Full wwPDB X-ray Structure Validation Report (i)

Aug 28, 2023 – 01:36 PM EDT

PDB ID	:	3JUX
Title	:	Structure of the translocation ATPase SecA from Thermotoga maritima
Authors	:	Zimmer, J.
Deposited on	:	2009-09-15
Resolution	:	3.10 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 (i) 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 (i)) were used in the production of this report:

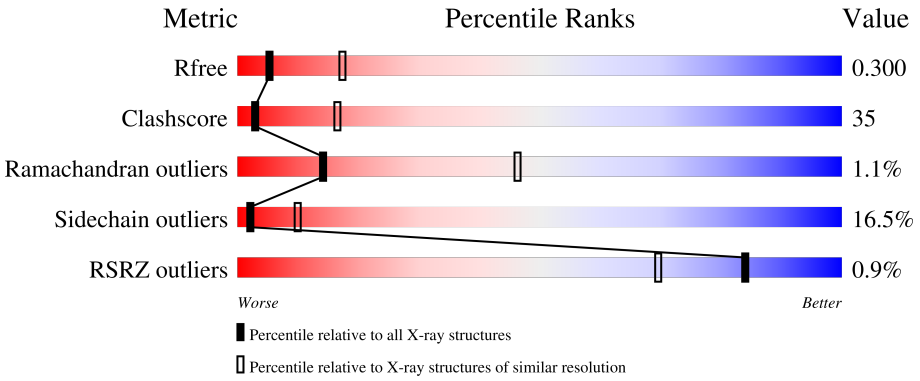
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1094 (3.10-3.10)
Clashscore	141614	1184 (3.10-3.10)
Ramachandran outliers	138981	1141 (3.10-3.10)
Sidechain outliers	138945	1141 (3.10-3.10)
RSRZ outliers	127900	1067 (3.10-3.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	822	% 53% 36% 9% ..

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6619 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 Protein translocase subunit secA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	813	Total	C	N	O	S	0	0	0
			6589	4198	1128	1236	27			

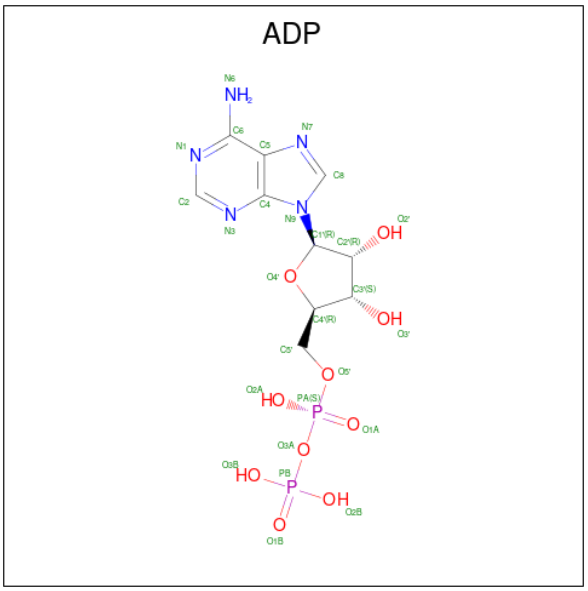
There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	817	HIS	-	expression tag	UNP Q9X1R4
A	818	HIS	-	expression tag	UNP Q9X1R4
A	819	HIS	-	expression tag	UNP Q9X1R4
A	820	HIS	-	expression tag	UNP Q9X1R4
A	821	HIS	-	expression tag	UNP Q9X1R4
A	822	HIS	-	expression tag	UNP Q9X1R4

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is water.

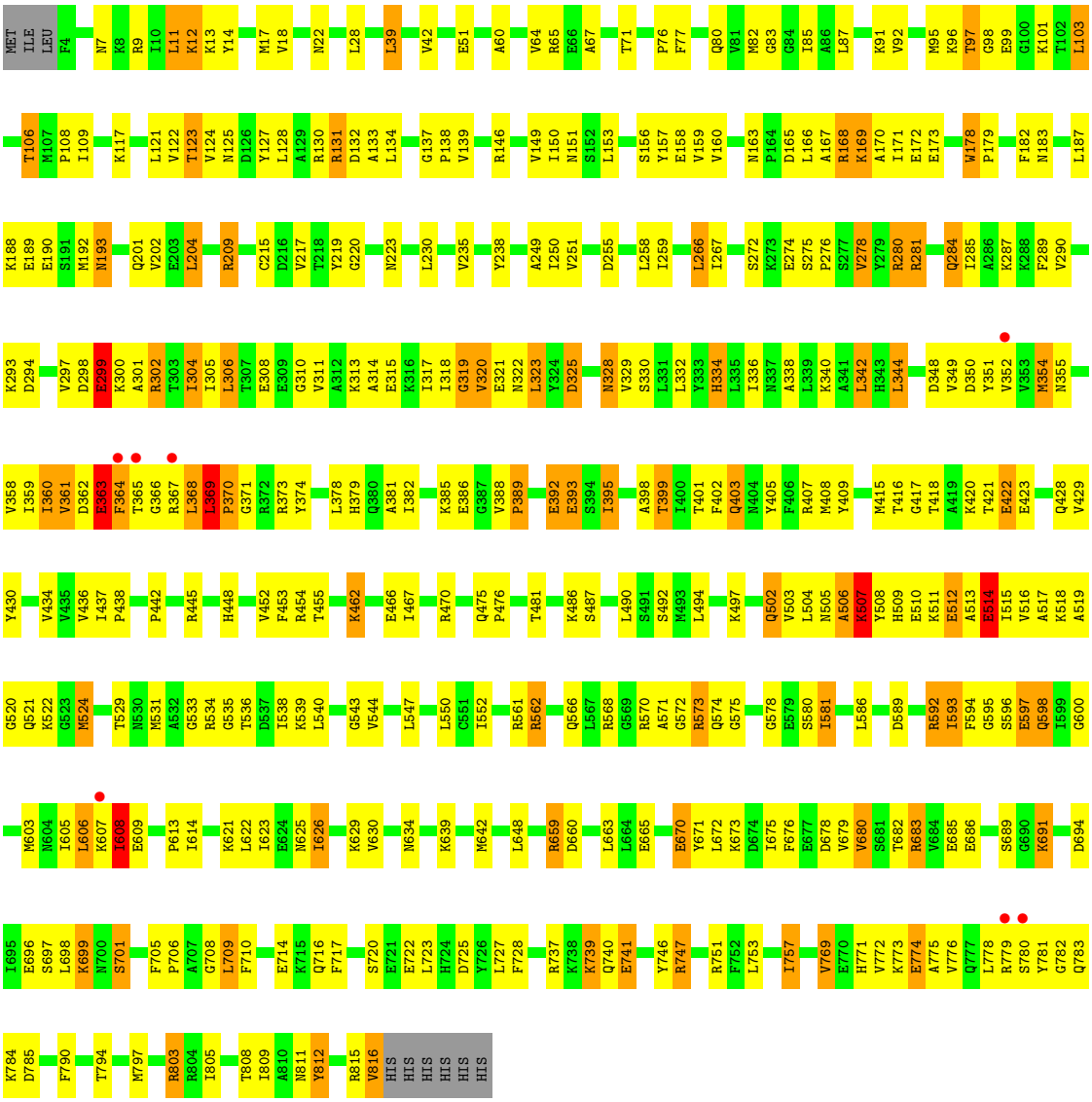
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	O	0	0
			2	2		

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: Protein translocase subunit secA

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	64.53Å 119.40Å 120.82Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.10 31.17 – 3.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (30.00-3.10) 99.2 (31.17-3.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$< I/\sigma(I) >$ [1]	1.68 (at 3.12Å)	Xtriage
Refinement program	REFMAC 5.0	Depositor
R, R_{free}	0.227 , 0.303 0.223 , 0.300	Depositor DCC
R_{free} test set	1810 reflections (10.38%)	wwPDB-VP
Wilson B-factor (Å^2)	56.2	Xtriage
Anisotropy	0.284	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.29 , 46.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.000 for -h,l,k	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6619	wwPDB-VP
Average B, all atoms (Å^2)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: ADP, MG

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	0.59	1/6706 (0.0%)	0.68	3/9016 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	514	GLU	CG-CD	-5.28	1.44	1.51

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	319	GLY	N-CA-C	-5.18	100.15	113.10
1	A	507	LYS	N-CA-C	-5.13	97.15	111.00
1	A	506	ALA	N-CA-C	5.11	124.80	111.00

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	6589	0	6655	462	0
2	A	1	0	0	0	0
3	A	27	0	12	2	0
4	A	2	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	6619	0	6667	462	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 35.

All (462) 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:369:LEU:C	1:A:371:GLY:HA3	1.34	1.41
1:A:368:LEU:C	1:A:370:PRO:HD3	1.40	1.38
1:A:708:GLY:C	1:A:709:LEU:HD23	1.45	1.36
1:A:515:ILE:HG21	1:A:536:THR:CG2	1.57	1.34
1:A:314:ALA:HA	1:A:317:ILE:CG2	1.68	1.24
1:A:17:MET:HE1	1:A:85:ILE:HG21	1.22	1.19
1:A:512:GLU:CG	1:A:536:THR:HB	1.73	1.17
1:A:157:TYR:CB	1:A:204:LEU:HD12	1.77	1.15
1:A:314:ALA:HA	1:A:317:ILE:HG21	1.27	1.13
1:A:95:MET:O	1:A:101:LYS:HE2	1.47	1.11
1:A:157:TYR:HB3	1:A:204:LEU:HD12	1.17	1.10
1:A:368:LEU:C	1:A:368:LEU:HD13	1.54	1.09
1:A:373:ARG:HA	1:A:379:HIS:CD2	1.88	1.07
1:A:512:GLU:HG2	1:A:536:THR:HB	1.35	1.07
1:A:709:LEU:HD23	1:A:709:LEU:N	1.52	1.07
1:A:515:ILE:HG21	1:A:536:THR:HG21	1.15	1.06
1:A:299:GLU:C	1:A:301:ALA:HA	1.76	1.05
1:A:300:LYS:N	1:A:301:ALA:HA	1.69	1.05
1:A:301:ALA:HB1	1:A:302:ARG:CB	1.85	1.05
1:A:368:LEU:HD13	1:A:368:LEU:O	1.56	1.04
1:A:368:LEU:O	1:A:368:LEU:HD22	1.55	1.04
1:A:362:ASP:HB3	1:A:369:LEU:HD21	1.40	1.03
1:A:361:VAL:HB	1:A:362:ASP:HA	1.38	1.02
1:A:364:PHE:C	1:A:366:GLY:HA2	1.80	1.02
1:A:470:ARG:HH11	1:A:475:GLN:HE22	1.04	1.02
1:A:365:THR:N	1:A:366:GLY:HA2	1.74	1.02
1:A:360:ILE:CG1	1:A:361:VAL:HG23	1.88	1.01
1:A:373:ARG:CA	1:A:379:HIS:HD2	1.72	1.01
1:A:359:ILE:HG21	1:A:370:PRO:HG3	1.02	1.01
1:A:301:ALA:HB1	1:A:302:ARG:HB3	1.05	1.01
1:A:368:LEU:C	1:A:370:PRO:CD	2.29	1.00
1:A:515:ILE:CG2	1:A:536:THR:HG21	1.91	1.00
1:A:373:ARG:HA	1:A:379:HIS:HD2	1.20	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:314:ALA:C	1:A:317:ILE:HG22	1.82	0.99
1:A:369:LEU:C	1:A:371:GLY:CA	2.30	0.99
1:A:360:ILE:HG12	1:A:361:VAL:HG23	1.01	0.99
1:A:515:ILE:CG2	1:A:536:THR:CG2	2.41	0.98
1:A:708:GLY:O	1:A:709:LEU:HD23	1.62	0.98
1:A:592:ARG:HH11	1:A:592:ARG:CG	1.76	0.98
1:A:369:LEU:N	1:A:370:PRO:HD3	1.68	0.98
1:A:369:LEU:O	1:A:371:GLY:HA3	1.64	0.97
1:A:603:MET:O	1:A:608:ILE:HG22	1.64	0.97
1:A:314:ALA:CA	1:A:317:ILE:HG22	1.93	0.97
1:A:360:ILE:HG12	1:A:361:VAL:CG2	1.95	0.96
1:A:368:LEU:HD12	1:A:368:LEU:N	1.77	0.96
1:A:314:ALA:CA	1:A:317:ILE:CG2	2.43	0.95
1:A:370:PRO:N	1:A:371:GLY:HA3	1.51	0.95
1:A:351:TYR:HB3	1:A:360:ILE:HG21	1.49	0.95
1:A:803:ARG:HH11	1:A:803:ARG:HG2	1.31	0.95
1:A:517:ALA:O	1:A:521:GLN:HG2	1.66	0.95
1:A:470:ARG:NH1	1:A:475:GLN:HE22	1.64	0.95
1:A:368:LEU:C	1:A:368:LEU:CD1	2.33	0.95
1:A:370:PRO:N	1:A:371:GLY:CA	2.30	0.94
1:A:512:GLU:HG3	1:A:536:THR:HB	1.48	0.94
1:A:533:GLY:O	1:A:536:THR:HG22	1.67	0.94
1:A:299:GLU:HA	1:A:302:ARG:HA	1.50	0.94
1:A:504:LEU:O	1:A:505:ASN:ND2	2.00	0.93
1:A:314:ALA:O	1:A:317:ILE:HG22	1.69	0.93
1:A:592:ARG:HH11	1:A:592:ARG:CB	1.81	0.93
1:A:368:LEU:HD12	1:A:368:LEU:H	1.29	0.92
1:A:159:VAL:HG13	1:A:202:VAL:HG11	1.50	0.92
1:A:515:ILE:HG21	1:A:536:THR:HG23	1.47	0.92
1:A:267:ILE:HG22	1:A:399:THR:HG23	1.51	0.91
1:A:361:VAL:HG12	1:A:363:GLU:N	1.84	0.91
1:A:342:LEU:HD22	1:A:385:LYS:HB3	1.53	0.91
1:A:779:ARG:HA	1:A:781:TYR:CE2	2.04	0.91
1:A:77:PHE:H	1:A:80:GLN:HE21	1.18	0.91
1:A:359:ILE:CG2	1:A:370:PRO:HG3	1.97	0.91
1:A:342:LEU:CD2	1:A:385:LYS:HB3	2.02	0.90
1:A:608:ILE:CG1	1:A:609:GLU:HA	2.01	0.90
1:A:519:ALA:HB3	1:A:538:ILE:HG21	1.53	0.90
1:A:709:LEU:N	1:A:709:LEU:CD2	2.29	0.89
1:A:512:GLU:HG3	1:A:536:THR:CB	2.03	0.89
1:A:159:VAL:CG1	1:A:202:VAL:HG11	2.02	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ARG:O	1:A:172:GLU:HB2	1.74	0.88
1:A:157:TYR:CB	1:A:204:LEU:CD1	2.52	0.87
1:A:314:ALA:HA	1:A:317:ILE:HG22	1.54	0.87
1:A:512:GLU:CG	1:A:536:THR:CB	2.52	0.87
1:A:361:VAL:CB	1:A:362:ASP:HA	2.05	0.87
1:A:362:ASP:HB3	1:A:369:LEU:CD2	2.05	0.87
1:A:373:ARG:HB3	1:A:379:HIS:CD2	2.09	0.87
1:A:359:ILE:HG21	1:A:370:PRO:CG	1.98	0.87
1:A:592:ARG:NH1	1:A:592:ARG:HG2	1.87	0.86
1:A:608:ILE:HG12	1:A:609:GLU:HA	1.56	0.86
1:A:705:PHE:HB3	1:A:706:PRO:HD2	1.58	0.86
1:A:17:MET:CE	1:A:85:ILE:HG21	2.03	0.86
1:A:361:VAL:HG12	1:A:362:ASP:C	1.95	0.86
1:A:603:MET:CE	1:A:614:ILE:HG22	2.05	0.86
1:A:373:ARG:CA	1:A:379:HIS:CD2	2.54	0.85
1:A:314:ALA:O	1:A:317:ILE:CG2	2.25	0.84
1:A:159:VAL:HG13	1:A:202:VAL:CG1	2.08	0.84
1:A:299:GLU:O	1:A:299:GLU:HG2	1.77	0.83
1:A:368:LEU:N	1:A:368:LEU:CD1	2.40	0.83
1:A:350:ASP:HB2	1:A:361:VAL:HG22	1.60	0.83
1:A:592:ARG:HH11	1:A:592:ARG:HG2	1.37	0.83
1:A:603:MET:HE2	1:A:614:ILE:HG22	1.61	0.83
1:A:512:GLU:HG3	1:A:536:THR:CG2	2.09	0.83
1:A:603:MET:O	1:A:608:ILE:CG2	2.27	0.82
1:A:683:ARG:CD	1:A:701:SER:OG	2.27	0.82
1:A:77:PHE:H	1:A:80:GLN:NE2	1.76	0.82
1:A:351:TYR:HB3	1:A:360:ILE:CG2	2.10	0.82
1:A:593:ILE:HG22	1:A:594:PHE:N	1.94	0.82
1:A:67:ALA:O	1:A:71:THR:HB	1.80	0.81
1:A:306:LEU:HD12	1:A:306:LEU:H	1.45	0.81
1:A:470:ARG:HH11	1:A:475:GLN:NE2	1.79	0.81
1:A:351:TYR:CB	1:A:360:ILE:HG22	2.10	0.81
1:A:95:MET:O	1:A:101:LYS:CE	2.28	0.81
1:A:17:MET:HE1	1:A:85:ILE:CG2	2.09	0.81
1:A:351:TYR:CB	1:A:360:ILE:CG2	2.58	0.80
1:A:71:THR:CG2	1:A:138:PRO:HB2	2.11	0.80
1:A:368:LEU:O	1:A:368:LEU:CD2	2.29	0.80
1:A:368:LEU:O	1:A:368:LEU:CD1	2.30	0.79
1:A:519:ALA:HB3	1:A:538:ILE:CG2	2.12	0.79
1:A:779:ARG:HA	1:A:781:TYR:HE2	1.47	0.79
1:A:373:ARG:CB	1:A:379:HIS:CD2	2.67	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:708:GLY:O	1:A:709:LEU:CD2	2.30	0.78
1:A:267:ILE:HG22	1:A:399:THR:CG2	2.13	0.78
1:A:515:ILE:CG2	1:A:536:THR:HG23	2.11	0.78
1:A:708:GLY:C	1:A:709:LEU:CD2	2.41	0.78
1:A:503:VAL:O	1:A:504:LEU:HD23	1.83	0.78
1:A:284:GLN:HA	1:A:287:LYS:HG2	1.65	0.77
1:A:676:PHE:O	1:A:680:VAL:HG22	1.85	0.76
1:A:255:ASP:OD1	1:A:416:THR:HG21	1.84	0.76
1:A:311:VAL:O	1:A:315:GLU:HG3	1.87	0.76
1:A:368:LEU:O	1:A:370:PRO:HD3	1.85	0.75
1:A:368:LEU:O	1:A:370:PRO:CD	2.33	0.75
1:A:531:MET:HA	1:A:531:MET:CE	2.17	0.75
1:A:592:ARG:HH11	1:A:592:ARG:HB3	1.50	0.74
1:A:130:ARG:HH11	1:A:151:ASN:ND2	1.85	0.74
1:A:281:ARG:NH1	1:A:285:ILE:HD11	2.01	0.74
1:A:420:LYS:HG3	1:A:436:VAL:CG2	2.16	0.74
1:A:131:ARG:HG2	1:A:131:ARG:HH11	1.52	0.74
1:A:626:ILE:O	1:A:630:VAL:HG23	1.89	0.73
1:A:595:GLY:HA2	1:A:598:GLN:NE2	2.04	0.73
1:A:803:ARG:HG2	1:A:803:ARG:NH1	1.97	0.72
1:A:157:TYR:HB2	1:A:204:LEU:CD1	2.20	0.72
1:A:320:VAL:HG21	1:A:328:ASN:ND2	2.05	0.71
1:A:351:TYR:HA	1:A:360:ILE:HG22	1.71	0.71
1:A:683:ARG:HD2	1:A:701:SER:OG	1.90	0.71
1:A:317:ILE:HG23	1:A:318:ILE:N	2.05	0.71
1:A:322:ASN:O	1:A:328:ASN:ND2	2.23	0.71
1:A:349:VAL:HA	1:A:350:ASP:OD1	1.91	0.71
1:A:506:ALA:N	1:A:511:LYS:HE3	2.06	0.71
1:A:365:THR:N	1:A:366:GLY:CA	2.53	0.71
1:A:670:GLU:HA	1:A:673:LYS:HE3	1.73	0.71
1:A:505:ASN:ND2	1:A:529:THR:OG1	2.23	0.71
1:A:757:ILE:HG12	1:A:808:THR:HG22	1.72	0.70
1:A:782:GLY:HA2	1:A:783:GLN:HB2	1.73	0.70
1:A:678:ASP:O	1:A:682:THR:HG23	1.91	0.70
1:A:683:ARG:HD3	1:A:701:SER:OG	1.91	0.70
1:A:476:PRO:HG2	1:A:550:LEU:HA	1.74	0.69
1:A:342:LEU:HD22	1:A:385:LYS:HD2	1.74	0.69
1:A:369:LEU:O	1:A:371:GLY:CA	2.36	0.69
1:A:502:GLN:HE21	1:A:502:GLN:HA	1.56	0.69
1:A:507:LYS:H	1:A:511:LYS:HE2	1.58	0.69
1:A:96:LYS:O	1:A:99:GLU:HB2	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:342:LEU:HD22	1:A:385:LYS:CB	2.22	0.68
1:A:531:MET:HA	1:A:531:MET:HE2	1.76	0.68
1:A:603:MET:HE3	1:A:614:ILE:HG22	1.76	0.68
1:A:178:TRP:HZ3	1:A:182:PHE:O	1.76	0.68
1:A:130:ARG:HH11	1:A:151:ASN:HD21	1.42	0.67
1:A:512:GLU:HG3	1:A:536:THR:HG21	1.75	0.67
1:A:322:ASN:HB3	1:A:325:ASP:HB3	1.77	0.67
1:A:368:LEU:CA	1:A:370:PRO:HD3	2.25	0.67
1:A:313:LYS:O	1:A:317:ILE:HG22	1.95	0.67
1:A:304:ILE:O	1:A:304:ILE:HG12	1.92	0.67
1:A:39:LEU:O	1:A:42:VAL:HG12	1.95	0.66
1:A:420:LYS:HG3	1:A:436:VAL:HG21	1.77	0.66
1:A:304:ILE:HG22	1:A:344:LEU:HD12	1.77	0.66
1:A:706:PRO:O	1:A:706:PRO:HG2	1.94	0.66
1:A:512:GLU:HG2	1:A:536:THR:CB	2.16	0.66
1:A:815:ARG:O	1:A:816:VAL:HG13	1.96	0.66
1:A:71:THR:HG23	1:A:138:PRO:HB2	1.78	0.65
1:A:131:ARG:HG2	1:A:131:ARG:NH1	2.07	0.65
1:A:534:ARG:HH21	1:A:566:GLN:NE2	1.94	0.65
1:A:351:TYR:CA	1:A:360:ILE:HG22	2.26	0.64
1:A:453:PHE:CE2	1:A:462:LYS:HG3	2.33	0.64
1:A:299:GLU:C	1:A:301:ALA:CA	2.62	0.64
1:A:131:ARG:HH11	1:A:131:ARG:CG	2.10	0.64
1:A:315:GLU:O	1:A:319:GLY:HA2	1.98	0.64
1:A:354:MET:O	1:A:355:ASN:HB2	1.97	0.64
1:A:543:GLY:O	1:A:547:LEU:HD12	1.99	0.63
1:A:680:VAL:HG11	1:A:727:LEU:HB3	1.80	0.63
1:A:416:THR:HG22	1:A:417:GLY:H	1.62	0.63
1:A:255:ASP:HB2	1:A:562:ARG:NH1	2.13	0.63
1:A:255:ASP:HB2	1:A:562:ARG:HH11	1.64	0.63
1:A:362:ASP:O	1:A:363:GLU:HB2	1.99	0.63
1:A:187:LEU:HD21	1:A:192:MET:HB3	1.81	0.62
1:A:361:VAL:HG12	1:A:362:ASP:CA	2.29	0.62
1:A:300:LYS:N	1:A:301:ALA:CA	2.54	0.62
1:A:342:LEU:HD21	1:A:385:LYS:HB3	1.80	0.62
1:A:124:VAL:HG22	1:A:128:LEU:HD12	1.82	0.62
1:A:169:LYS:HE3	1:A:173:GLU:OE2	2.00	0.62
1:A:351:TYR:HA	1:A:360:ILE:CG2	2.29	0.62
1:A:519:ALA:CB	1:A:538:ILE:HG21	2.26	0.62
1:A:352:VAL:HG22	1:A:359:ILE:O	1.99	0.61
1:A:315:GLU:O	1:A:319:GLY:CA	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:368:LEU:O	1:A:368:LEU:CG	2.48	0.61
1:A:22:ASN:ND2	1:A:65:ARG:HH12	1.97	0.61
1:A:373:ARG:CB	1:A:379:HIS:HD2	2.09	0.61
1:A:442:PRO:O	1:A:575:GLY:HA2	2.00	0.61
1:A:757:ILE:HG12	1:A:808:THR:CG2	2.31	0.60
1:A:361:VAL:CB	1:A:362:ASP:CA	2.79	0.60
1:A:281:ARG:HG3	1:A:281:ARG:HH11	1.66	0.60
1:A:423:GLU:HG3	1:A:434:VAL:HB	1.82	0.60
1:A:514:GLU:O	1:A:518:LYS:HG2	2.02	0.60
1:A:280:ARG:HH22	1:A:389:PRO:HA	1.66	0.60
1:A:168:ARG:HH11	1:A:168:ARG:CG	2.15	0.60
1:A:168:ARG:NH1	1:A:168:ARG:HG2	2.17	0.60
1:A:386:GLU:OE2	1:A:386:GLU:HA	2.02	0.59
1:A:486:LYS:O	1:A:490:LEU:HD23	2.02	0.59
1:A:407:ARG:NH1	1:A:429:VAL:O	2.35	0.59
1:A:170:ALA:O	1:A:173:GLU:O	2.21	0.59
1:A:776:VAL:O	1:A:780:SER:HB2	2.03	0.59
1:A:504:LEU:C	1:A:505:ASN:ND2	2.55	0.58
1:A:518:LYS:HD2	1:A:524:MET:HE2	1.85	0.58
1:A:462:LYS:HE3	1:A:462:LYS:HA	1.83	0.58
1:A:476:PRO:HB2	1:A:519:ALA:O	2.04	0.58
1:A:369:LEU:N	1:A:370:PRO:CD	2.53	0.58
1:A:281:ARG:O	1:A:285:ILE:HG13	2.03	0.58
1:A:534:ARG:HH21	1:A:566:GLN:HE22	1.52	0.58
1:A:639:LYS:HG2	1:A:642:MET:HE3	1.84	0.58
1:A:416:THR:HG22	1:A:417:GLY:N	2.19	0.58
1:A:536:THR:HG23	1:A:536:THR:O	2.01	0.58
1:A:381:ALA:O	1:A:385:LYS:HG2	2.03	0.57
1:A:622:LEU:O	1:A:626:ILE:HG23	2.04	0.57
1:A:342:LEU:HD22	1:A:385:LYS:CG	2.34	0.57
1:A:157:TYR:HB2	1:A:204:LEU:HD11	1.86	0.57
1:A:266:LEU:HD12	1:A:402:PHE:CE2	2.39	0.57
1:A:178:TRP:CZ3	1:A:182:PHE:O	2.57	0.57
1:A:534:ARG:NH2	1:A:566:GLN:HE22	2.01	0.57
1:A:445:ARG:HD3	1:A:572:GLY:H	1.70	0.57
1:A:97:THR:HA	1:A:101:LYS:NZ	2.20	0.57
1:A:351:TYR:CA	1:A:360:ILE:CG2	2.83	0.56
1:A:359:ILE:HD13	1:A:370:PRO:HB3	1.87	0.56
1:A:568:ARG:HG3	1:A:580:SER:OG	2.05	0.56
1:A:621:LYS:HE2	1:A:625:ASN:HD21	1.70	0.56
1:A:235:VAL:O	1:A:659:ARG:NH2	2.39	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:GLU:HG3	1:A:392:GLU:O	2.06	0.56
1:A:275:SER:O	1:A:278:VAL:HG13	2.06	0.55
1:A:507:LYS:N	1:A:511:LYS:HE2	2.21	0.55
1:A:109:ILE:HD11	1:A:121:LEU:HD12	1.88	0.55
1:A:360:ILE:HG12	1:A:361:VAL:N	2.20	0.55
1:A:358:VAL:HB	1:A:379:HIS:HE1	1.71	0.55
1:A:314:ALA:O	1:A:317:ILE:HG23	2.06	0.55
1:A:784:LYS:O	1:A:785:ASP:C	2.45	0.55
1:A:351:TYR:HA	1:A:360:ILE:CB	2.36	0.55
1:A:691:LYS:HE3	1:A:691:LYS:HA	1.89	0.55
1:A:466:GLU:OE1	1:A:466:GLU:HA	2.06	0.54
1:A:685:GLU:O	1:A:689:SER:OG	2.25	0.54
1:A:544:VAL:HA	1:A:547:LEU:HD12	1.90	0.54
1:A:14:TYR:HD1	1:A:17:MET:HE2	1.72	0.54
1:A:351:TYR:HB2	1:A:360:ILE:HG22	1.85	0.54
1:A:706:PRO:O	1:A:706:PRO:CG	2.51	0.54
1:A:272:SER:HB3	1:A:393:GLU:H	1.72	0.54
1:A:168:ARG:HH11	1:A:168:ARG:HG2	1.72	0.54
1:A:504:LEU:HD12	1:A:515:ILE:HD13	1.90	0.53
1:A:517:ALA:O	1:A:521:GLN:CG	2.49	0.53
1:A:189:GLU:HA	1:A:192:MET:CE	2.38	0.53
1:A:354:MET:O	1:A:355:ASN:CB	2.57	0.53
1:A:362:ASP:CB	1:A:369:LEU:HD21	2.27	0.53
1:A:520:GLY:HA3	1:A:539:LYS:O	2.08	0.53
1:A:71:THR:HG21	1:A:139:VAL:N	2.24	0.53
1:A:153:LEU:N	1:A:153:LEU:HD12	2.24	0.53
1:A:276:PRO:O	1:A:280:ARG:HG3	2.09	0.53
1:A:342:LEU:HD22	1:A:385:LYS:CD	2.37	0.53
1:A:14:TYR:HD1	1:A:17:MET:CE	2.22	0.52
1:A:167:ALA:O	1:A:171:ILE:HD12	2.09	0.52
1:A:359:ILE:C	1:A:360:ILE:CG2	2.78	0.52
1:A:360:ILE:HD13	1:A:360:ILE:O	2.09	0.52
1:A:178:TRP:NE1	1:A:187:LEU:HB2	2.23	0.52
1:A:512:GLU:O	1:A:516:VAL:HG23	2.08	0.52
1:A:361:VAL:C	1:A:367:ARG:HA	2.30	0.52
1:A:675:ILE:O	1:A:679:VAL:HG23	2.09	0.52
1:A:317:ILE:CG2	1:A:318:ILE:N	2.72	0.52
1:A:349:VAL:N	1:A:350:ASP:HA	2.24	0.52
1:A:470:ARG:HG2	1:A:475:GLN:NE2	2.25	0.52
1:A:608:ILE:HG12	1:A:609:GLU:CA	2.35	0.52
1:A:77:PHE:N	1:A:80:GLN:HE21	1.98	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:TRP:CD1	1:A:187:LEU:HD22	2.45	0.52
1:A:238:TYR:CD2	1:A:238:TYR:O	2.63	0.52
1:A:358:VAL:C	1:A:359:ILE:HG13	2.30	0.52
1:A:361:VAL:CG1	1:A:362:ASP:HA	2.40	0.51
1:A:374:TYR:H	1:A:379:HIS:CD2	2.28	0.51
1:A:665:GLU:O	1:A:751:ARG:NH2	2.43	0.51
1:A:753:LEU:HD13	1:A:812:TYR:HB3	1.91	0.51
1:A:11:LEU:HD11	1:A:438:PRO:HD3	1.93	0.51
1:A:445:ARG:HG3	1:A:578:GLY:O	2.10	0.51
1:A:80:GLN:HE22	3:A:873:ADP:N6	2.09	0.51
1:A:151:ASN:O	1:A:209:ARG:NH2	2.43	0.51
1:A:360:ILE:HD13	1:A:360:ILE:C	2.31	0.51
1:A:361:VAL:CG1	1:A:362:ASP:CA	2.89	0.50
1:A:453:PHE:CE1	1:A:613:PRO:HB3	2.45	0.50
1:A:445:ARG:HG3	1:A:578:GLY:C	2.32	0.50
1:A:503:VAL:C	1:A:504:LEU:HD23	2.32	0.50
1:A:251:VAL:HG11	1:A:258:LEU:HG	1.94	0.50
1:A:607:LYS:NZ	1:A:607:LYS:HB3	2.26	0.50
1:A:83:GLY:O	1:A:87:LEU:HG	2.12	0.50
1:A:274:GLU:HG2	1:A:334:HIS:HE1	1.76	0.50
1:A:325:ASP:OD1	1:A:325:ASP:C	2.50	0.50
1:A:71:THR:HG23	1:A:138:PRO:CB	2.42	0.49
1:A:123:THR:HG21	1:A:128:LEU:HB3	1.93	0.49
1:A:401:THR:HB	1:A:403:GLN:HE21	1.77	0.49
1:A:592:ARG:CB	1:A:592:ARG:NH1	2.64	0.49
1:A:160:VAL:O	1:A:202:VAL:HG13	2.12	0.49
1:A:274:GLU:HG2	1:A:334:HIS:CE1	2.47	0.49
1:A:359:ILE:C	1:A:360:ILE:HG22	2.33	0.49
1:A:361:VAL:O	1:A:367:ARG:HA	2.11	0.49
1:A:510:GLU:OE2	1:A:510:GLU:O	2.30	0.49
1:A:361:VAL:O	1:A:367:ARG:CA	2.60	0.49
1:A:281:ARG:HH11	1:A:285:ILE:HD11	1.73	0.49
1:A:64:VAL:CG1	1:A:106:THR:HG23	2.42	0.49
1:A:370:PRO:HA	1:A:371:GLY:C	2.32	0.49
1:A:739:LYS:HE3	1:A:746:TYR:HD2	1.78	0.49
1:A:405:TYR:O	1:A:408:MET:HG3	2.13	0.49
1:A:188:LYS:HD3	1:A:190:GLU:HB2	1.95	0.49
1:A:97:THR:HA	1:A:101:LYS:HZ2	1.76	0.48
1:A:98:GLY:O	1:A:574:GLN:NE2	2.46	0.48
1:A:188:LYS:HG2	1:A:190:GLU:HG2	1.94	0.48
1:A:280:ARG:HH22	1:A:388:VAL:HA	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:514:GLU:O	1:A:518:LYS:CG	2.61	0.48
1:A:294:ASP:O	1:A:310:GLY:HA3	2.14	0.48
1:A:298:ASP:O	1:A:300:LYS:N	2.45	0.48
1:A:60:ALA:O	1:A:64:VAL:HG23	2.14	0.48
1:A:728:PHE:CD1	1:A:728:PHE:C	2.87	0.48
1:A:403:GLN:O	1:A:407:ARG:HG3	2.13	0.47
1:A:179:PRO:HB2	1:A:182:PHE:CD2	2.49	0.47
1:A:505:ASN:H	1:A:511:LYS:HE3	1.79	0.47
1:A:603:MET:CE	1:A:614:ILE:CG2	2.87	0.47
1:A:448:HIS:HB2	1:A:581:ILE:HG23	1.97	0.47
1:A:805:ILE:O	1:A:809:ILE:HG13	2.14	0.47
1:A:361:VAL:O	1:A:367:ARG:HB3	2.15	0.47
1:A:281:ARG:HA	1:A:284:GLN:OE1	2.15	0.47
1:A:130:ARG:HH21	1:A:509:HIS:CE1	2.32	0.47
1:A:351:TYR:HA	1:A:360:ILE:HB	1.96	0.47
1:A:510:GLU:O	1:A:513:ALA:HB3	2.15	0.47
1:A:159:VAL:CG1	1:A:202:VAL:CG1	2.77	0.47
1:A:774:GLU:HG3	1:A:775:ALA:N	2.29	0.47
1:A:12:LYS:HA	1:A:12:LYS:HD3	1.55	0.46
1:A:230:LEU:HD22	1:A:398:ALA:HB1	1.97	0.46
1:A:680:VAL:CG1	1:A:727:LEU:HB3	2.44	0.46
1:A:304:ILE:CG2	1:A:344:LEU:HD12	2.45	0.46
1:A:714:GLU:N	1:A:714:GLU:OE1	2.48	0.46
1:A:691:LYS:O	1:A:691:LYS:HG3	2.16	0.46
1:A:314:ALA:C	1:A:317:ILE:CG2	2.61	0.46
1:A:76:PRO:HG3	1:A:103:LEU:HD22	1.97	0.46
1:A:360:ILE:HG21	1:A:374:TYR:OH	2.16	0.46
1:A:454:ARG:HA	1:A:586:LEU:HG	1.97	0.46
1:A:13:LYS:O	1:A:17:MET:HG3	2.16	0.46
1:A:293:LYS:HE3	1:A:293:LYS:HB2	1.60	0.46
1:A:80:GLN:HE22	3:A:873:ADP:HN61	1.63	0.46
1:A:368:LEU:O	1:A:370:PRO:HD2	2.15	0.46
1:A:772:VAL:HG21	1:A:797:MET:SD	2.55	0.46
1:A:157:TYR:HB3	1:A:204:LEU:CD1	2.11	0.45
1:A:313:LYS:O	1:A:317:ILE:CG2	2.62	0.45
1:A:358:VAL:C	1:A:359:ILE:CG1	2.84	0.45
1:A:352:VAL:O	1:A:358:VAL:HA	2.16	0.45
1:A:536:THR:CG2	1:A:536:THR:O	2.64	0.45
1:A:157:TYR:CG	1:A:204:LEU:HD12	2.47	0.45
1:A:358:VAL:HG11	1:A:382:ILE:HG21	1.97	0.45
1:A:595:GLY:HA2	1:A:598:GLN:CD	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:600:GLY:O	1:A:603:MET:HB2	2.16	0.45
1:A:95:MET:HG2	1:A:437:ILE:HB	1.99	0.45
1:A:124:VAL:HG23	1:A:125:ASN:ND2	2.32	0.45
1:A:747:ARG:N	1:A:747:ARG:HD2	2.31	0.45
1:A:259:ILE:HD13	1:A:422:GLU:HG2	1.99	0.45
1:A:452:VAL:O	1:A:603:MET:CE	2.65	0.45
1:A:365:THR:HG22	1:A:365:THR:O	2.17	0.45
1:A:589:ASP:OD2	1:A:589:ASP:N	2.46	0.45
1:A:323:LEU:CD2	1:A:332:LEU:HB2	2.47	0.44
1:A:467:ILE:HG21	1:A:494:LEU:HD11	1.98	0.44
1:A:694:ASP:OD2	1:A:697:SER:OG	2.34	0.44
1:A:518:LYS:O	1:A:524:MET:HB3	2.17	0.44
1:A:317:ILE:HG23	1:A:318:ILE:H	1.79	0.44
1:A:388:VAL:HG13	1:A:389:PRO:CG	2.47	0.44
1:A:109:ILE:HG13	1:A:250:ILE:HD12	1.99	0.44
1:A:369:LEU:HD13	1:A:369:LEU:HA	1.57	0.44
1:A:505:ASN:HD22	1:A:529:THR:HB	1.83	0.44
1:A:518:LYS:O	1:A:524:MET:HG2	2.18	0.44
1:A:131:ARG:NH1	1:A:132:ASP:OD1	2.51	0.44
1:A:369:LEU:O	1:A:371:GLY:C	2.56	0.44
1:A:717:PHE:HA	1:A:722:GLU:OE1	2.18	0.44
1:A:121:LEU:HD22	1:A:219:TYR:CD2	2.52	0.44
1:A:122:VAL:HG22	1:A:251:VAL:HA	1.99	0.44
1:A:362:ASP:O	1:A:363:GLU:CB	2.65	0.44
1:A:648:LEU:HD11	1:A:769:VAL:HG11	2.00	0.44
1:A:133:ALA:O	1:A:137:GLY:N	2.50	0.43
1:A:504:LEU:HB3	1:A:511:LYS:HD3	2.01	0.43
1:A:149:VAL:HA	1:A:219:TYR:O	2.18	0.43
1:A:603:MET:HE3	1:A:614:ILE:CG2	2.47	0.43
1:A:395:ILE:HD13	1:A:395:ILE:H	1.83	0.43
1:A:597:GLU:H	1:A:597:GLU:HG3	1.50	0.43
1:A:740:GLN:HB3	1:A:741:GLU:OE2	2.19	0.43
1:A:92:VAL:HB	1:A:434:VAL:HG22	1.99	0.43
1:A:150:ILE:HG12	1:A:220:GLY:HA3	2.00	0.43
1:A:266:LEU:HD12	1:A:402:PHE:CZ	2.54	0.43
1:A:348:ASP:C	1:A:350:ASP:HA	2.39	0.43
1:A:753:LEU:O	1:A:757:ILE:HD12	2.18	0.43
1:A:17:MET:HE3	1:A:85:ILE:HD13	1.99	0.43
1:A:223:ASN:HD22	1:A:223:ASN:H	1.66	0.43
1:A:320:VAL:HG23	1:A:321:GLU:N	2.33	0.43
1:A:593:ILE:O	1:A:594:PHE:CD2	2.71	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:299:GLU:O	1:A:299:GLU:CG	2.52	0.43
1:A:505:ASN:C	1:A:511:LYS:HE3	2.39	0.43
1:A:699:LYS:HZ2	1:A:699:LYS:C	2.22	0.43
1:A:811:ASN:OD1	1:A:815:ARG:HD2	2.18	0.43
1:A:127:TYR:CZ	1:A:131:ARG:HD3	2.53	0.43
1:A:481:THR:HG1	1:A:487:SER:HG	1.67	0.43
1:A:811:ASN:O	1:A:815:ARG:HG3	2.19	0.43
1:A:7:ASN:O	1:A:11:LEU:HB2	2.18	0.42
1:A:297:VAL:HG13	1:A:304:ILE:HG22	2.01	0.42
1:A:388:VAL:HG13	1:A:389:PRO:HB3	1.99	0.42
1:A:595:GLY:HA2	1:A:598:GLN:HE22	1.79	0.42
1:A:420:LYS:CG	1:A:436:VAL:CG2	2.91	0.42
1:A:670:GLU:O	1:A:673:LYS:HG2	2.20	0.42
1:A:705:PHE:HB3	1:A:706:PRO:CD	2.38	0.42
1:A:18:VAL:HG21	1:A:82:MET:HG2	2.01	0.42
1:A:134:LEU:HD21	1:A:204:LEU:HD22	2.00	0.42
1:A:428:GLN:HE22	1:A:639:LYS:HE2	1.85	0.42
1:A:504:LEU:CD1	1:A:515:ILE:HD13	2.49	0.42
1:A:146:ARG:O	1:A:215:CYS:HB3	2.19	0.42
1:A:388:VAL:HG13	1:A:389:PRO:CB	2.50	0.42
1:A:403:GLN:HA	1:A:430:TYR:CE2	2.55	0.42
1:A:505:ASN:ND2	1:A:529:THR:CB	2.83	0.42
1:A:249:ALA:HB2	1:A:409:TYR:CE1	2.55	0.42
1:A:290:VAL:N	1:A:294:ASP:OD2	2.49	0.42
1:A:502:GLN:HA	1:A:502:GLN:NE2	2.29	0.42
1:A:514:GLU:O	1:A:518:LYS:CB	2.67	0.42
1:A:515:ILE:HD12	1:A:515:ILE:HA	1.90	0.42
1:A:519:ALA:HB3	1:A:538:ILE:HG23	1.98	0.42
1:A:370:PRO:HA	1:A:371:GLY:O	2.20	0.41
1:A:505:ASN:HD22	1:A:529:THR:CB	2.33	0.41
1:A:374:TYR:CD1	1:A:378:LEU:HD23	2.55	0.41
1:A:608:ILE:HG13	1:A:609:GLU:HA	1.97	0.41
1:A:648:LEU:HD21	1:A:790:PHE:CZ	2.55	0.41
1:A:101:LYS:HB3	1:A:415:MET:SD	2.60	0.41
1:A:361:VAL:HG12	1:A:363:GLU:H	1.76	0.41
1:A:573:ARG:HE	1:A:573:ARG:HB3	1.27	0.41
1:A:623:ILE:O	1:A:626:ILE:HG13	2.20	0.41
1:A:535:GLY:HA2	4:A:823:HOH:O	2.20	0.41
1:A:698:LEU:HD21	1:A:727:LEU:HD11	2.03	0.41
1:A:660:ASP:O	1:A:663:LEU:HB2	2.21	0.41
1:A:739:LYS:HZ1	1:A:747:ARG:HD3	1.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ARG:HH11	1:A:168:ARG:CB	2.34	0.41
1:A:605:ILE:HG22	1:A:606:LEU:HD13	2.01	0.41
1:A:304:ILE:HD13	1:A:340:LYS:HB2	2.03	0.41
1:A:350:ASP:C	1:A:360:ILE:HB	2.40	0.41
1:A:518:LYS:HD2	1:A:524:MET:CE	2.50	0.41
1:A:373:ARG:HB3	1:A:379:HIS:CG	2.54	0.41
1:A:671:TYR:CZ	1:A:675:ILE:HD11	2.56	0.41
1:A:683:ARG:HE	1:A:683:ARG:HB2	1.76	0.41
1:A:552:ILE:HG12	1:A:571:ALA:HB2	2.03	0.40
1:A:289:PHE:HD1	1:A:294:ASP:HB3	1.86	0.40
1:A:475:GLN:HG2	1:A:476:PRO:HD2	2.02	0.40
1:A:671:TYR:CE2	1:A:675:ILE:HD11	2.56	0.40
1:A:138:PRO:HG3	1:A:202:VAL:HG23	2.03	0.40
1:A:453:PHE:CZ	1:A:613:PRO:HG3	2.56	0.40
1:A:518:LYS:CD	1:A:524:MET:CE	2.99	0.40
1:A:781:TYR:HA	1:A:782:GLY:HA2	1.65	0.40
1:A:87:LEU:HD12	1:A:108:PRO:HG3	2.02	0.40
1:A:338:ALA:O	1:A:385:LYS:HE3	2.22	0.40
1:A:354:MET:HE3	1:A:354:MET:HB3	1.84	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	811/822 (99%)	749 (92%)	53 (6%)	9 (1%)	14 46

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	363	GLU
1	A	370	PRO

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Mol	Chain	Res	Type
1	A	193	ASN
1	A	369	LEU
1	A	608	ILE
1	A	299	GLU
1	A	364	PHE
1	A	361	VAL
1	A	389	PRO

5.3.2 Protein sidechains (i)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	714/723 (99%)	596 (84%)	118 (16%)	2 10

All (118) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ARG
1	A	11	LEU
1	A	12	LYS
1	A	28	LEU
1	A	39	LEU
1	A	51	GLU
1	A	91	LYS
1	A	97	THR
1	A	103	LEU
1	A	106	THR
1	A	117	LYS
1	A	123	THR
1	A	131	ARG
1	A	156	SER
1	A	158	GLU
1	A	163	ASN
1	A	165	ASP
1	A	166	LEU
1	A	168	ARG

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Mol	Chain	Res	Type
1	A	169	LYS
1	A	178	TRP
1	A	183	ASN
1	A	193	ASN
1	A	201	GLN
1	A	204	LEU
1	A	209	ARG
1	A	217	VAL
1	A	266	LEU
1	A	278	VAL
1	A	280	ARG
1	A	281	ARG
1	A	284	GLN
1	A	299	GLU
1	A	302	ARG
1	A	304	ILE
1	A	305	ILE
1	A	306	LEU
1	A	308	GLU
1	A	320	VAL
1	A	323	LEU
1	A	325	ASP
1	A	328	ASN
1	A	329	VAL
1	A	330	SER
1	A	334	HIS
1	A	336	ILE
1	A	342	LEU
1	A	344	LEU
1	A	354	MET
1	A	360	ILE
1	A	363	GLU
1	A	368	LEU
1	A	369	LEU
1	A	392	GLU
1	A	393	GLU
1	A	395	ILE
1	A	399	THR
1	A	403	GLN
1	A	418	THR
1	A	421	THR
1	A	422	GLU

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Mol	Chain	Res	Type
1	A	455	THR
1	A	462	LYS
1	A	492	SER
1	A	497	LYS
1	A	502	GLN
1	A	507	LYS
1	A	508	TYR
1	A	512	GLU
1	A	514	GLU
1	A	522	LYS
1	A	524	MET
1	A	540	LEU
1	A	561	ARG
1	A	562	ARG
1	A	570	ARG
1	A	573	ARG
1	A	581	ILE
1	A	592	ARG
1	A	593	ILE
1	A	596	SER
1	A	597	GLU
1	A	598	GLN
1	A	606	LEU
1	A	608	ILE
1	A	626	ILE
1	A	629	LYS
1	A	634	ASN
1	A	659	ARG
1	A	670	GLU
1	A	672	LEU
1	A	680	VAL
1	A	683	ARG
1	A	686	GLU
1	A	691	LYS
1	A	696	GLU
1	A	699	LYS
1	A	701	SER
1	A	709	LEU
1	A	710	PHE
1	A	716	GLN
1	A	720	SER
1	A	723	LEU

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Mol	Chain	Res	Type
1	A	725	ASP
1	A	737	ARG
1	A	739	LYS
1	A	741	GLU
1	A	747	ARG
1	A	757	ILE
1	A	769	VAL
1	A	771	HIS
1	A	773	LYS
1	A	774	GLU
1	A	778	LEU
1	A	794	THR
1	A	803	ARG
1	A	812	TYR
1	A	816	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	22	ASN
1	A	80	GLN
1	A	120	HIS
1	A	151	ASN
1	A	163	ASN
1	A	193	ASN
1	A	334	HIS
1	A	379	HIS
1	A	403	GLN
1	A	428	GLN
1	A	440	HIS
1	A	475	GLN
1	A	502	GLN
1	A	505	ASN
1	A	509	HIS
1	A	558	HIS
1	A	566	GLN
1	A	598	GLN
1	A	616	HIS
1	A	625	ASN
1	A	634	ASN
1	A	716	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

Of 2 ligands modelled in this entry, 1 is 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	$\#\|Z\| > 2$
3	ADP	A	873	-	24,29,29	1.12	2 (8%)	29,45,45	1.42	5 (17%)

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
3	ADP	A	873	-	-	1/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	873	ADP	C5-C4	2.93	1.48	1.40
3	A	873	ADP	C2-N3	2.32	1.35	1.32

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	873	ADP	N3-C2-N1	-3.04	123.92	128.68
3	A	873	ADP	C3'-C2'-C1'	2.64	104.95	100.98
3	A	873	ADP	C4-C5-N7	-2.52	106.77	109.40
3	A	873	ADP	C5'-C4'-C3'	-2.37	106.31	115.18
3	A	873	ADP	PA-O3A-PB	-2.16	125.40	132.83

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	873	ADP	C5'-O5'-PA-O1A

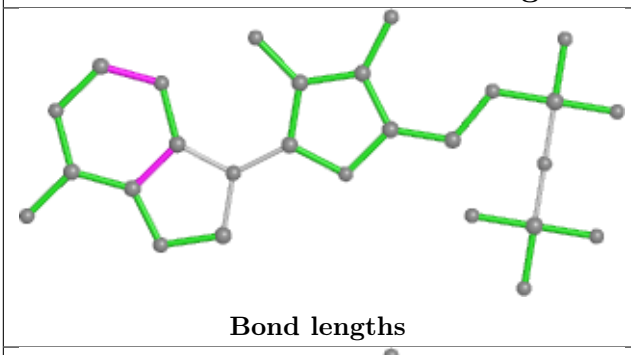
There are no ring outliers.

1 monomer is involved in 2 short contacts:

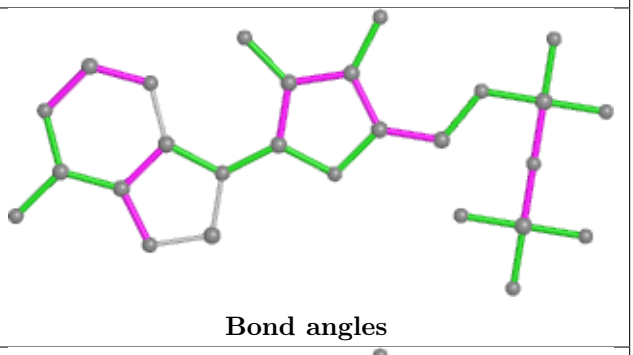
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	873	ADP	2	0

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 then 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.

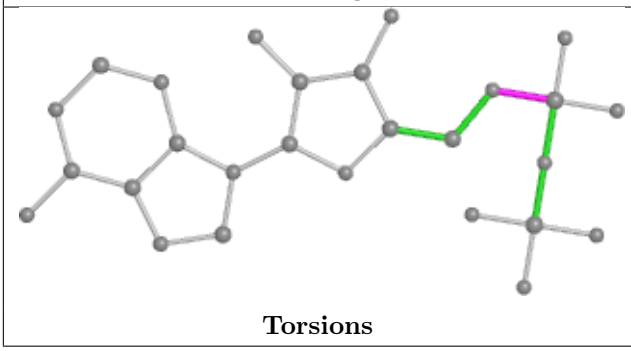
Ligand ADP A 873



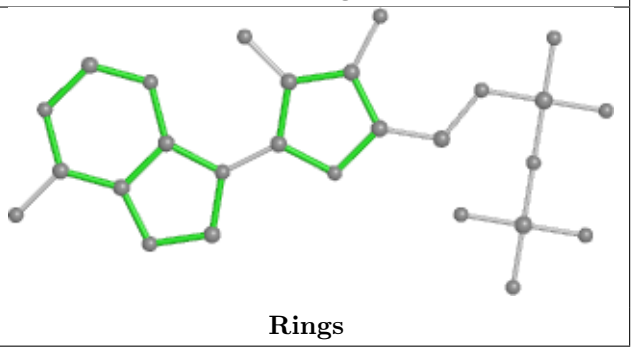
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	813/822 (98%)	-0.32	7 (0%)	84	69	8, 44, 87, 131	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	780	SER	4.1
1	A	367	ARG	3.1
1	A	607	LYS	2.8
1	A	352	VAL	2.7
1	A	365	THR	2.7
1	A	779	ARG	2.5
1	A	364	PHE	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 monosaccharides 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, 95^{th} 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	ADP	A	873	27/27	0.88	0.28	51,52,53,54	0

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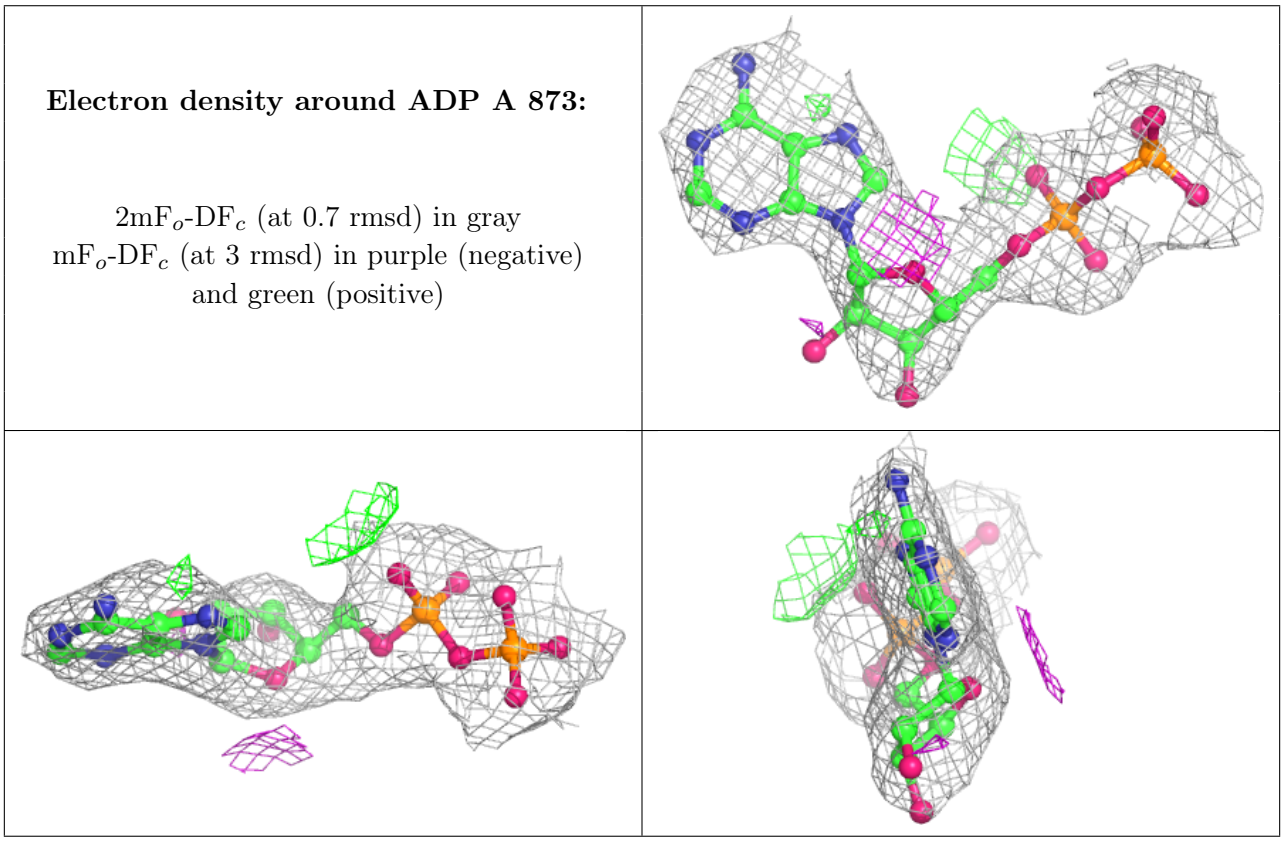
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	MG	A	872	1/1	0.97	0.50	36,36,36,36	0

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 ADP A 873:

$2mF_o$-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.