3	1:A:131:ARG:HH11	1.77	0.50
1:A:856:LEU:HD12	1:A:856:LEU:N	2.27	0.50
1:A:882:PHE:O	1:A:883:GLU:HB2	2.10	0.50
1:A:479:MET:HG3	1:A:498:CYS:HB3	1.94	0.50
1:A:502:LYS:HB2	1:A:504:ARG:HH21	1.77	0.50
1:A:650:ARG:HB2	1:A:650:ARG:NH1	2.27	0.50
1:A:704:VAL:HG13	1:A:725:VAL:HG11	1.94	0.50
1:A:18:VAL:HG21	1:A:24:LEU:CD1	2.42	0.49
1:A:278:HIS:HA	1:A:281:ASP:CG	2.36	0.49
1:A:174:ARG:HB3	1:A:186:SER:HB3	1.93	0.49
1:A:284:HIS:C	1:A:286:GLY:N	2.70	0.49
1:A:391:PRO:HD2	1:A:434:TYR:CD2	2.47	0.49
1:A:527:VAL:HG21	1:A:540:VAL:HG11	1.95	0.49
1:A:961:LEU:O	1:A:965:HIS:HB2	2.13	0.49
1:A:119:LEU:HD13	1:A:119:LEU:O	2.12	0.49
1:A:367:PHE:HD1	1:A:551:TRP:CH2	2.30	0.49
1:A:761:ARG:HH21	1:A:917:GLU:HA	1.78	0.49
1:A:436:LYS:CB	1:A:443:THR:HG21	2.42	0.49
1:A:15:TYR:C	1:A:15:TYR:CD1	2.90	0.49
1:A:339:VAL:O	1:A:749:GLY:HA3	2.13	0.49
1:A:893:PRO:C	1:A:895:PRO:HD2	2.37	0.49
1:A:893:PRO:CB	1:A:957:LYS:HG3	2.41	0.49
1:A:864:VAL:CG2	1:A:868:GLN:HA	2.43	0.49
1:A:334:ARG:HH11	1:A:334:ARG:HB2	1.74	0.49
1:A:773:CYS:O	1:A:777:THR:HG22	2.13	0.49
1:A:938:LEU:O	1:A:938:LEU:HD22	2.13	0.49
1:A:84:THR:HA	1:A:87:ALA:HB3	1.94	0.48
1:A:743:VAL:O	1:A:746:VAL:CG1	2.61	0.48
1:A:874:LYS:HB2	1:A:882:PHE:HB3	1.94	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:908:MET:HE2	1:A:939:SER:HB2	1.95	0.48
1:A:49:LEU:O	1:A:50:TRP:C	2.56	0.48
1:A:164:ARG:HG3	1:A:164:ARG:HH11	1.78	0.48
1:A:517:PRO:HD3	1:A:561:LEU:HA	1.96	0.48
1:A:609:SER:OG	1:A:740:SER:HA	2.13	0.48
1:A:59:ASP:CG	1:A:60:LEU:HD23	2.38	0.48
1:A:882:PHE:O	1:A:883:GLU:CB	2.61	0.48
1:A:913:ASN:HD21	1:A:977:ILE:HA	1.78	0.48
1:A:814:ASP:H	1:A:818:ARG:HH21	1.57	0.48
1:A:860:ASP:O	1:A:861:GLY:C	2.57	0.48
1:A:58:GLU:HA	1:A:63:ARG:NH2	2.29	0.48
1:A:166:LEU:HD21	1:A:222:ILE:CG2	2.43	0.48
1:A:585:GLU:O	1:A:588:THR:HG23	2.14	0.48
1:A:145:ILE:HD11	1:A:223:VAL:HG11	1.94	0.48
1:A:835:ARG:HG3	1:A:983:LEU:HD13	1.96	0.48
1:A:970:LEU:O	1:A:974:LEU:HB2	2.14	0.48
1:A:60:LEU:C	1:A:61:LEU:O	2.55	0.48
1:A:151:VAL:CG1	1:A:163:ILE:HD13	2.41	0.48
1:A:603:ARG:HG2	1:A:603:ARG:HH11	1.78	0.48
1:A:699:MET:HE2	1:A:709:ALA:CB	2.44	0.48
1:A:862:PRO:HD3	1:A:889:VAL:CG1	2.38	0.48
1:A:932:LEU:O	1:A:936:ILE:HG13	2.14	0.48
1:A:41:LEU:CD2	1:A:228:VAL:HG22	2.44	0.47
1:A:191:THR:HG23	1:A:192:GLU:CD	2.39	0.47
1:A:280:ASN:C	1:A:280:ASN:ND2	2.70	0.47
1:A:76:ALA:HB1	1:A:88:PHE:HD2	1.79	0.47
1:A:580:SER:HA	1:A:583:PHE:CE2	2.49	0.47
1:A:605:GLU:CD	1:A:605:GLU:H	2.21	0.47
1:A:796:LEU:O	1:A:796:LEU:HD13	2.13	0.47
1:A:54:LEU:O	1:A:55:GLU:CD	2.57	0.47
1:A:59:ASP:CG	1:A:312:PRO:CB	2.87	0.47
1:A:174:ARG:HE	1:A:186:SER:HB2	1.78	0.47
1:A:284:HIS:HE1	1:A:295:TYR:CE2	2.32	0.47
1:A:610:ILE:CD1	1:A:620:VAL:HG11	2.39	0.47
1:A:885:VAL:HG12	1:A:885:VAL:O	2.15	0.47
1:A:954:MET:SD	1:A:954:MET:C	2.98	0.47
1:A:119:LEU:HD12	1:A:332:ILE:HG12	1.95	0.47
1:A:628:LYS:HD3	1:A:653:THR:CG2	2.43	0.47
1:A:979:LEU:C	1:A:979:LEU:CD2	2.85	0.47
1:A:171:THR:CG2	1:A:577:LEU:HD23	2.44	0.47
1:A:235:ILE:HG22	1:A:235:ILE:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:484:THR:HB	1:A:496:VAL:CG2	2.44	0.47
1:A:711:LYS:HG3	1:A:729:ALA:HB1	1.97	0.47
1:A:809:ASN:HD21	1:A:915:LEU:HD23	1.79	0.47
1:A:41:LEU:HD21	1:A:228:VAL:HA	1.97	0.47
1:A:341:THR:HB	1:A:715:ILE:HD11	1.95	0.47
1:A:417:CYS:HB3	1:A:445:LEU:HB3	1.95	0.47
1:A:908:MET:HG3	1:A:940:MET:CE	2.44	0.47
1:A:962:ASP:O	1:A:963:LEU:HB2	2.15	0.47
1:A:195:PRO:O	1:A:197:PRO:HD3	2.15	0.47
1:A:271:VAL:O	1:A:275:ASN:ND2	2.48	0.47
1:A:425:LEU:HD11	1:A:447:THR:HG22	1.97	0.47
1:A:572:ARG:HE	1:A:572:ARG:C	2.21	0.47
1:A:575:MET:HE3	1:A:586:TYR:CG	2.49	0.47
1:A:750:ARG:NH1	1:A:816:MET:HE3	2.29	0.47
1:A:912:LEU:O	1:A:921:LEU:HD11	2.14	0.47
1:A:990:TYR:C	1:A:992:GLU:H	2.22	0.47
1:A:606:VAL:O	1:A:610:ILE:HG12	2.14	0.47
1:A:771:VAL:C	1:A:773:CYS:N	2.70	0.47
1:A:11:GLU:OE1	1:A:11:GLU:N	2.43	0.47
1:A:236:ARG:NH2	1:A:237:ASP:HA	2.27	0.47
1:A:345:THR:O	1:A:618:ILE:CD1	2.63	0.47
1:A:505:ALA:O	1:A:506:ALA:HB3	2.15	0.47
1:A:282:PRO:HG2	1:A:283:VAL:HG23	1.97	0.47
1:A:621:ILE:HD12	1:A:690:LEU:HD21	1.96	0.47
1:A:64:ILE:HG21	1:A:307:ILE:HD13	1.96	0.46
1:A:193:PRO:HA	1:A:206:ASN:ND2	2.30	0.46
1:A:396:LEU:HD23	1:A:401:PRO:HA	1.96	0.46
1:A:949:VAL:O	1:A:949:VAL:HG12	2.14	0.46
1:A:24:LEU:HD22	1:A:149:ASP:CB	2.40	0.46
1:A:236:ARG:NH2	1:A:237:ASP:HB3	2.31	0.46
1:A:334:ARG:CB	1:A:334:ARG:NH1	2.68	0.46
1:A:266:LEU:O	1:A:269:VAL:HG12	2.15	0.46
1:A:603:ARG:HG2	1:A:603:ARG:NH1	2.30	0.46
1:A:796:LEU:HD13	1:A:796:LEU:C	2.40	0.46
1:A:883:GLU:OE1	1:A:883:GLU:HA	2.15	0.46
1:A:196:ASP:C	1:A:198:ARG:NH2	2.73	0.46
1:A:602:PRO:HB3	1:A:638:ILE:CD1	2.31	0.46
1:A:666:ARG:NH1	1:A:693:PHE:CZ	2.83	0.46
1:A:315:ILE:CG1	1:A:316:THR:N	2.78	0.46
1:A:339:VAL:N	6:A:1023:HOH:O	2.48	0.46
1:A:806:LEU:O	1:A:809:ASN:HB2	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:862:PRO:HG3	1:A:889:VAL:CG2	2.41	0.46
1:A:198:ARG:NE	1:A:198:ARG:CA	2.79	0.46
1:A:867:SER:O	1:A:868:GLN:HG3	2.15	0.46
1:A:918:ASN:ND2	1:A:987:ALA:HB3	2.29	0.46
1:A:51:GLU:O	1:A:52:LEU:C	2.58	0.46
1:A:83:GLU:C	1:A:85:VAL:H	2.24	0.46
1:A:303:ALA:O	1:A:306:ALA:N	2.43	0.46
1:A:2:GLU:HG2	1:A:16:PHE:CE1	2.51	0.45
1:A:18:VAL:HG21	1:A:24:LEU:HD11	1.98	0.45
1:A:276:ILE:C	1:A:278:HIS:H	2.24	0.45
1:A:502:LYS:N	1:A:502:LYS:HD2	2.31	0.45
1:A:769:GLY:CA	1:A:840:GLY:O	2.64	0.45
1:A:822:THR:HG23	1:A:823:PRO:HD2	1.98	0.45
1:A:122:TYR:O	1:A:123:GLU:CB	2.64	0.45
1:A:236:ARG:CZ	1:A:237:ASP:HB3	2.47	0.45
1:A:559:ARG:HH22	5:A:1001:ACP:PB	2.39	0.45
1:A:758:GLN:NE2	1:A:917:GLU:N	2.65	0.45
1:A:6:SER:O	1:A:193:PRO:HB2	2.16	0.45
1:A:670:ARG:HD2	1:A:693:PHE:CD1	2.51	0.45
1:A:866:TYR:O	1:A:866:TYR:CD1	2.69	0.45
5:A:1001:ACP:H3'	5:A:1001:ACP:O2B	2.16	0.45
1:A:94:ILE:HG23	1:A:304:VAL:HG11	1.98	0.45
1:A:209:PHE:CD1	1:A:231:GLU:HG3	2.52	0.45
1:A:344:CYS:O	1:A:696:ILE:HB	2.17	0.45
1:A:920:SER:CB	1:A:922:VAL:HG12	2.46	0.45
1:A:76:ALA:HB1	1:A:88:PHE:CD2	2.52	0.45
1:A:276:ILE:C	1:A:278:HIS:N	2.74	0.45
1:A:809:ASN:HD22	1:A:809:ASN:HA	1.54	0.45
1:A:52:LEU:O	1:A:55:GLU:HG2	2.17	0.45
1:A:120:LYS:C	1:A:122:TYR:N	2.73	0.45
1:A:865:THR:O	1:A:866:TYR:C	2.60	0.45
1:A:1:MET:HG2	1:A:225:THR:CA	2.46	0.45
1:A:145:ILE:HD12	1:A:145:ILE:C	2.41	0.45
1:A:798:THR:CB	1:A:907:GLU:OE2	2.64	0.45
1:A:161:ALA:O	1:A:163:ILE:HG13	2.17	0.45
1:A:241:ALA:HB1	1:A:243:GLU:CD	2.42	0.45
1:A:331:ALA:HB2	1:A:741:THR:HG21	1.98	0.45
1:A:824:LYS:O	1:A:825:GLU:C	2.60	0.45
1:A:863:HIS:O	1:A:864:VAL:C	2.59	0.45
1:A:174:ARG:NE	1:A:186:SER:CB	2.79	0.45
1:A:839:ILE:O	1:A:843:VAL:HG12	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:32:HIS:HD2	1:A:147:PRO:O	2.00	0.45
1:A:177:GLN:O	1:A:178:SER:C	2.59	0.45
1:A:819:PRO:HA	1:A:820:PRO:HD3	1.86	0.45
1:A:361:MET:HE1	1:A:441:THR:OG1	2.16	0.44
1:A:843:VAL:HA	1:A:906:ILE:CD1	2.45	0.44
1:A:86:THR:CG2	1:A:789:VAL:HG21	2.46	0.44
1:A:177:GLN:NE2	1:A:189:LYS:HZ3	2.16	0.44
1:A:679:GLU:N	1:A:682:HIS:ND1	2.61	0.44
1:A:16:PHE:CD1	1:A:222:ILE:HD11	2.52	0.44
1:A:860:ASP:O	1:A:861:GLY:O	2.35	0.44
1:A:972:ILE:C	1:A:975:PRO:HD2	2.42	0.44
1:A:980:ASP:OD2	1:A:984:LYS:HE3	2.17	0.44
1:A:457:THR:HG22	1:A:459:VAL:HG13	1.98	0.44
1:A:863:HIS:C	1:A:865:THR:N	2.75	0.44
1:A:78:PHE:O	1:A:79:GLU:C	2.61	0.44
1:A:181:THR:HB	1:A:202:GLN:HG3	2.00	0.44
1:A:263:VAL:O	1:A:267:ILE:HG12	2.17	0.44
1:A:389:TYR:HB3	1:A:425:LEU:HD21	1.99	0.44
1:A:718:ALA:HB2	1:A:730:SER:HB2	1.98	0.44
1:A:864:VAL:HG12	1:A:869:LEU:CD1	2.48	0.44
1:A:991:LEU:O	1:A:992:GLU:HB3	2.18	0.44
1:A:488:SER:OG	1:A:491:ARG:NH1	2.50	0.44
1:A:669:CYS:HB3	1:A:690:LEU:HD11	1.98	0.44
1:A:866:TYR:O	1:A:867:SER:HB3	2.17	0.44
1:A:162:ASP:OD2	1:A:230:THR:CA	2.61	0.44
1:A:196:ASP:CB	1:A:198:ARG:NH2	2.73	0.44
1:A:813:LEU:C	1:A:813:LEU:HD23	2.42	0.44
1:A:952:LEU:HA	1:A:955:ILE:HD12	2.00	0.44
1:A:507:VAL:O	1:A:509:ASN:N	2.51	0.44
1:A:92:PHE:O	1:A:96:LEU:HB2	2.18	0.44
1:A:478:LEU:O	1:A:478:LEU:HD13	2.17	0.44
1:A:617:GLY:HA3	1:A:820:PRO:HD3	2.00	0.43
1:A:891:GLU:HG2	1:A:891:GLU:O	2.17	0.43
1:A:20:GLU:OE2	1:A:167:THR:HG21	2.17	0.43
1:A:864:VAL:O	1:A:865:THR:C	2.61	0.43
1:A:341:THR:CB	1:A:715:ILE:HD11	2.48	0.43
1:A:39:ASN:HB2	1:A:226:THR:CB	2.47	0.43
1:A:194:VAL:HG23	1:A:194:VAL:O	2.18	0.43
1:A:315:ILE:HG22	1:A:756:MET:SD	2.59	0.43
1:A:511:MET:HE2	1:A:570:PRO:HD2	2.00	0.43
1:A:580:SER:O	1:A:582:LYS:N	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:769:GLY:O	1:A:844:GLY:HA2	2.19	0.43
1:A:874:LYS:NZ	1:A:874:LYS:CB	2.81	0.43
1:A:919:GLN:HA	1:A:988:ARG:HD3	2.01	0.43
1:A:90:GLU:N	1:A:91:PRO:HD2	2.33	0.43
1:A:42:PRO:O	1:A:43:ALA:C	2.62	0.43
1:A:58:GLU:HA	1:A:63:ARG:NE	2.33	0.43
1:A:119:LEU:HD12	1:A:332:ILE:HD11	2.01	0.43
1:A:269:VAL:CG1	1:A:270:ALA:N	2.81	0.43
1:A:288:TRP:H	1:A:288:TRP:HE3	1.57	0.43
1:A:306:ALA:O	1:A:308:PRO:HD3	2.18	0.43
1:A:761:ARG:HA	1:A:836:TYR:CE1	2.53	0.43
1:A:866:TYR:O	1:A:866:TYR:CG	2.72	0.43
1:A:354:GLY:HA2	1:A:359:ASN:HB2	1.99	0.43
1:A:528:ARG:HH22	1:A:567:ASP:CG	2.26	0.43
1:A:743:VAL:CA	1:A:746:VAL:HG12	2.49	0.43
1:A:303:ALA:C	1:A:305:ALA:N	2.76	0.43
1:A:460:ARG:HG3	1:A:460:ARG:HH11	1.83	0.43
1:A:335:SER:C	1:A:337:PRO:HD2	2.42	0.43
1:A:204:LYS:C	1:A:206:ASN:H	2.27	0.43
1:A:239:MET:C	1:A:241:ALA:H	2.27	0.43
1:A:339:VAL:HG12	1:A:749:GLY:CA	2.49	0.43
1:A:661:PRO:O	1:A:662:LEU:C	2.62	0.43
1:A:90:GLU:O	1:A:94:ILE:HG13	2.19	0.42
1:A:200:VAL:O	1:A:201:ASN:C	2.62	0.42
1:A:760:ILE:O	1:A:764:ILE:HG12	2.19	0.42
1:A:842:TYR:OH	1:A:975:PRO:HB2	2.19	0.42
1:A:166:LEU:CD2	1:A:222:ILE:HG22	2.47	0.42
1:A:559:ARG:NH2	5:A:1001:ACP:PB	2.92	0.42
1:A:795:ASN:C	1:A:797:VAL:H	2.28	0.42
1:A:957:LYS:HA	1:A:957:LYS:HZ2	1.84	0.42
1:A:275:ASN:C	1:A:277:GLY:N	2.78	0.42
1:A:284:HIS:ND1	1:A:291:GLY:HA2	2.34	0.42
1:A:321:LEU:CG	1:A:325:ARG:HH21	2.30	0.42
1:A:441:THR:OG1	1:A:559:ARG:NH1	2.52	0.42
1:A:797:VAL:O	1:A:797:VAL:CG1	2.68	0.42
1:A:256:PHE:O	1:A:260:LEU:HD22	2.19	0.42
1:A:276:ILE:HA	1:A:279:PHE:CD2	2.53	0.42
1:A:304:VAL:O	1:A:304:VAL:HG12	2.20	0.42
1:A:691:GLN:HE21	1:A:714:GLU:CD	2.26	0.42
1:A:719:MET:HE3	1:A:737:ASP:OD2	2.20	0.42
1:A:894:GLN:N	1:A:895:PRO:CD	2.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:908:MET:CE	1:A:939:SER:HB2	2.49	0.42
1:A:307:ILE:O	1:A:309:GLU:N	2.52	0.42
1:A:352:LYS:HE2	1:A:352:LYS:HB3	1.93	0.42
1:A:371:ARG:HG3	1:A:378:LEU:HB2	2.02	0.42
1:A:601:PRO:HA	1:A:602:PRO:HD3	1.91	0.42
1:A:623:ILE:HD11	1:A:686:ILE:HG21	2.01	0.42
1:A:676:ALA:O	1:A:677:ARG:C	2.63	0.42
1:A:783:PRO:O	1:A:784:GLU:C	2.63	0.42
1:A:788:PRO:O	1:A:789:VAL:C	2.62	0.42
1:A:206:ASN:OD1	1:A:207:MET:HG2	2.18	0.42
1:A:271:VAL:HA	1:A:274:ILE:HD11	2.02	0.42
1:A:842:TYR:CD1	1:A:842:TYR:C	2.97	0.42
1:A:854:TRP:CZ2	1:A:894:GLN:HB2	2.54	0.42
1:A:864:VAL:CG1	1:A:869:LEU:HG	2.50	0.42
1:A:991:LEU:HD23	1:A:991:LEU:C	2.44	0.42
1:A:59:ASP:OD2	1:A:312:PRO:HG3	2.20	0.42
1:A:892:ALA:C	1:A:895:PRO:HD2	2.45	0.42
1:A:198:ARG:HE	1:A:198:ARG:CA	2.32	0.42
1:A:230:THR:HB	1:A:232:ILE:CG2	2.49	0.42
1:A:511:MET:CE	1:A:570:PRO:HD2	2.49	0.42
1:A:246:LYS:CG	1:A:251:GLN:HG2	2.46	0.42
1:A:309:GLU:CD	1:A:309:GLU:H	2.28	0.42
1:A:500:PRO:HG2	1:A:503:SER:HA	2.01	0.42
1:A:538:GLY:O	1:A:542:GLU:HG3	2.20	0.42
1:A:874:LYS:NZ	1:A:882:PHE:CD2	2.87	0.42
1:A:968:MET:HE2	6:A:1013:HOH:O	2.20	0.42
1:A:837:MET:O	1:A:841:GLY:N	2.44	0.42
1:A:856:LEU:HG	1:A:864:VAL:HG23	2.01	0.42
1:A:897:THR:HG23	1:A:947:LEU:HD11	2.02	0.42
1:A:147:PRO:HA	1:A:223:VAL:CG1	2.50	0.41
1:A:231:GLU:O	1:A:235:ILE:HD12	2.20	0.41
1:A:164:ARG:HG3	1:A:164:ARG:NH1	2.36	0.41
1:A:768:VAL:HG21	1:A:837:MET:CE	2.49	0.41
1:A:105:GLY:O	1:A:109:GLU:HB2	2.20	0.41
1:A:166:LEU:CG	1:A:222:ILE:HG22	2.51	0.41
1:A:485:LEU:O	1:A:486:GLU:C	2.63	0.41
1:A:809:ASN:HD22	1:A:929:ASN:ND2	2.16	0.41
1:A:843:VAL:HG23	1:A:906:ILE:HD13	2.02	0.41
1:A:870:THR:HG22	1:A:871:HIS:CE1	2.55	0.41
1:A:949:VAL:O	1:A:951:PRO:CD	2.68	0.41
1:A:58:GLU:HA	1:A:63:ARG:CZ	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:LEU:HD22	1:A:119:LEU:HA	1.94	0.41
1:A:174:ARG:NE	1:A:186:SER:HB2	2.35	0.41
1:A:191:THR:HG23	1:A:192:GLU:OE2	2.19	0.41
1:A:837:MET:HA	1:A:837:MET:CE	2.38	0.41
1:A:184:SER:C	1:A:185:VAL:CG2	2.94	0.41
1:A:920:SER:C	1:A:922:VAL:N	2.78	0.41
1:A:83:GLU:O	1:A:84:THR:HB	2.20	0.41
1:A:231:GLU:H	1:A:231:GLU:HG2	1.64	0.41
1:A:269:VAL:HG13	1:A:270:ALA:N	2.34	0.41
1:A:919:GLN:CA	1:A:919:GLN:HE21	2.34	0.41
1:A:51:GLU:C	1:A:53:VAL:N	2.75	0.41
1:A:147:PRO:HA	1:A:223:VAL:HG12	2.01	0.41
1:A:242:THR:O	1:A:242:THR:HG22	2.20	0.41
1:A:336:LEU:N	1:A:337:PRO:CD	2.83	0.41
1:A:622:MET:HE1	1:A:634:ILE:HG22	2.03	0.41
1:A:168:ILE:HG22	1:A:170:SER:O	2.21	0.41
1:A:623:ILE:CG2	1:A:683:LYS:HG2	2.47	0.41
1:A:63:ARG:HD3	1:A:66:LEU:HD12	2.03	0.41
1:A:155:VAL:CG1	1:A:216:ALA:HA	2.43	0.41
1:A:198:ARG:CD	1:A:198:ARG:H	2.33	0.41
1:A:282:PRO:CG	1:A:283:VAL:H	2.29	0.41
1:A:303:ALA:C	1:A:305:ALA:H	2.29	0.41
1:A:636:ARG:HG2	1:A:636:ARG:HH11	1.85	0.41
1:A:801:LEU:HD22	1:A:801:LEU:HA	1.77	0.41
1:A:154:ALA:O	1:A:155:VAL:C	2.64	0.41
1:A:162:ASP:OD2	1:A:230:THR:HG22	2.20	0.41
1:A:480:LYS:HD3	1:A:482:GLU:OE2	2.20	0.41
1:A:209:PHE:CD2	1:A:209:PHE:N	2.89	0.40
1:A:371:ARG:CD	1:A:378:LEU:HD23	2.51	0.40
1:A:517:PRO:HB3	1:A:548:ILE:HD13	2.02	0.40
1:A:76:ALA:HA	1:A:87:ALA:HB1	2.04	0.40
1:A:197:PRO:C	1:A:199:ALA:H	2.28	0.40
1:A:782:LEU:N	1:A:782:LEU:HD22	2.35	0.40
1:A:980:ASP:C	1:A:982:ILE:N	2.78	0.40
1:A:246:LYS:HE3	1:A:251:GLN:HG2	2.03	0.40
1:A:370:ASP:HB3	1:A:378:LEU:O	2.21	0.40
1:A:803:ALA:HA	1:A:806:LEU:HD13	2.02	0.40
1:A:930:ILE:HD12	1:A:930:ILE:HA	1.90	0.40
1:A:34:GLU:OE1	1:A:34:GLU:HA	2.22	0.40
1:A:136:SER:O	1:A:137:VAL:C	2.64	0.40
1:A:177:GLN:NE2	1:A:189:LYS:HZ1	2.19	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:276:ILE:HA	1:A:279:PHE:CD1	2.57	0.40
1:A:314:VAL:HG13	1:A:315:ILE:N	2.35	0.40
1:A:412:GLU:OE2	1:A:565:THR:HG21	2.21	0.40
1:A:514:LYS:O	5:A:1001:ACP:H2	2.22	0.40
1:A:42:PRO:C	1:A:44:GLU:H	2.29	0.40
1:A:291:GLY:O	1:A:295:TYR:HD2	2.05	0.40
1:A:369:ILE:HG13	1:A:527:VAL:CG1	2.51	0.40
1:A:445:LEU:N	1:A:445:LEU:CD1	2.84	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	983/992 (99%)	792 (81%)	139 (14%)	52 (5%)	1 3

All (52) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	43	ALA
1	A	197	PRO
1	A	204	LYS
1	A	486	GLU
1	A	857	TYR
1	A	864	VAL
1	A	867	SER
1	A	887	CYS
1	A	950	ASP
1	A	54	LEU
1	A	61	LEU
1	A	183	GLU
1	A	231	GLU

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Mol	Chain	Res	Type
1	A	236	ARG
1	A	274	ILE
1	A	338	SER
1	A	503	SER
1	A	508	GLY
1	A	581	THR
1	A	776	LEU
1	A	788	PRO
1	A	812	ASP
1	A	861	GLY
1	A	865	THR
1	A	866	TYR
1	A	883	GLU
1	A	988	ARG
1	A	9	THR
1	A	123	GLU
1	A	202	GLN
1	A	796	LEU
1	A	870	THR
1	A	24	LEU
1	A	155	VAL
1	A	185	VAL
1	A	198	ARG
1	A	241	ALA
1	A	244	GLN
1	A	964	TYR
1	A	58	GLU
1	A	223	VAL
1	A	506	ALA
1	A	662	LEU
1	A	44	GLU
1	A	235	ILE
1	A	282	PRO
1	A	557	THR
1	A	680	PRO
1	A	763	LEU
1	A	308	PRO
1	A	884	GLY
1	A	304	VAL

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	833/838 (99%)	756 (91%)	77 (9%)	8 23

All (77) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	GLU
1	A	6	SER
1	A	50	TRP
1	A	60	LEU
1	A	62	VAL
1	A	74	VAL
1	A	89	VAL
1	A	108	GLN
1	A	114	ASN
1	A	116	ILE
1	A	119	LEU
1	A	137	VAL
1	A	145	ILE
1	A	167	THR
1	A	175	VAL
1	A	179	ILE
1	A	185	VAL
1	A	188	ILE
1	A	198	ARG
1	A	225	THR
1	A	231	GLU
1	A	232	ILE
1	A	236	ARG
1	A	244	GLN
1	A	249	LEU
1	A	253	LEU
1	A	258	GLU
1	A	260	LEU
1	A	271	VAL
1	A	280	ASN

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Mol	Chain	Res	Type
1	A	283	VAL
1	A	319	LEU
1	A	323	THR
1	A	336	LEU
1	A	356	LEU
1	A	375	ASP
1	A	399	ASP
1	A	433	ILE
1	A	457	THR
1	A	484	THR
1	A	496	VAL
1	A	517	PRO
1	A	521	ILE
1	A	533	ARG
1	A	553	THR
1	A	572	ARG
1	A	638	ILE
1	A	650	ARG
1	A	662	LEU
1	A	728	THR
1	A	758	GLN
1	A	760	ILE
1	A	763	LEU
1	A	788	PRO
1	A	789	VAL
1	A	796	LEU
1	A	801	LEU
1	A	809	ASN
1	A	812	ASP
1	A	824	LYS
1	A	859	GLU
1	A	860	ASP
1	A	868	GLN
1	A	870	THR
1	A	873	MET
1	A	874	LYS
1	A	886	ASP
1	A	903	LEU
1	A	942	LEU
1	A	946	ILE
1	A	952	LEU
1	A	957	LYS

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Mol	Chain	Res	Type
1	A	959	GLN
1	A	962	ASP
1	A	974	LEU
1	A	986	VAL
1	A	992	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (27) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	38	HIS
1	A	56	GLN
1	A	108	GLN
1	A	177	GLN
1	A	201	ASN
1	A	213	ASN
1	A	244	GLN
1	A	275	ASN
1	A	280	ASN
1	A	360	GLN
1	A	398	ASN
1	A	456	ASN
1	A	472	ASN
1	A	611	GLN
1	A	627	ASN
1	A	665	GLN
1	A	691	GLN
1	A	754	ASN
1	A	758	GLN
1	A	767	ASN
1	A	795	ASN
1	A	809	ASN
1	A	868	GLN
1	A	894	GLN
1	A	910	ASN
1	A	913	ASN
1	A	918	ASN

5.3.3 RNA ⓘ

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	ACP	A	1001	3	31,33,33	1.77	8 (25%)	47,52,52	1.92	13 (27%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ACP	A	1001	3	-	0/19/38/38	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	1001	ACP	PG-O1G	5.48	1.61	1.50
5	A	1001	ACP	PB-O2B	-3.24	1.48	1.56
5	A	1001	ACP	C5-N7	-3.13	1.33	1.39
5	A	1001	ACP	PG-O2G	-2.90	1.48	1.55
5	A	1001	ACP	PG-O3G	2.83	1.61	1.55
5	A	1001	ACP	PB-O3A	2.67	1.61	1.58
5	A	1001	ACP	C8-N9	-2.38	1.33	1.37
5	A	1001	ACP	C4-N9	-2.03	1.33	1.37

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1001	ACP	C5-C4-N3	-5.37	119.32	126.72
5	A	1001	ACP	N3-C2-N1	-4.53	121.73	128.58
5	A	1001	ACP	N3-C4-N9	3.80	133.64	127.17
5	A	1001	ACP	C2-N3-C4	3.61	120.64	111.83
5	A	1001	ACP	PB-O3A-PA	-3.60	120.62	132.37
5	A	1001	ACP	O3G-PG-O1G	-3.04	104.52	112.39
5	A	1001	ACP	N9-C8-N7	-3.04	109.63	113.94
5	A	1001	ACP	C5-N7-C8	2.80	107.86	103.45
5	A	1001	ACP	O2G-PG-C3B	2.80	113.20	106.40
5	A	1001	ACP	C4-C5-N7	-2.79	107.39	110.58
5	A	1001	ACP	C2'-C3'-C4'	-2.69	97.42	102.61
5	A	1001	ACP	O2B-PB-O1B	2.43	117.87	109.95
5	A	1001	ACP	C4-N9-C8	2.23	108.08	105.74

There are no chirality outliers.

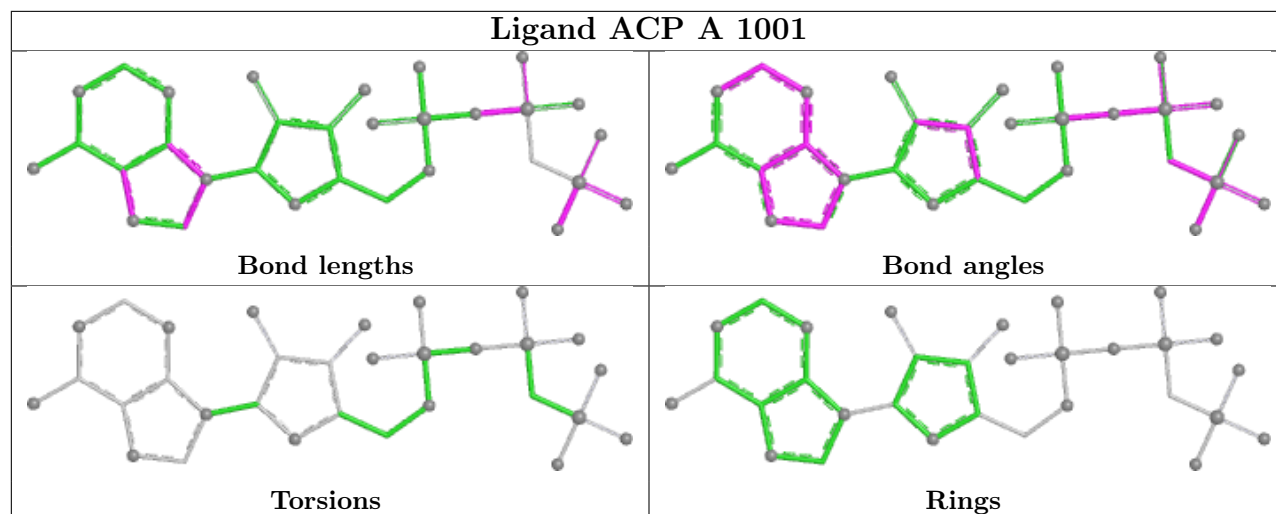
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1001	ACP	7	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	987/992 (99%)	-0.02	27 (2%) 56 48	33, 75, 131, 179	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	872	PHE	4.5
1	A	869	LEU	3.9
1	A	507	VAL	3.8
1	A	886	ASP	3.6
1	A	784	GLU	3.5
1	A	868	GLN	3.4
1	A	1	MET	3.2
1	A	875	CYS	3.2
1	A	85	VAL	3.1
1	A	508	GLY	3.1
1	A	43	ALA	2.9
1	A	336	LEU	2.8
1	A	296	PHE	2.8
1	A	50	TRP	2.7
1	A	890	PHE	2.6
1	A	781	GLY	2.6
1	A	959	GLN	2.5
1	A	44	GLU	2.4
1	A	84	THR	2.3
1	A	235	ILE	2.3
1	A	376	LEU	2.2
1	A	5	HIS	2.2
1	A	916	SER	2.2
1	A	964	TYR	2.2
1	A	217	GLY	2.1
1	A	663	ALA	2.1
1	A	882	PHE	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](#)

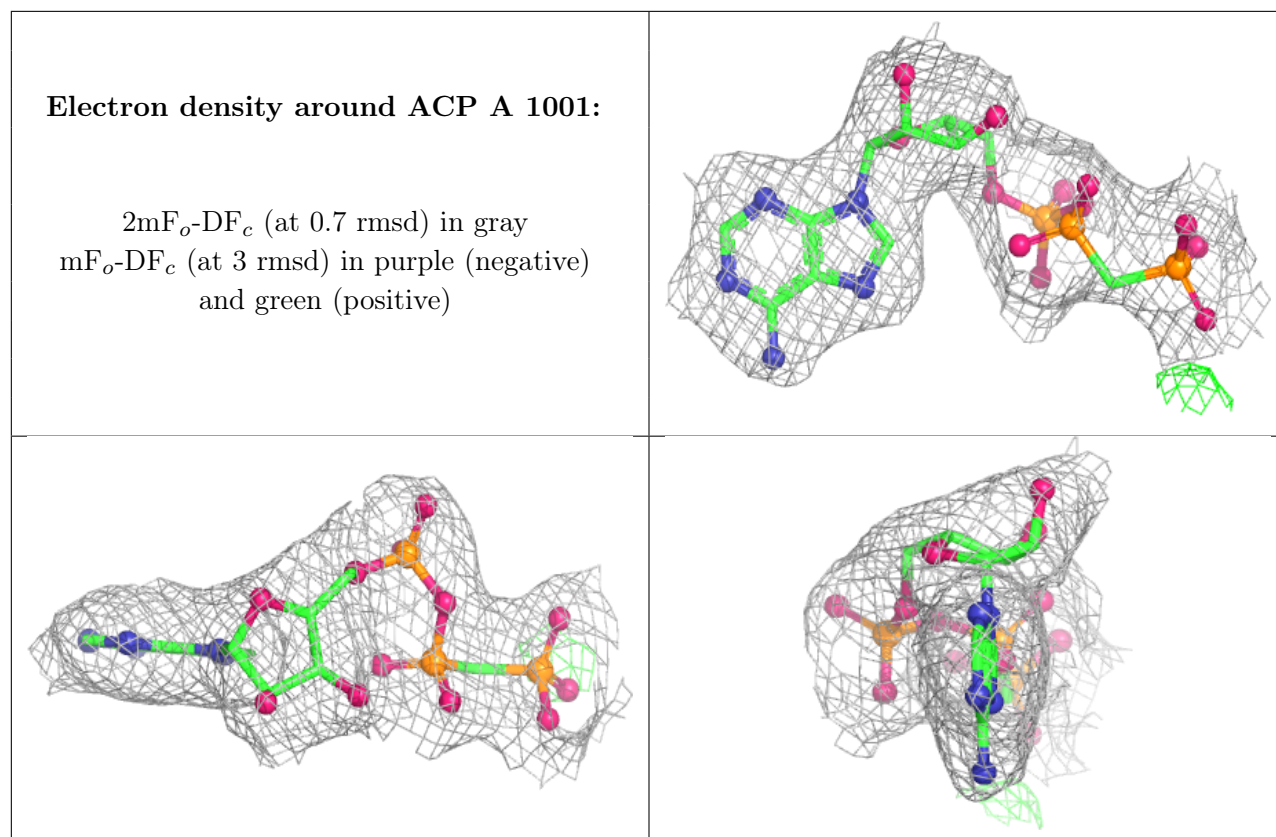
There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
2	CA	A	1004	1/1	0.85	0.09	70,70,70,70	0
3	MG	A	1005	1/1	0.96	0.10	41,41,41,41	0
4	K	A	1006	1/1	0.97	0.10	80,80,80,80	0
2	CA	A	1003	1/1	0.98	0.08	61,61,61,61	0
5	ACP	A	1001	31/31	0.99	0.04	21,42,61,73	0

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



6.5 Other polymers [i](#)

There are no such residues in this entry.