



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2021 – 05:19 AM EDT

PDB ID : 3BXZ
Title : Crystal structure of the isolated DEAD motor domains from Escherichia coli SecA
Authors : Nithianantham, S.; Namjoshi, S.; Shilton, B.H.
Deposited on : 2008-01-15
Resolution : 3.00 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
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)	:	2.23.2

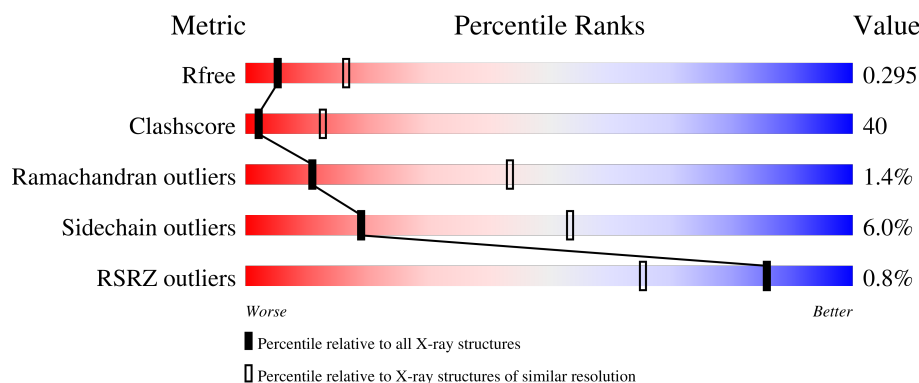
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	471	<div> <div></div> <div>37%</div> <div>52%</div> <div>7%</div> </div>
1	B	471	<div> <div></div> <div>39%</div> <div>51%</div> <div>7%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SPD	A	905	-	-	-	X
3	SPD	B	906	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7106 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 Preprotein translocase subunit secA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	438	Total	C	N	O	S	0	0	0
			3420	2143	608	655	14			
1	B	440	Total	C	N	O	S	0	0	0
			3439	2154	613	657	15			

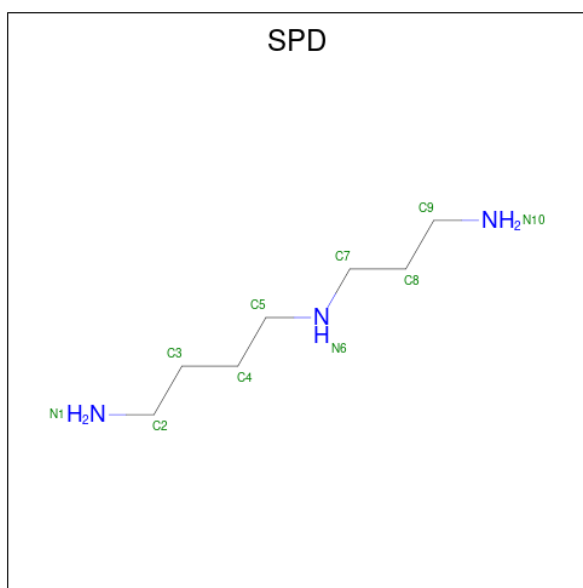
There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P10408
A	0	HIS	-	expression tag	UNP P10408
A	1	HIS	-	expression tag	UNP P10408
A	2	HIS	-	expression tag	UNP P10408
A	3	HIS	-	expression tag	UNP P10408
A	4	HIS	-	expression tag	UNP P10408
A	5	HIS	-	expression tag	UNP P10408
A	368	ALA	GLU	engineered mutation	UNP P10408
B	-1	MET	-	expression tag	UNP P10408
B	0	HIS	-	expression tag	UNP P10408
B	1	HIS	-	expression tag	UNP P10408
B	2	HIS	-	expression tag	UNP P10408
B	3	HIS	-	expression tag	UNP P10408
B	4	HIS	-	expression tag	UNP P10408
B	5	HIS	-	expression tag	UNP P10408
B	368	ALA	GLU	engineered mutation	UNP P10408

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

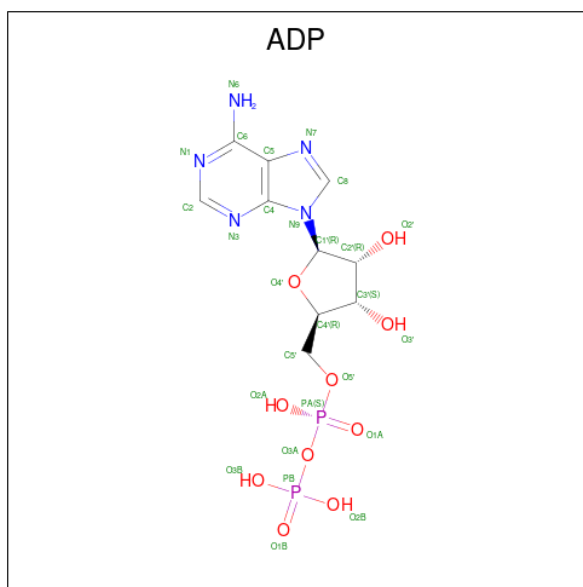
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		
2	B	1	Total	Mg	0	0
			1	1		

- Molecule 3 is SPERMIDINE (three-letter code: SPD) (formula: $C_7H_{19}N_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	N	0	0
			10	7	3		
3	B	1	Total	C	N	0	0
			10	7	3		

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

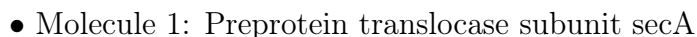


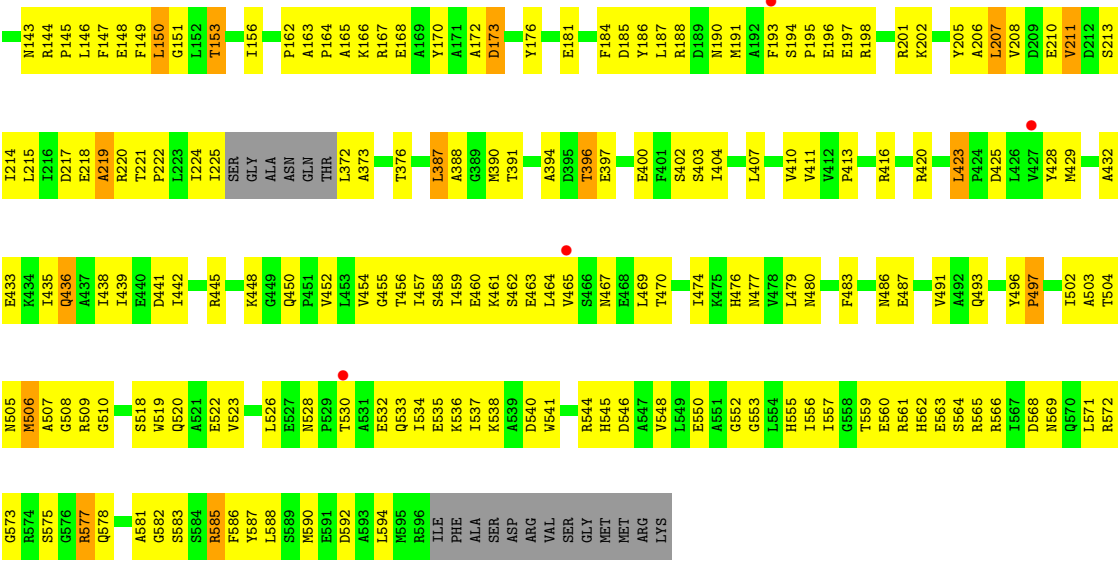
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
4	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	89	Total	O	0	0
			89	89		
5	B	82	Total	O	0	0
			82	82		

- Molecule 1: Preprotein translocase subunit secA





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.82Å 71.36Å 119.54Å 90.00° 128.82° 90.00°	Depositor
Resolution (Å)	46.58 – 3.00 46.57 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.58-3.00) 84.1 (46.57-3.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.54 (at 3.01Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.245 , 0.305 0.238 , 0.295	Depositor DCC
R_{free} test set	2317 reflections (9.86%)	wwPDB-VP
Wilson B-factor (Å ²)	83.2	Xtriage
Anisotropy	0.140	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 63.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	7106	wwPDB-VP
Average B, all atoms (Å ²)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.73% 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, ADP, SPD

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	0.40	0/3472	0.63	1/4689 (0.0%)
1	B	0.39	0/3491	0.63	0/4713
All	All	0.39	0/6963	0.63	1/9402 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	486	ASN	CB-CA-C	-5.01	100.38	110.40

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3420	0	3431	283	0
1	B	3439	0	3453	275	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	10	0	19	4	0
3	B	10	0	19	0	0
4	A	27	0	12	1	0
4	B	27	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	89	0	0	19	0
5	B	82	0	0	22	0
All	All	7106	0	6946	550	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 40.

All (550) 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:506:MET:HE2	1:A:506:MET:H	1.12	1.13
1:B:506:MET:HE2	1:B:506:MET:H	1.12	1.06
1:A:221:THR:HG22	1:A:376:THR:HG22	1.05	1.03
1:B:556:ILE:HD13	1:B:571:LEU:HG	1.45	0.98
1:A:504:THR:HG22	1:A:505:ASN:H	1.28	0.98
1:A:556:ILE:HD13	1:A:571:LEU:HG	1.45	0.94
1:B:99:ILE:HD11	1:B:407:LEU:HD13	1.48	0.94
1:A:64:ILE:HG13	1:A:65:PRO:CD	1.96	0.94
1:A:99:ILE:HD11	1:A:407:LEU:HD13	1.49	0.93
1:A:457:ILE:HG23	1:A:560:GLU:HG3	1.49	0.93
1:A:64:ILE:HG13	1:A:65:PRO:HD3	1.51	0.93
1:B:561:ARG:HH22	1:B:572:ARG:HH22	1.14	0.93
1:B:64:ILE:HG13	1:B:65:PRO:CD	1.98	0.92
1:B:504:THR:HG22	1:B:505:ASN:H	1.31	0.92
1:B:64:ILE:HG13	1:B:65:PRO:HD3	1.52	0.91
1:B:562:HIS:HD2	1:B:564:SER:H	1.17	0.91
1:A:221:THR:CG2	1:A:376:THR:HG22	1.98	0.89
1:A:436:GLN:HG3	5:A:951:HOH:O	1.72	0.87
1:A:221:THR:HG22	1:A:376:THR:CG2	2.00	0.85
1:B:506:MET:HE2	1:B:506:MET:N	1.91	0.85
1:B:63:LEU:HD23	1:B:63:LEU:H	1.41	0.84
1:A:506:MET:HE2	1:A:506:MET:N	1.92	0.83
1:B:60:LEU:HD12	1:B:61:GLU:N	1.94	0.83
1:A:445:ARG:HA	1:A:448:LYS:HD3	1.60	0.83
1:A:63:LEU:HD23	1:A:63:LEU:H	1.44	0.82
1:B:225:ILE:HG22	1:B:372:LEU:HD22	1.61	0.81
1:B:445:ARG:HA	1:B:448:LYS:HD3	1.60	0.81
1:B:14:ASN:HD21	1:B:411:VAL:H	1.30	0.80
1:A:454:VAL:HG22	1:A:557:ILE:HD11	1.64	0.80
1:A:60:LEU:HD12	1:A:61:GLU:N	1.96	0.79
1:A:14:ASN:HD21	1:A:411:VAL:H	1.29	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:529:PRO:HD3	5:A:990:HOH:O	1.84	0.77
1:B:94:LEU:HD13	1:B:207:LEU:HD21	1.66	0.77
1:B:568:ASP:HB3	5:B:964:HOH:O	1.83	0.77
1:B:425:ASP:HB3	1:B:588:LEU:HD13	1.67	0.76
1:B:553:GLY:HA3	1:B:581:ALA:O	1.85	0.76
1:B:454:VAL:HG22	1:B:557:ILE:HD11	1.65	0.76
1:B:491:VAL:HG21	1:B:508:GLY:HA3	1.68	0.75
1:A:491:VAL:HG21	1:A:508:GLY:HA3	1.67	0.75
1:A:425:ASP:HB3	1:A:588:LEU:HD13	1.68	0.75
1:A:53:ARG:HA	1:A:56:LYS:HE2	1.69	0.75
1:B:562:HIS:CD2	1:B:564:SER:H	2.02	0.75
1:B:459:ILE:O	1:B:463:GLU:HG2	1.86	0.75
1:A:459:ILE:O	1:A:463:GLU:HG2	1.87	0.75
1:A:562:HIS:HD2	1:A:564:SER:H	1.30	0.74
1:A:577:ARG:NH1	1:A:578:GLN:HB2	2.03	0.74
1:A:553:GLY:HA3	1:A:581:ALA:O	1.86	0.74
1:B:53:ARG:HA	1:B:56:LYS:HE2	1.67	0.74
1:B:201:ARG:HD2	5:B:961:HOH:O	1.87	0.74
1:B:217:ASP:O	1:B:220:ARG:HG2	1.87	0.74
1:A:66:GLU:O	1:A:70:VAL:HG23	1.87	0.74
1:B:561:ARG:HH22	1:B:572:ARG:NH2	1.84	0.74
1:B:577:ARG:NH1	1:B:578:GLN:HB2	2.03	0.74
1:A:76:LYS:O	1:A:80:GLY:HA2	1.88	0.73
1:A:94:LEU:HD13	1:A:207:LEU:HD21	1.69	0.73
1:A:504:THR:HG22	1:A:505:ASN:N	2.04	0.73
1:B:457:ILE:HG23	1:B:560:GLU:HG3	1.68	0.73
1:A:18:LEU:HD21	1:A:413:PRO:HD3	1.69	0.72
1:A:561:ARG:HH22	1:A:572:ARG:HH22	1.36	0.72
1:B:66:GLU:O	1:B:70:VAL:HG23	1.89	0.72
1:B:526:LEU:HD23	1:B:528:ASN:H	1.54	0.72
1:B:18:LEU:HD21	1:B:413:PRO:HD3	1.70	0.72
5:A:979:HOH:O	1:B:222:PRO:HB3	1.88	0.72
1:A:115:PRO:HG2	1:A:207:LEU:HD11	1.72	0.72
1:B:25:VAL:HG21	1:B:89:LEU:HD13	1.72	0.72
1:B:115:PRO:HG2	1:B:207:LEU:HD11	1.72	0.72
1:B:76:LYS:O	1:B:80:GLY:HA2	1.90	0.71
1:A:562:HIS:CD2	1:A:564:SER:H	2.08	0.71
1:B:50:PHE:CD2	1:B:63:LEU:HD12	2.26	0.70
1:A:526:LEU:HD23	1:A:528:ASN:H	1.55	0.70
1:B:504:THR:HG22	1:B:505:ASN:N	2.05	0.70
1:A:544:ARG:O	1:A:548:VAL:HG23	1.92	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:25:VAL:HG21	1:A:89:LEU:HD13	1.73	0.69
1:B:68:PHE:CD2	1:B:114:LEU:HD13	2.27	0.69
1:A:210:GLU:HG3	5:A:981:HOH:O	1.91	0.69
1:A:455:GLY:O	1:A:559:THR:HG23	1.93	0.68
1:A:225:ILE:HG12	1:A:372:LEU:HG	1.73	0.68
1:B:455:GLY:O	1:B:559:THR:HG23	1.93	0.68
1:A:50:PHE:CD2	1:A:63:LEU:HD12	2.28	0.68
1:B:79:PHE:CE1	1:B:146:LEU:HB2	2.29	0.68
1:B:144:ARG:HG2	1:B:148:GLU:HG3	1.76	0.67
1:A:469:LEU:HD23	1:A:474:ILE:HB	1.76	0.67
1:B:544:ARG:O	1:B:548:VAL:HG23	1.94	0.67
1:B:538:LYS:O	1:B:538:LYS:HD3	1.95	0.67
1:A:213:SER:O	1:A:218:GLU:HG2	1.95	0.67
1:A:538:LYS:O	1:A:538:LYS:HD3	1.95	0.67
1:A:123:GLY:HA2	5:A:957:HOH:O	1.95	0.66
1:A:79:PHE:CE1	1:A:146:LEU:HB2	2.29	0.66
1:A:60:LEU:HB2	5:A:909:HOH:O	1.96	0.66
1:A:68:PHE:CD2	1:A:114:LEU:HD13	2.30	0.66
1:B:469:LEU:HD23	1:B:474:ILE:HB	1.76	0.66
1:B:396:THR:HB	1:B:397:GLU:OE1	1.95	0.66
1:B:503:ALA:HB1	1:B:507:ALA:HB3	1.77	0.66
1:A:503:ALA:HB1	1:A:507:ALA:HB3	1.78	0.65
1:B:467:ASN:HA	1:B:470:THR:HG22	1.78	0.65
1:B:506:MET:HB3	1:B:509:ARG:HD2	1.79	0.65
1:B:39:SER:OG	1:B:42:GLU:HG3	1.96	0.65
1:A:504:THR:H	1:A:507:ALA:HB2	1.61	0.64
1:B:43:LEU:O	1:B:46:LYS:HB2	1.97	0.64
1:A:39:SER:OG	1:A:42:GLU:HG3	1.97	0.64
1:A:467:ASN:HA	1:A:470:THR:HG22	1.79	0.64
1:A:454:VAL:HG22	1:A:557:ILE:CD1	2.28	0.64
1:A:506:MET:HB3	1:A:509:ARG:HD2	1.79	0.64
1:A:377:PHE:HA	1:B:191:MET:CE	2.27	0.63
1:B:60:LEU:HD11	5:B:968:HOH:O	1.97	0.63
1:B:87:GLN:NE2	4:B:902:ADP:N7	2.47	0.63
1:A:23:LYS:HA	1:A:26:ASN:HD22	1.64	0.63
1:B:504:THR:H	1:B:507:ALA:HB2	1.62	0.63
1:A:373:ALA:HB2	5:B:966:HOH:O	1.98	0.63
1:A:441:ASP:O	1:A:445:ARG:HG3	1.98	0.62
1:B:454:VAL:HG22	1:B:557:ILE:CD1	2.29	0.62
1:A:114:LEU:HB2	1:A:115:PRO:CD	2.29	0.62
1:A:196:GLU:CD	1:A:196:GLU:H	2.02	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:441:ASP:O	1:B:445:ARG:HG3	1.99	0.62
1:B:153:THR:N	1:B:173:ASP:OD2	2.28	0.62
1:B:214:ILE:O	1:B:218:GLU:HB2	1.99	0.62
1:A:94:LEU:HD21	1:A:390:MET:HB3	1.82	0.62
1:A:144:ARG:HG2	1:A:148:GLU:HG3	1.81	0.62
1:A:165:ALA:O	1:A:168:GLU:HB2	1.99	0.62
1:B:561:ARG:NH2	1:B:572:ARG:HH22	1.93	0.62
1:A:43:LEU:O	1:A:46:LYS:HB2	1.99	0.62
1:B:165:ALA:O	1:B:168:GLU:HB2	1.99	0.62
1:A:487:GLU:O	1:A:491:VAL:HG23	1.99	0.62
1:B:60:LEU:HD12	1:B:61:GLU:H	1.65	0.62
1:B:108:LYS:HE2	5:B:914:HOH:O	2.00	0.62
1:B:526:LEU:HD22	1:B:528:ASN:O	2.00	0.62
1:A:395:ASP:HA	1:A:398:ALA:HB2	1.83	0.61
1:B:94:LEU:HD21	1:B:390:MET:HB3	1.82	0.61
1:A:434:LYS:HE3	1:A:589:SER:HB2	1.81	0.61
1:B:130:THR:HG21	1:B:135:LEU:HB3	1.81	0.61
1:A:130:THR:HG21	1:A:135:LEU:HB3	1.81	0.61
1:B:114:LEU:HB2	1:B:115:PRO:CD	2.31	0.61
1:A:457:ILE:HD13	5:A:948:HOH:O	2.01	0.60
1:A:49:GLU:O	1:A:53:ARG:HG3	2.01	0.60
1:A:153:THR:N	1:A:173:ASP:OD2	2.29	0.60
1:B:23:LYS:HA	1:B:26:ASN:HD22	1.66	0.60
1:B:196:GLU:CD	1:B:196:GLU:H	2.04	0.60
1:A:61:GLU:HG2	1:A:64:ILE:HD13	1.83	0.60
1:A:526:LEU:HD22	1:A:528:ASN:O	2.01	0.60
1:B:102:MET:O	1:B:108:LYS:HE3	2.01	0.60
1:A:493:GLN:NE2	1:A:518:SER:H	1.99	0.59
1:B:139:ASP:O	1:B:143:ASN:HB2	2.03	0.59
1:B:487:GLU:O	1:B:491:VAL:HG23	2.02	0.59
1:A:434:LYS:CE	1:A:589:SER:HB2	2.33	0.59
1:B:454:VAL:HG22	1:B:557:ILE:CG1	2.32	0.59
1:B:493:GLN:NE2	1:B:518:SER:H	2.01	0.59
1:B:387:LEU:HG	5:B:970:HOH:O	2.01	0.59
1:A:454:VAL:HG22	1:A:557:ILE:CG1	2.33	0.59
1:A:493:GLN:HE22	1:A:518:SER:H	1.51	0.59
1:B:113:THR:HG22	1:B:143:ASN:HD21	1.67	0.59
1:B:506:MET:H	1:B:506:MET:CE	2.02	0.59
1:A:83:HIS:ND1	1:A:114:LEU:HD21	2.18	0.58
1:B:509:ARG:HG2	5:B:976:HOH:O	2.02	0.58
1:B:194:SER:HB2	1:B:196:GLU:OE2	2.04	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:GLU:HG2	1:B:64:ILE:HD13	1.85	0.58
1:A:138:ARG:NH2	1:A:510:GLY:O	2.35	0.58
1:A:457:ILE:CG2	1:A:560:GLU:HG3	2.29	0.58
1:A:506:MET:H	1:A:506:MET:CE	2.00	0.58
1:A:18:LEU:O	1:A:22:ARG:HB2	2.04	0.58
1:B:503:ALA:HB1	1:B:507:ALA:CB	2.34	0.57
1:A:102:MET:O	1:A:108:LYS:HE3	2.04	0.57
1:B:114:LEU:HB2	1:B:115:PRO:HD3	1.87	0.57
1:A:376:THR:O	1:B:191:MET:HE3	2.04	0.57
1:B:224:ILE:HB	1:B:373:ALA:HB3	1.87	0.57
1:B:519:TRP:O	1:B:522:GLU:HB2	2.05	0.57
1:A:114:LEU:HB2	1:A:115:PRO:HD3	1.87	0.57
1:B:49:GLU:O	1:B:53:ARG:HG3	2.05	0.57
1:A:60:LEU:HD12	1:A:61:GLU:HB2	1.86	0.57
1:A:113:THR:HG22	1:A:143:ASN:HD21	1.68	0.57
1:B:18:LEU:O	1:B:22:ARG:HB2	2.04	0.57
1:B:211:VAL:HG22	1:B:390:MET:N	2.20	0.56
1:A:503:ALA:HB1	1:A:507:ALA:CB	2.34	0.56
1:A:568:ASP:HB2	1:A:586:PHE:CZ	2.40	0.56
1:B:16:ARG:O	1:B:20:ARG:HB2	2.05	0.56
1:B:59:VAL:HB	1:B:62:ASN:HB2	1.87	0.56
1:B:63:LEU:HD23	1:B:63:LEU:N	2.18	0.56
1:B:432:ALA:O	1:B:436:GLN:HB2	2.05	0.56
1:A:194:SER:HB2	1:A:196:GLU:OE2	2.05	0.56
1:A:432:ALA:O	1:A:436:GLN:HB2	2.05	0.56
1:A:585:ARG:HG3	1:A:585:ARG:HH11	1.71	0.56
1:A:211:VAL:HG22	1:A:390:MET:N	2.20	0.56
1:B:60:LEU:HD12	1:B:61:GLU:HB2	1.88	0.56
1:B:496:TYR:HE2	1:B:544:ARG:HH11	1.53	0.55
1:B:83:HIS:ND1	1:B:114:LEU:HD21	2.21	0.55
1:B:493:GLN:HE22	1:B:518:SER:H	1.53	0.55
1:A:59:VAL:HB	1:A:62:ASN:HB2	1.87	0.55
1:A:16:ARG:O	1:A:20:ARG:HB2	2.06	0.55
1:A:60:LEU:HD12	1:A:61:GLU:H	1.67	0.55
1:A:496:TYR:HE2	1:A:544:ARG:HH11	1.54	0.54
1:A:377:PHE:HA	1:B:191:MET:HE1	1.89	0.54
1:B:568:ASP:HB2	1:B:586:PHE:CZ	2.41	0.54
1:A:137:GLN:HG3	1:A:156:ILE:HG21	1.90	0.54
1:A:191:MET:SD	1:B:186:TYR:CE2	3.01	0.54
1:A:126:VAL:HG13	1:A:205:TYR:HD2	1.73	0.54
1:A:504:THR:CG2	1:A:505:ASN:H	2.09	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:519:TRP:O	1:A:522:GLU:HB2	2.08	0.54
1:B:469:LEU:HD23	1:B:469:LEU:O	2.07	0.54
1:B:585:ARG:HG3	1:B:585:ARG:HH11	1.71	0.54
1:A:469:LEU:HD23	1:A:469:LEU:O	2.07	0.54
1:A:493:GLN:NE2	1:A:518:SER:HB3	2.23	0.54
1:B:218:GLU:O	1:B:220:ARG:N	2.32	0.54
1:B:206:ALA:HB3	5:B:970:HOH:O	2.07	0.54
1:B:397:GLU:OE1	1:B:566:ARG:HD3	2.07	0.54
1:B:460:GLU:O	1:B:464:LEU:HG	2.08	0.54
1:B:565:ARG:NH1	1:B:572:ARG:HH12	2.05	0.54
1:B:32:GLU:N	1:B:33:PRO:HD2	2.23	0.53
1:B:552:GLY:O	1:B:582:GLY:HA2	2.08	0.53
1:A:541:TRP:HA	1:A:544:ARG:NH2	2.23	0.53
1:B:420:ARG:HH12	1:B:573:GLY:HA2	1.72	0.53
1:A:565:ARG:NH1	1:A:572:ARG:HH12	2.06	0.53
1:B:590:MET:C	1:B:592:ASP:H	2.11	0.53
1:A:64:ILE:HG13	1:A:65:PRO:HD2	1.83	0.53
1:A:420:ARG:HH12	1:A:573:GLY:HA2	1.73	0.53
1:A:460:GLU:O	1:A:464:LEU:HG	2.07	0.53
1:B:450:GLN:HG3	1:B:553:GLY:O	2.08	0.53
1:B:541:TRP:HA	1:B:544:ARG:NH2	2.23	0.53
1:B:64:ILE:HG13	1:B:65:PRO:HD2	1.86	0.53
1:A:63:LEU:HD23	1:A:63:LEU:N	2.20	0.53
1:A:225:ILE:CG2	1:A:372:LEU:HD12	2.39	0.53
1:A:450:GLN:HG3	1:A:553:GLY:O	2.08	0.53
1:A:463:GLU:HG3	3:A:905:SPD:N6	2.24	0.53
1:A:191:MET:SD	1:B:186:TYR:HE2	2.32	0.53
1:A:438:ILE:HG22	1:A:587:TYR:CD2	2.44	0.53
1:A:456:THR:HG21	1:A:462:SER:HA	1.90	0.53
1:B:438:ILE:HG22	1:B:587:TYR:CD2	2.43	0.53
1:B:530:THR:HB	1:B:533:GLN:HE22	1.74	0.53
1:B:456:THR:HG21	1:B:462:SER:HA	1.91	0.53
1:A:108:LYS:HD2	5:A:966:HOH:O	2.08	0.52
1:B:572:ARG:HD3	5:B:919:HOH:O	2.08	0.52
1:B:126:VAL:HG13	1:B:205:TYR:HD2	1.74	0.52
1:A:127:HIS:CD2	5:A:973:HOH:O	2.61	0.52
1:B:172:ALA:O	1:B:201:ARG:NH2	2.41	0.52
1:B:479:LEU:CD1	1:B:491:VAL:HG22	2.39	0.52
1:A:377:PHE:HA	1:B:191:MET:HE3	1.90	0.52
1:B:101:GLU:HG2	5:B:982:HOH:O	2.09	0.52
1:A:442:ILE:HG22	1:A:452:VAL:HG21	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:117:TYR:CE1	1:B:150:LEU:HD13	2.44	0.52
1:A:21:MET:O	1:A:25:VAL:HG23	2.10	0.52
1:A:400:GLU:CG	1:A:404:ILE:HD11	2.40	0.52
1:B:144:ARG:O	1:B:147:PHE:N	2.42	0.52
1:A:463:GLU:HG3	3:A:905:SPD:HN6	1.74	0.52
1:A:530:THR:HB	1:A:533:GLN:HE22	1.74	0.52
1:B:173:ASP:HA	5:B:971:HOH:O	2.10	0.52
1:A:32:GLU:N	1:A:33:PRO:HD2	2.24	0.52
1:B:166:LYS:NZ	1:B:181:GLU:OE1	2.42	0.52
1:B:217:ASP:OD1	1:B:566:ARG:NH2	2.39	0.52
1:B:442:ILE:HG22	1:B:452:VAL:HG21	1.91	0.52
1:B:137:GLN:HG3	1:B:156:ILE:HG21	1.91	0.51
1:B:400:GLU:CG	1:B:404:ILE:HD11	2.40	0.51
1:B:504:THR:CG2	1:B:505:ASN:H	2.12	0.51
1:A:589:SER:HB3	1:A:592:ASP:OD2	2.10	0.51
1:A:400:GLU:O	1:A:404:ILE:HG13	2.10	0.51
1:B:391:THR:CG2	1:B:394:ALA:HB2	2.39	0.51
1:A:499:ALA:HA	5:A:937:HOH:O	2.10	0.51
1:A:593:ALA:O	1:A:594:LEU:HD23	2.10	0.51
1:A:166:LYS:NZ	1:A:181:GLU:OE1	2.43	0.51
1:A:534:ILE:HG13	1:A:535:GLU:N	2.26	0.51
1:B:461:LYS:O	1:B:465:VAL:HG23	2.10	0.51
1:A:103:ARG:O	1:A:106:GLU:HB2	2.11	0.51
1:B:93:VAL:O	1:B:98:CYS:HB2	2.11	0.51
1:A:81:MET:HA	5:A:983:HOH:O	2.10	0.51
1:A:83:HIS:CE1	1:A:114:LEU:HD21	2.46	0.50
1:B:103:ARG:HD3	5:B:977:HOH:O	2.11	0.50
1:B:493:GLN:NE2	1:B:518:SER:HB3	2.26	0.50
1:A:400:GLU:HG2	1:A:404:ILE:HD11	1.94	0.50
1:A:479:LEU:CD1	1:A:491:VAL:HG22	2.41	0.50
1:A:588:LEU:HD12	1:A:588:LEU:N	2.26	0.50
1:B:60:LEU:CD1	1:B:61:GLU:N	2.72	0.50
1:A:93:VAL:O	1:A:98:CYS:HB2	2.11	0.50
1:A:461:LYS:O	1:A:465:VAL:HG23	2.10	0.50
1:A:520:GLN:N	1:A:520:GLN:OE1	2.45	0.50
1:B:53:ARG:HB3	1:B:58:GLU:OE2	2.10	0.50
1:A:552:GLY:O	1:A:582:GLY:HA2	2.10	0.50
1:B:149:PHE:C	1:B:151:GLY:H	2.15	0.50
1:B:400:GLU:O	1:B:404:ILE:HG13	2.11	0.50
1:A:22:ARG:NH1	5:A:968:HOH:O	2.36	0.50
1:A:372:LEU:C	1:A:372:LEU:HD23	2.31	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:577:ARG:HH11	1:A:578:GLN:HB2	1.75	0.50
1:B:134:TYR:HD2	1:B:135:LEU:HD22	1.77	0.50
1:B:219:ALA:HA	5:B:975:HOH:O	2.11	0.50
1:A:541:TRP:HA	1:A:544:ARG:CZ	2.42	0.49
1:A:555:HIS:HA	1:A:583:SER:O	2.12	0.49
1:B:89:LEU:O	1:B:93:VAL:HG23	2.11	0.49
1:A:149:PHE:C	1:A:151:GLY:H	2.15	0.49
1:A:211:VAL:CG2	1:A:390:MET:N	2.76	0.49
1:B:534:ILE:HG13	1:B:535:GLU:N	2.26	0.49
1:B:213:SER:O	1:B:218:GLU:HG2	2.11	0.49
1:A:76:LYS:HE2	1:A:82:ARG:HB2	1.94	0.49
1:A:457:ILE:HG21	5:A:948:HOH:O	2.11	0.49
1:A:561:ARG:HG2	1:A:561:ARG:HH11	1.76	0.49
1:B:113:THR:HG22	1:B:143:ASN:ND2	2.28	0.49
1:A:465:VAL:O	1:A:469:LEU:HB2	2.13	0.49
1:A:541:TRP:CA	1:A:544:ARG:HH21	2.26	0.49
1:B:35:MET:HA	1:B:38:LEU:HD13	1.94	0.49
1:B:555:HIS:HA	1:B:583:SER:O	2.13	0.49
1:A:117:TYR:CE1	1:A:150:LEU:HD13	2.47	0.49
1:B:21:MET:HB2	1:B:92:MET:SD	2.53	0.49
1:A:21:MET:HB2	1:A:92:MET:SD	2.53	0.49
1:B:76:LYS:HE2	1:B:82:ARG:HB2	1.95	0.49
1:B:429:MET:HB2	1:B:433:GLU:OE2	2.13	0.49
1:B:526:LEU:CD2	1:B:528:ASN:H	2.23	0.49
1:B:21:MET:O	1:B:25:VAL:HG23	2.12	0.49
1:A:469:LEU:HD13	1:A:502:ILE:HD11	1.95	0.49
1:A:530:THR:HG22	1:A:532:GLU:H	1.78	0.49
1:B:60:LEU:CD1	1:B:61:GLU:H	2.25	0.49
1:B:530:THR:HG22	1:B:532:GLU:H	1.78	0.49
1:A:163:ALA:HB3	1:A:164:PRO:HD3	1.95	0.48
1:A:454:VAL:CG2	1:A:557:ILE:HD11	2.38	0.48
1:A:541:TRP:HA	1:A:544:ARG:NE	2.28	0.48
1:B:400:GLU:HG2	1:B:404:ILE:HD11	1.94	0.48
1:B:577:ARG:HH11	1:B:578:GLN:HB2	1.75	0.48
1:A:97:ARG:O	1:A:97:ARG:HG2	2.13	0.48
1:A:461:LYS:HA	1:A:464:LEU:HD12	1.94	0.48
1:A:128:VAL:HG11	1:A:176:TYR:CE2	2.48	0.48
1:A:457:ILE:HG13	1:A:458:SER:N	2.28	0.48
1:B:22:ARG:O	1:B:25:VAL:HB	2.13	0.48
1:B:541:TRP:HA	1:B:544:ARG:CZ	2.43	0.48
1:A:144:ARG:O	1:A:147:PHE:N	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:402:SER:HA	1:B:407:LEU:H	1.77	0.48
1:A:35:MET:HA	1:A:38:LEU:HD13	1.94	0.48
1:A:493:GLN:HE22	1:A:518:SER:N	2.10	0.48
1:A:496:TYR:CD1	1:A:497:PRO:HD2	2.48	0.48
1:B:24:VAL:O	1:B:28:ILE:HG13	2.14	0.48
1:B:461:LYS:HA	1:B:464:LEU:HD12	1.95	0.48
1:B:541:TRP:HA	1:B:544:ARG:NE	2.29	0.48
1:A:163:ALA:CB	1:A:167:ARG:HH12	2.27	0.48
1:B:201:ARG:HB3	5:B:961:HOH:O	2.13	0.48
1:B:225:ILE:HG22	1:B:372:LEU:CD2	2.37	0.47
1:B:465:VAL:O	1:B:469:LEU:HB2	2.13	0.47
1:A:134:TYR:HD2	1:A:135:LEU:HD22	1.76	0.47
1:A:541:TRP:CA	1:A:544:ARG:NH2	2.78	0.47
1:B:128:VAL:HG11	1:B:176:TYR:CE2	2.48	0.47
1:B:541:TRP:CA	1:B:544:ARG:HH21	2.26	0.47
1:A:167:ARG:HH21	1:A:197:GLU:HA	1.79	0.47
1:B:51:ARG:HD3	5:B:910:HOH:O	2.14	0.47
1:B:93:VAL:HG11	1:B:410:VAL:HB	1.96	0.47
1:B:428:TYR:O	1:B:590:MET:N	2.47	0.47
1:A:89:LEU:O	1:A:93:VAL:HG23	2.13	0.47
1:B:30:ALA:O	1:B:33:PRO:HD2	2.15	0.47
1:B:214:ILE:HA	1:B:218:GLU:HG3	1.96	0.47
1:B:493:GLN:HE22	1:B:518:SER:N	2.12	0.47
1:B:520:GLN:N	1:B:520:GLN:OE1	2.47	0.47
1:B:562:HIS:CD2	1:B:563:GLU:N	2.82	0.47
1:A:429:MET:HB2	1:A:433:GLU:OE2	2.15	0.47
1:A:113:THR:HG22	1:A:143:ASN:ND2	2.29	0.47
1:A:126:VAL:HG13	1:A:205:TYR:CD2	2.49	0.47
1:A:397:GLU:OE2	1:A:566:ARG:HD3	2.15	0.47
1:B:144:ARG:HB3	1:B:145:PRO:HD3	1.95	0.47
1:B:195:PRO:HD3	5:B:920:HOH:O	2.15	0.47
1:B:496:TYR:CD1	1:B:497:PRO:HD2	2.49	0.47
1:A:163:ALA:N	1:A:164:PRO:CD	2.77	0.47
1:B:97:ARG:HG2	1:B:97:ARG:O	2.15	0.47
1:B:163:ALA:HB3	1:B:164:PRO:HD3	1.97	0.47
1:B:186:TYR:O	1:B:190:ASN:ND2	2.48	0.47
1:A:30:ALA:O	1:A:33:PRO:HD2	2.15	0.47
1:A:60:LEU:CD1	1:A:61:GLU:H	2.27	0.47
1:A:479:LEU:HB2	1:A:507:ALA:HB1	1.96	0.47
1:B:541:TRP:CA	1:B:544:ARG:NH2	2.78	0.47
1:A:221:THR:HB	1:A:375:ILE:O	2.14	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:402:SER:HA	1:A:407:LEU:H	1.79	0.46
1:A:526:LEU:CD2	1:A:528:ASN:H	2.24	0.46
1:A:564:SER:HB3	5:A:972:HOH:O	2.15	0.46
1:B:103:ARG:O	1:B:106:GLU:HB2	2.15	0.46
1:B:137:GLN:HG3	1:B:156:ILE:HD13	1.97	0.46
1:B:163:ALA:N	1:B:164:PRO:CD	2.78	0.46
1:B:219:ALA:CA	5:B:975:HOH:O	2.63	0.46
1:B:457:ILE:HG13	1:B:458:SER:N	2.30	0.46
1:A:442:ILE:HG13	1:A:443:LYS:N	2.30	0.46
1:B:167:ARG:HH21	1:B:197:GLU:HA	1.79	0.46
1:B:454:VAL:CG2	1:B:557:ILE:HD11	2.39	0.46
1:B:522:GLU:OE1	1:B:537:ILE:HD12	2.15	0.46
1:A:51:ARG:O	1:A:55:GLU:HB2	2.16	0.46
1:A:128:VAL:HG11	1:A:176:TYR:HE2	1.81	0.46
1:A:530:THR:HB	1:A:533:GLN:NE2	2.31	0.46
1:B:423:LEU:HB2	1:B:585:ARG:HG2	1.97	0.46
1:A:108:LYS:HB3	1:A:390:MET:SD	2.55	0.46
1:B:126:VAL:HG13	1:B:205:TYR:CD2	2.50	0.46
1:B:588:LEU:N	1:B:588:LEU:HD12	2.30	0.46
1:B:138:ARG:NH2	1:B:510:GLY:O	2.40	0.46
1:B:573:GLY:C	1:B:575:SER:N	2.69	0.46
1:A:122:THR:HG21	5:A:946:HOH:O	2.15	0.46
1:A:211:VAL:HG22	1:A:390:MET:H	1.80	0.46
1:A:566:ARG:O	1:A:569:ASN:HB2	2.15	0.46
1:A:589:SER:O	1:A:592:ASP:HB2	2.15	0.46
1:B:128:VAL:HG11	1:B:176:TYR:HE2	1.80	0.46
1:B:211:VAL:CG2	1:B:390:MET:N	2.79	0.46
1:B:520:GLN:HA	1:B:523:VAL:HG22	1.97	0.46
1:A:493:GLN:HE22	1:A:518:SER:CA	2.29	0.46
1:A:573:GLY:C	1:A:575:SER:N	2.68	0.46
1:A:585:ARG:HH11	1:A:585:ARG:CG	2.28	0.46
1:B:565:ARG:HH12	1:B:572:ARG:HH12	1.64	0.46
1:B:566:ARG:O	1:B:569:ASN:HB2	2.15	0.46
1:B:585:ARG:HH11	1:B:585:ARG:CG	2.29	0.46
1:A:85:ASP:HA	1:A:88:LEU:HD12	1.98	0.45
1:A:522:GLU:OE1	1:A:537:ILE:HD12	2.16	0.45
1:A:536:LYS:O	1:A:540:ASP:HB2	2.16	0.45
1:A:573:GLY:C	1:A:575:SER:H	2.19	0.45
1:A:431:GLU:HG2	1:A:591:GLU:OE1	2.16	0.45
1:B:467:ASN:O	1:B:470:THR:HG22	2.16	0.45
1:A:186:TYR:O	1:A:190:ASN:ND2	2.48	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:LYS:O	1:B:170:TYR:HD2	2.00	0.45
1:B:530:THR:HB	1:B:533:GLN:NE2	2.31	0.45
1:B:573:GLY:C	1:B:575:SER:H	2.19	0.45
1:A:85:ASP:OD1	1:A:85:ASP:N	2.50	0.45
1:B:194:SER:HA	5:B:920:HOH:O	2.15	0.45
1:B:208:VAL:CG1	1:B:214:ILE:HD12	2.46	0.45
1:B:416:ARG:HG3	1:B:416:ARG:HH11	1.82	0.45
1:A:24:VAL:O	1:A:28:ILE:HG13	2.17	0.45
1:A:550:GLU:HB3	5:A:964:HOH:O	2.16	0.45
1:A:93:VAL:HG11	1:A:410:VAL:HB	1.98	0.45
1:A:423:LEU:HB2	1:A:585:ARG:HG2	1.98	0.45
1:A:578:GLN:HG3	5:A:949:HOH:O	2.16	0.45
1:B:108:LYS:HB3	1:B:390:MET:SD	2.57	0.45
1:B:479:LEU:HB2	1:B:507:ALA:HB1	1.97	0.45
1:B:487:GLU:HB2	5:B:980:HOH:O	2.16	0.45
1:A:53:ARG:HB3	1:A:58:GLU:OE2	2.15	0.45
1:A:463:GLU:OE2	3:A:905:SPD:H81	2.17	0.45
1:A:476:HIS:HD2	1:A:502:ILE:HD12	1.82	0.45
1:B:51:ARG:O	1:B:55:GLU:HB2	2.17	0.45
1:A:108:LYS:HG3	4:A:901:ADP:O3B	2.16	0.44
1:B:60:LEU:CG	1:B:61:GLU:H	2.30	0.44
1:A:427:VAL:HG11	1:A:590:MET:HE3	2.00	0.44
1:A:565:ARG:HH12	1:A:572:ARG:HH12	1.65	0.44
1:A:60:LEU:CD1	1:A:61:GLU:N	2.74	0.44
1:A:520:GLN:HA	1:A:523:VAL:HG22	1.98	0.44
1:B:387:LEU:HD22	1:B:388:ALA:N	2.32	0.44
1:A:60:LEU:CG	1:A:61:GLU:H	2.31	0.44
1:A:137:GLN:HG3	1:A:156:ILE:HD13	1.98	0.44
1:A:225:ILE:HG23	1:A:372:LEU:HD12	2.00	0.44
1:B:469:LEU:HD13	1:B:502:ILE:HD11	1.99	0.44
1:A:21:MET:HA	1:A:24:VAL:HG23	2.00	0.44
1:A:138:ARG:NH1	1:A:139:ASP:OD1	2.49	0.44
1:A:425:ASP:HB3	1:A:588:LEU:CD1	2.45	0.44
1:B:13:ARG:HD3	1:B:13:ARG:C	2.38	0.44
1:B:425:ASP:HB3	1:B:588:LEU:CD1	2.42	0.44
1:A:223:LEU:CD2	1:A:372:LEU:HD21	2.48	0.44
1:B:184:PHE:O	1:B:188:ARG:HG3	2.17	0.44
1:B:53:ARG:HA	1:B:56:LYS:CE	2.44	0.43
1:B:202:LYS:HG3	5:B:984:HOH:O	2.18	0.43
1:B:211:VAL:HG22	1:B:390:MET:H	1.83	0.43
1:B:224:ILE:O	1:B:372:LEU:HA	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:400:GLU:HA	1:B:403:SER:OG	2.18	0.43
1:A:184:PHE:O	1:A:188:ARG:HG3	2.18	0.43
1:A:400:GLU:HA	1:A:403:SER:OG	2.19	0.43
1:A:416:ARG:HG3	1:A:416:ARG:HH11	1.83	0.43
1:A:427:VAL:HG11	1:A:590:MET:CE	2.49	0.43
1:B:536:LYS:O	1:B:540:ASP:HB2	2.17	0.43
1:A:93:VAL:HB	1:A:100:ALA:HB2	2.00	0.43
1:B:546:ASP:O	1:B:550:GLU:HG3	2.18	0.43
1:B:590:MET:O	1:B:594:LEU:HG	2.18	0.43
1:A:166:LYS:O	1:A:170:TYR:HD2	2.01	0.43
1:A:483:PHE:HB3	1:A:486:ASN:HD22	1.83	0.43
1:B:522:GLU:OE1	1:B:537:ILE:HG23	2.19	0.43
1:A:557:ILE:HG13	1:A:557:ILE:O	2.19	0.43
1:B:163:ALA:CB	1:B:167:ARG:HH12	2.31	0.43
1:B:397:GLU:OE1	1:B:397:GLU:N	2.43	0.43
1:A:375:ILE:HG22	1:B:188:ARG:HG2	2.01	0.43
1:A:467:ASN:O	1:A:470:THR:HG22	2.18	0.43
1:A:163:ALA:HB1	1:A:167:ARG:HH12	1.84	0.43
1:B:138:ARG:NH1	1:B:139:ASP:OD1	2.45	0.43
1:B:493:GLN:HE22	1:B:518:SER:CA	2.32	0.43
1:A:22:ARG:O	1:A:25:VAL:HB	2.19	0.42
1:B:117:TYR:HE1	1:B:150:LEU:HB3	1.84	0.42
1:A:63:LEU:H	1:A:63:LEU:CD2	2.25	0.42
1:A:493:GLN:NE2	1:A:518:SER:O	2.51	0.42
1:B:129:VAL:HG12	1:B:214:ILE:HD13	2.01	0.42
1:B:18:LEU:HD21	1:B:413:PRO:CD	2.46	0.42
1:B:218:GLU:C	1:B:220:ARG:H	2.20	0.42
1:B:493:GLN:NE2	1:B:518:SER:O	2.51	0.42
1:B:557:ILE:HG13	1:B:557:ILE:O	2.19	0.42
1:A:25:VAL:HG11	1:A:85:ASP:HB2	2.02	0.42
1:A:208:VAL:CG1	1:A:214:ILE:HD12	2.49	0.42
1:A:387:LEU:HD22	1:A:388:ALA:N	2.35	0.42
1:A:517:GLY:O	1:A:541:TRP:NE1	2.51	0.42
1:A:565:ARG:N	5:A:972:HOH:O	2.52	0.42
1:B:476:HIS:HD2	1:B:502:ILE:HD12	1.84	0.42
1:A:13:ARG:HD3	1:A:13:ARG:C	2.39	0.42
1:A:393:THR:HB	1:A:566:ARG:HG2	2.02	0.42
1:A:423:LEU:H	1:A:423:LEU:HD22	1.84	0.42
1:B:25:VAL:HG11	1:B:85:ASP:HB2	2.01	0.42
1:B:68:PHE:CE2	1:B:114:LEU:HD13	2.54	0.42
1:A:144:ARG:HB3	1:A:145:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:460:GLU:OE1	3:A:905:SPD:H32	2.20	0.42
1:B:132:ASN:ND2	1:B:135:LEU:HD23	2.34	0.42
1:B:561:ARG:NH1	1:B:568:ASP:OD2	2.53	0.42
1:B:52:ALA:O	1:B:56:LYS:HG3	2.20	0.42
1:B:83:HIS:CE1	1:B:114:LEU:HD21	2.54	0.42
1:A:187:LEU:HD23	1:A:187:LEU:HA	1.85	0.42
1:A:225:ILE:HG21	1:A:372:LEU:HD12	2.01	0.42
1:A:426:LEU:HD12	1:A:587:TYR:HE1	1.85	0.42
1:A:519:TRP:HB2	1:A:537:ILE:HG22	2.02	0.42
1:A:546:ASP:O	1:A:550:GLU:HG3	2.19	0.42
1:A:223:LEU:HD21	1:A:372:LEU:HD21	2.02	0.42
1:A:505:ASN:HB3	1:A:506:MET:HE2	2.01	0.42
1:B:94:LEU:HD22	1:B:207:LEU:HD21	2.01	0.42
1:A:108:LYS:HB3	1:A:390:MET:CE	2.49	0.41
1:B:469:LEU:CD2	1:B:474:ILE:HB	2.48	0.41
1:A:89:LEU:HA	1:A:89:LEU:HD12	1.78	0.41
1:A:18:LEU:HD21	1:A:413:PRO:CD	2.44	0.41
1:A:117:TYR:HE1	1:A:150:LEU:HB3	1.85	0.41
1:B:85:ASP:N	1:B:85:ASP:OD1	2.54	0.41
1:B:470:THR:HB	1:B:476:HIS:HE1	1.85	0.41
1:A:461:LYS:HG3	1:A:560:GLU:OE2	2.21	0.41
1:A:493:GLN:C	1:A:495:GLY:H	2.24	0.41
1:B:21:MET:HA	1:B:24:VAL:HG23	2.01	0.41
1:B:85:ASP:HA	1:B:88:LEU:HD12	2.02	0.41
1:B:166:LYS:NZ	1:B:185:ASP:OD2	2.49	0.41
1:A:87:GLN:O	1:A:111:THR:HG23	2.20	0.41
1:A:170:TYR:O	1:A:201:ARG:NH2	2.52	0.41
1:B:416:ARG:HD3	5:B:957:HOH:O	2.20	0.41
1:B:435:ILE:O	1:B:439:ILE:HG23	2.20	0.41
1:A:43:LEU:HD22	1:A:77:ARG:NH1	2.36	0.41
1:A:60:LEU:C	1:A:62:ASN:H	2.24	0.41
1:A:225:ILE:HG23	1:A:372:LEU:HB2	2.03	0.41
1:B:60:LEU:C	1:B:62:ASN:H	2.24	0.41
1:B:93:VAL:HB	1:B:100:ALA:HB2	2.03	0.41
1:B:483:PHE:HB3	1:B:486:ASN:HD22	1.85	0.41
1:B:519:TRP:HB2	1:B:537:ILE:HG22	2.02	0.41
1:A:97:ARG:HA	1:A:387:LEU:O	2.21	0.41
1:A:195:PRO:HA	1:A:198:ARG:HD2	2.02	0.41
1:A:435:ILE:O	1:A:439:ILE:HG23	2.21	0.41
1:A:541:TRP:N	1:A:544:ARG:HH21	2.18	0.41
1:A:585:ARG:CG	1:A:585:ARG:NH1	2.82	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:214:ILE:HG22	1:B:215:LEU:HD23	2.02	0.41
1:B:423:LEU:HD22	1:B:423:LEU:H	1.84	0.41
1:B:592:ASP:C	1:B:594:LEU:N	2.74	0.41
1:A:216:ILE:HG21	1:A:566:ARG:HH12	1.86	0.41
1:A:504:THR:N	1:A:507:ALA:HB2	2.33	0.41
1:B:82:ARG:HD2	5:B:938:HOH:O	2.21	0.41
1:B:163:ALA:HB1	1:B:167:ARG:HH12	1.86	0.41
1:B:195:PRO:HA	1:B:198:ARG:HD2	2.03	0.41
1:B:457:ILE:CG2	1:B:560:GLU:HG3	2.44	0.41
1:B:541:TRP:N	1:B:544:ARG:HH21	2.19	0.41
1:A:52:ALA:O	1:A:56:LYS:HG3	2.21	0.40
1:A:470:THR:HB	1:A:476:HIS:HE1	1.86	0.40
1:B:25:VAL:CG1	1:B:85:ASP:HB2	2.51	0.40
1:B:31:MET:CE	1:B:66:GLU:HG3	2.51	0.40
1:B:108:LYS:HB3	1:B:390:MET:CE	2.51	0.40
1:B:146:LEU:HD23	1:B:146:LEU:O	2.21	0.40
1:A:469:LEU:CD2	1:A:474:ILE:HB	2.48	0.40
1:B:467:ASN:CA	1:B:470:THR:HG22	2.48	0.40
1:A:60:LEU:O	1:A:63:LEU:HD23	2.22	0.40
1:A:187:LEU:HD22	1:B:187:LEU:HD22	2.04	0.40
1:A:567:ILE:C	1:A:569:ASN:H	2.25	0.40
1:B:470:THR:HB	1:B:476:HIS:CE1	2.57	0.40
1:A:555:HIS:HE2	1:A:557:ILE:CG2	2.35	0.40
1:B:43:LEU:O	1:B:46:LYS:CB	2.67	0.40
1:A:101:GLU:HB3	1:A:411:VAL:HA	2.03	0.40
1:A:467:ASN:CA	1:A:470:THR:HG22	2.49	0.40
1:A:574:ARG:NH1	5:A:906:HOH:O	2.53	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	434/471 (92%)	380 (88%)	49 (11%)	5 (1%)	13	48
1	B	436/471 (93%)	382 (88%)	47 (11%)	7 (2%)	9	40
All	All	870/942 (92%)	762 (88%)	96 (11%)	12 (1%)	11	43

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	396	THR
1	A	396	THR
1	B	219	ALA
1	A	150	LEU
1	B	221	THR
1	B	545	HIS
1	A	61	GLU
1	A	545	HIS
1	B	61	GLU
1	B	150	LEU
1	B	497	PRO
1	A	497	PRO

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	359/388 (92%)	338 (94%)	21 (6%)	20	55
1	B	361/388 (93%)	339 (94%)	22 (6%)	18	53
All	All	720/776 (93%)	677 (94%)	43 (6%)	19	53

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	40	ASP
1	A	63	LEU
1	A	86	VAL

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Mol	Chain	Res	Type
1	A	130	THR
1	A	153	THR
1	A	173	ASP
1	A	193	PHE
1	A	201	ARG
1	A	207	LEU
1	A	210	GLU
1	A	211	VAL
1	A	223	LEU
1	A	387	LEU
1	A	423	LEU
1	A	436	GLN
1	A	477	ASN
1	A	480	ASN
1	A	506	MET
1	A	577	ARG
1	A	585	ARG
1	B	13	ARG
1	B	40	ASP
1	B	63	LEU
1	B	86	VAL
1	B	130	THR
1	B	135	LEU
1	B	153	THR
1	B	162	PRO
1	B	173	ASP
1	B	193	PHE
1	B	207	LEU
1	B	210	GLU
1	B	211	VAL
1	B	376	THR
1	B	387	LEU
1	B	423	LEU
1	B	436	GLN
1	B	477	ASN
1	B	480	ASN
1	B	506	MET
1	B	577	ARG
1	B	585	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	14	ASN
1	A	26	ASN
1	A	127	HIS
1	A	143	ASN
1	A	415	ASN
1	A	486	ASN
1	A	493	GLN
1	A	528	ASN
1	A	562	HIS
1	B	14	ASN
1	B	26	ASN
1	B	127	HIS
1	B	143	ASN
1	B	415	ASN
1	B	486	ASN
1	B	493	GLN
1	B	528	ASN
1	B	533	GLN
1	B	562	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 2 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	$\# Z > 2$
4	ADP	A	901	2	24,29,29	1.83	7 (29%)	29,45,45	1.78	6 (20%)
3	SPD	A	905	-	9,9,9	0.72	0	8,8,8	0.57	0
3	SPD	B	906	-	9,9,9	0.72	0	8,8,8	0.50	0
4	ADP	B	902	-	24,29,29	1.72	7 (29%)	29,45,45	1.75	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
4	ADP	A	901	2	-	3/12/32/32	0/3/3/3
3	SPD	A	905	-	-	1/7/7/7	-
3	SPD	B	906	-	-	2/7/7/7	-
4	ADP	B	902	-	-	5/12/32/32	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	ADP	O4'-C1'	4.48	1.47	1.41
4	B	902	ADP	O4'-C1'	4.24	1.47	1.41
4	B	902	ADP	C4-N3	3.13	1.40	1.35
4	A	901	ADP	C2-N3	3.02	1.37	1.32
4	A	901	ADP	C2-N1	2.82	1.39	1.33
4	B	902	ADP	C2-N3	2.68	1.36	1.32
4	A	901	ADP	C4-N3	2.60	1.39	1.35
4	B	902	ADP	C2'-C1'	-2.42	1.50	1.53
4	A	901	ADP	C2'-C1'	-2.32	1.50	1.53
4	B	902	ADP	PA-O2A	-2.20	1.45	1.55
4	A	901	ADP	PA-O2A	-2.15	1.45	1.55
4	B	902	ADP	C2-N1	2.14	1.37	1.33
4	A	901	ADP	PB-O2B	2.10	1.62	1.54
4	B	902	ADP	PB-O2B	2.06	1.62	1.54

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	901	ADP	N3-C2-N1	-6.81	118.03	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	902	ADP	N3-C2-N1	-6.05	119.22	128.68
4	B	902	ADP	C4-C5-N7	-3.61	105.63	109.40
4	B	902	ADP	C2'-C3'-C4'	3.42	109.28	102.64
4	A	901	ADP	C2'-C3'-C4'	3.09	108.64	102.64
4	A	901	ADP	C4-C5-N7	-2.89	106.38	109.40
4	A	901	ADP	C3'-C2'-C1'	2.58	104.86	100.98
4	B	902	ADP	O4'-C1'-C2'	2.48	110.55	106.93
4	B	902	ADP	C2-N1-C6	2.12	122.38	118.75
4	A	901	ADP	C2-N1-C6	2.11	122.36	118.75
4	A	901	ADP	O5'-C5'-C4'	-2.07	101.85	108.99

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	902	ADP	O4'-C4'-C5'-O5'
4	A	901	ADP	C3'-C4'-C5'-O5'
4	B	902	ADP	C3'-C4'-C5'-O5'
4	A	901	ADP	O4'-C4'-C5'-O5'
3	B	906	SPD	C7-C8-C9-N10
4	B	902	ADP	PA-O3A-PB-O2B
4	A	901	ADP	PB-O3A-PA-O1A
4	B	902	ADP	PB-O3A-PA-O1A
3	A	905	SPD	C2-C3-C4-C5
3	B	906	SPD	C2-C3-C4-C5
4	B	902	ADP	PA-O3A-PB-O3B

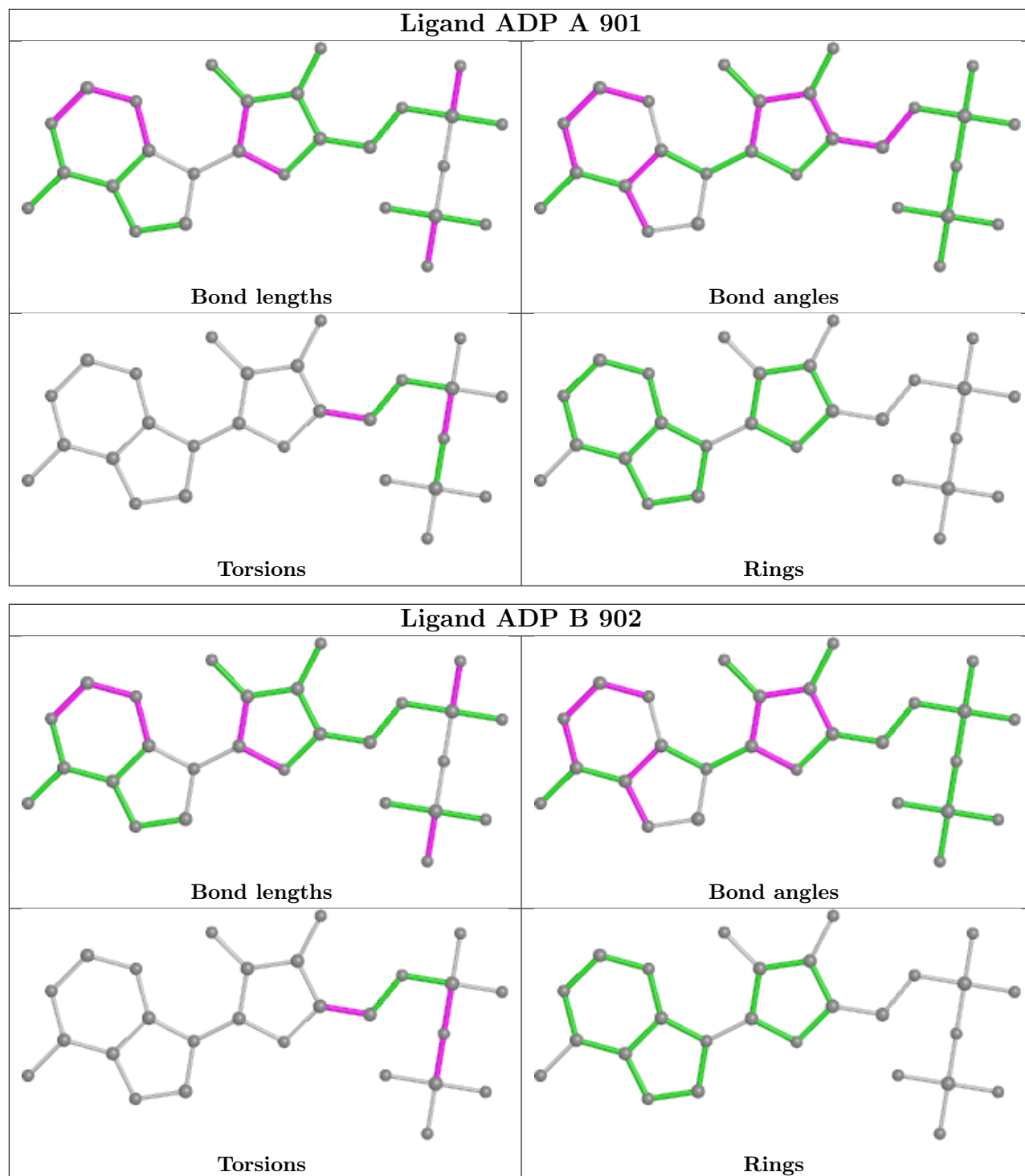
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	901	ADP	1	0
3	A	905	SPD	4	0
4	B	902	ADP	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

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

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	438/471 (92%)	0.02	3 (0%) 87 69	46, 78, 128, 152	0
1	B	440/471 (93%)	0.02	4 (0%) 84 63	48, 78, 129, 152	0
All	All	878/942 (93%)	0.02	7 (0%) 86 65	46, 78, 129, 152	0

All (7) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	530	THR	3.3
1	B	465	VAL	3.2
1	A	474	ILE	2.7
1	A	11	GLY	2.1
1	B	427	VAL	2.1
1	A	395	ASP	2.1
1	B	193	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](#)

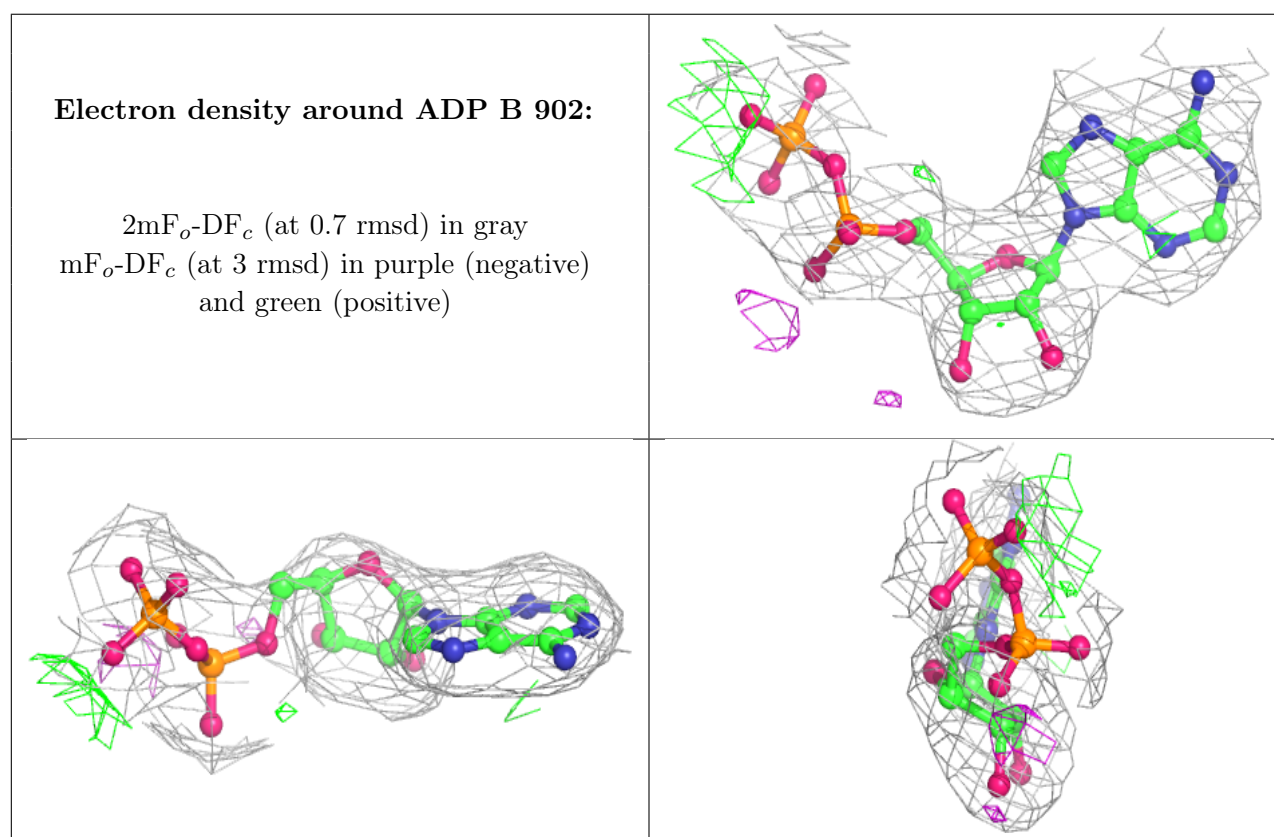
There are no monosaccharides in this entry.

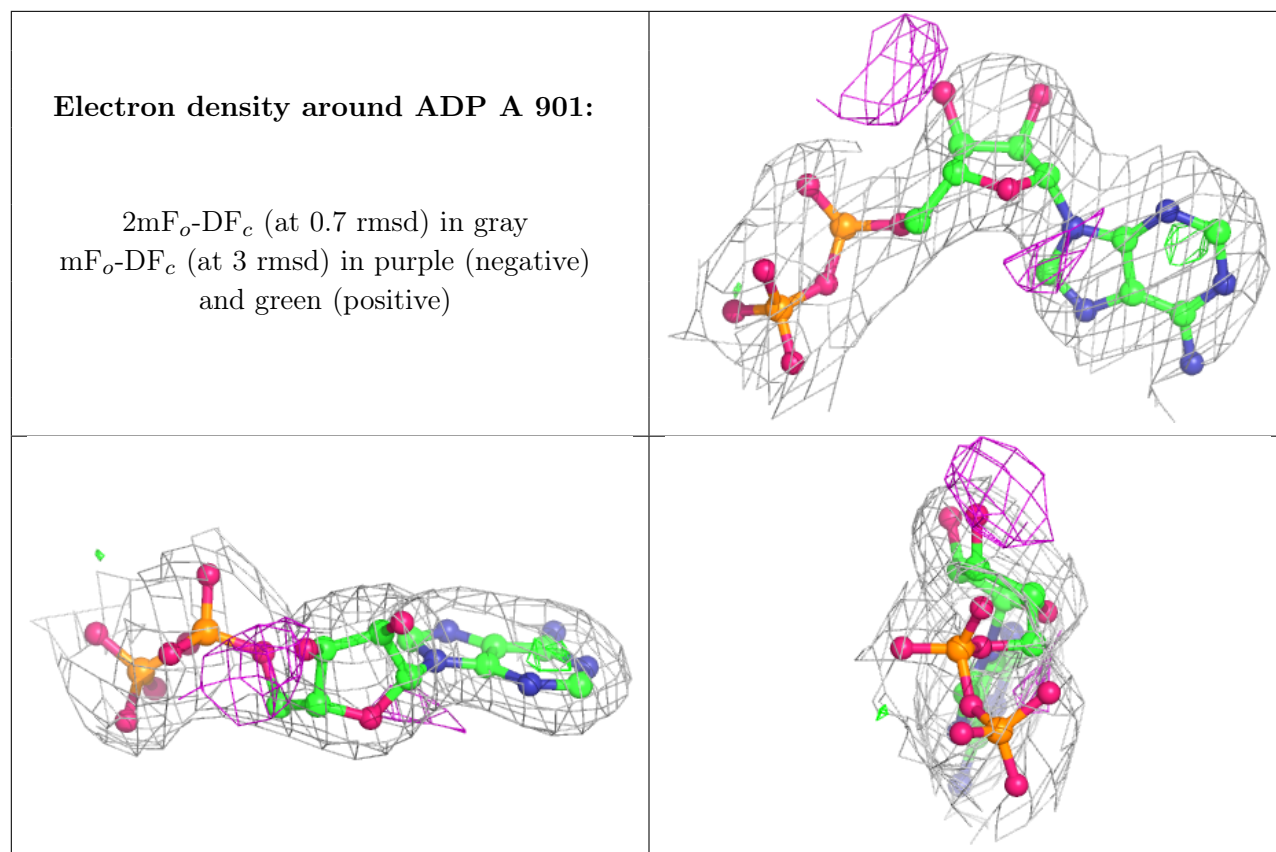
6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	SPD	B	906	10/10	0.67	0.46	74,80,82,82	0
3	SPD	A	905	10/10	0.69	0.50	76,78,80,81	0
4	ADP	B	902	27/27	0.93	0.22	64,70,71,72	0
4	ADP	A	901	27/27	0.96	0.21	57,63,68,72	0
2	MG	A	903	1/1	0.97	0.23	23,23,23,23	0
2	MG	B	904	1/1	0.98	0.36	41,41,41,41	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.