



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2026 – 05:46 AM UTC

PDB ID : 2ONJ / pdb_00002onj
Title : Structure of the multidrug ABC transporter Sav1866 from *S. aureus* in complex with AMP-PNP
Authors : Dawson, R.J.P.; Locher, K.P.
Deposited on : 2007-01-24
Resolution : 3.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

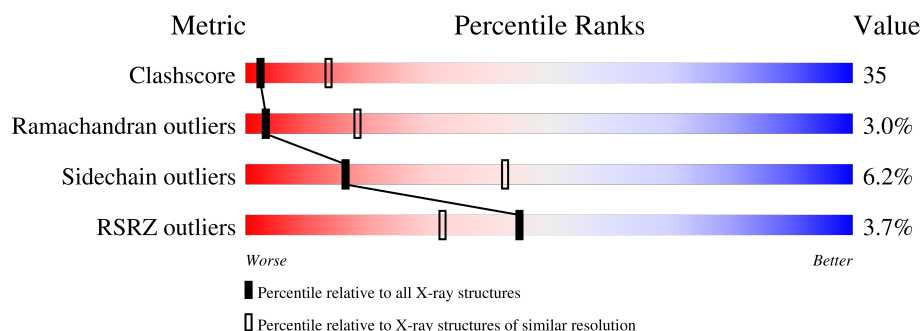
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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))
Clashscore	190562	1022 (3.44-3.36)
Ramachandran outliers	187476	1012 (3.44-3.36)
Sidechain outliers	187428	1012 (3.44-3.36)
RSRZ outliers	180081	1001 (3.44-3.36)

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	578	3% 45% 47% 8%
1	B	578	4% 43% 50% 7%

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	ANP	A	701	-	X	-	-
3	ANP	B	700	-	X	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 9254 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.

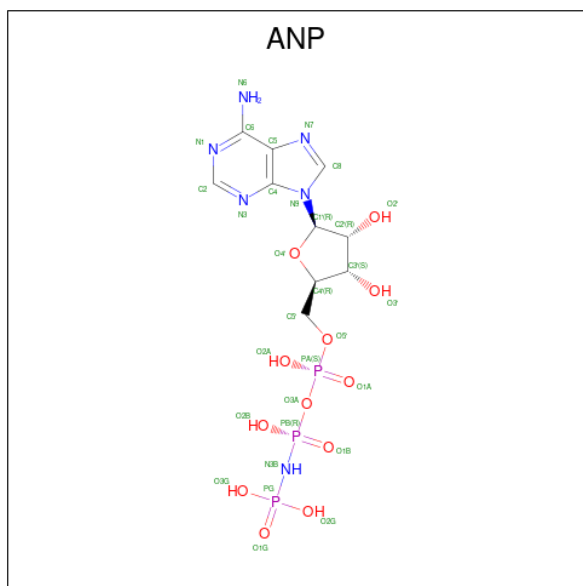
- Molecule 1 is a protein called Multidrug export ATP-binding/permease protein SAV1866.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	578	Total	C	N	O	S	0	0	0
			4584	2967	774	834	9			
1	B	578	Total	C	N	O	S	0	0	0
			4584	2967	774	834	9			

- Molecule 2 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	2	Total	Na	0	0
			2	2		
2	B	2	Total	Na	0	0
			2	2		

- Molecule 3 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
3	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

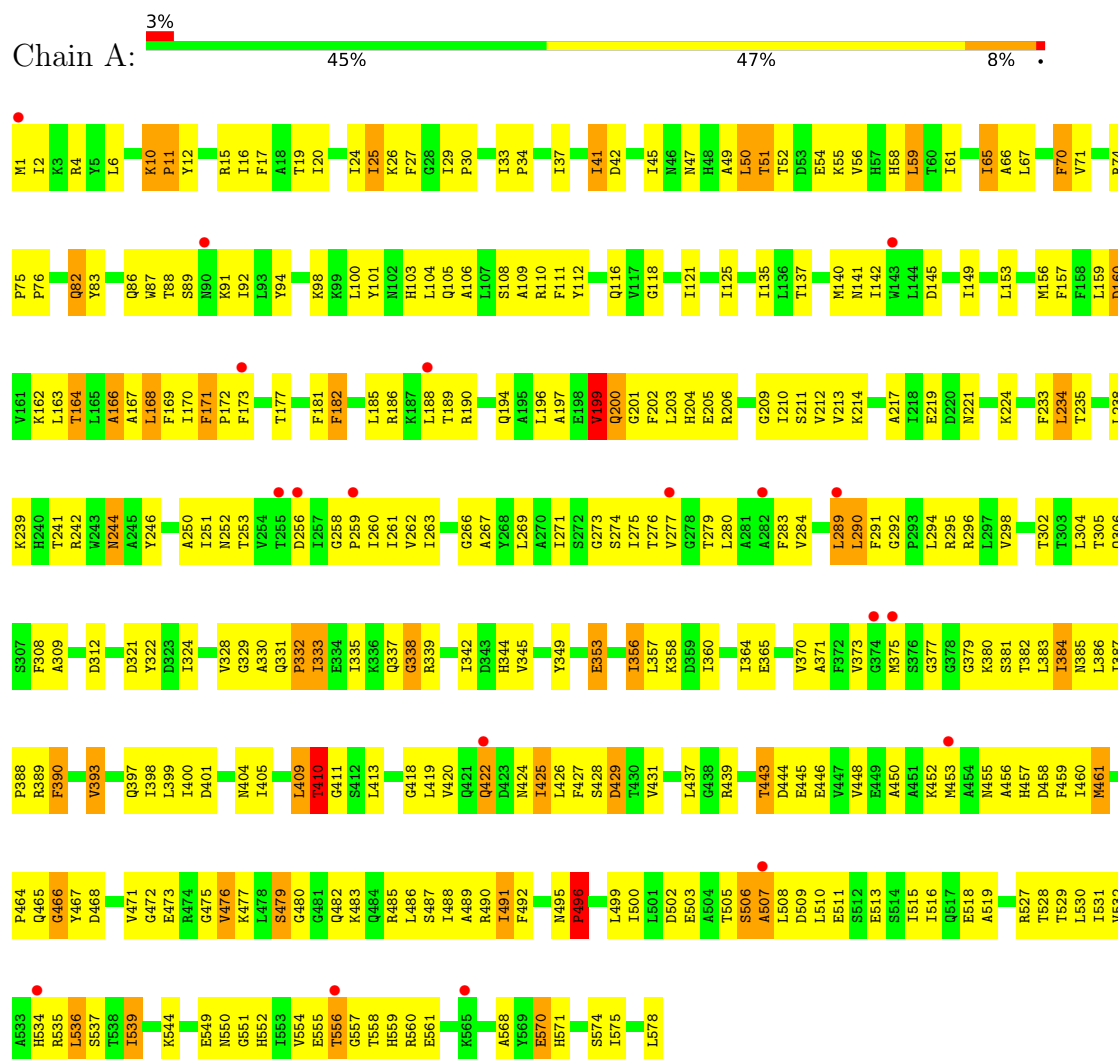
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	10	Total	O	0	0
			10	10		
4	B	10	Total	O	0	0
			10	10		

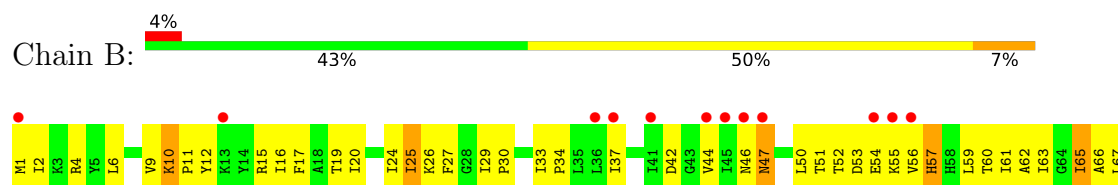
3 Residue-property plots [i](#)

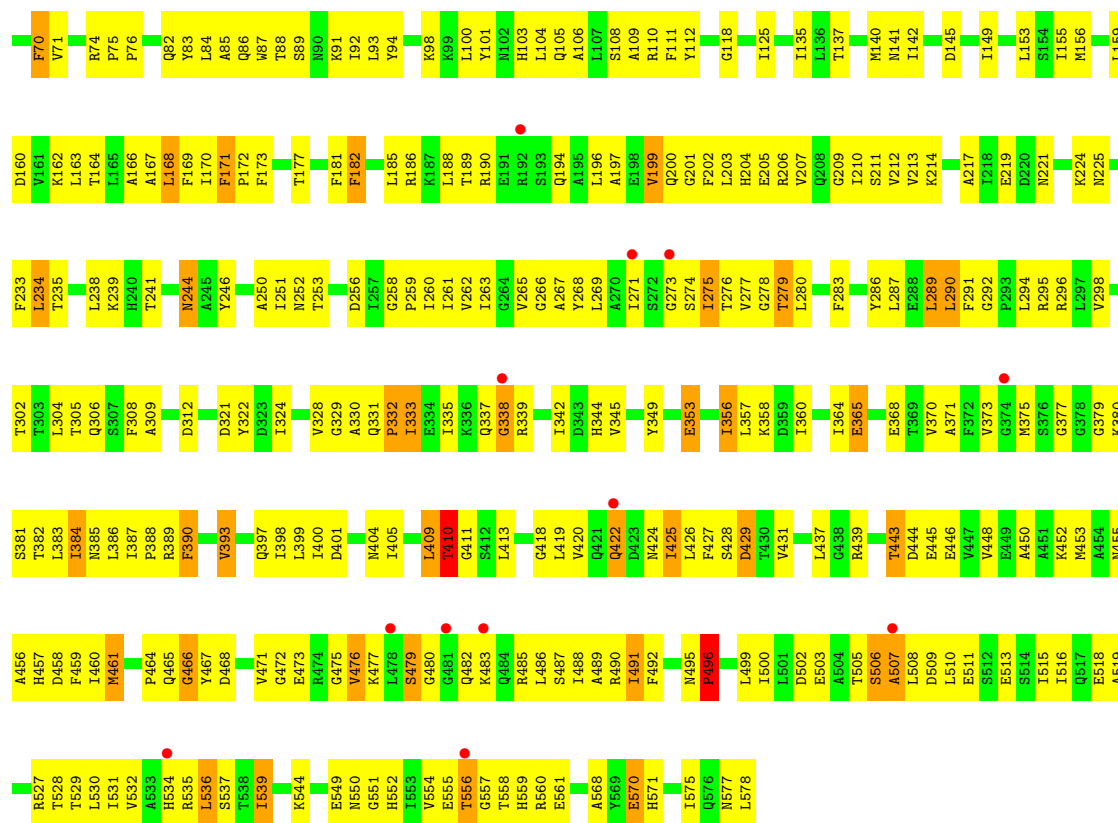
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Multidrug export ATP-binding/permease protein SAV1866



- Molecule 1: Multidrug export ATP-binding/permease protein SAV1866





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	160.96Å 104.45Å 181.39Å 90.00° 98.23° 90.00°	Depositor
Resolution (Å)	20.00 – 3.40 20.00 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-3.40) 99.3 (20.00-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.58 (at 3.39Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.254 , 0.278 0.245 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	101.1	Xtriage
Anisotropy	0.613	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.24 , 77.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9254	wwPDB-VP
Average B, all atoms (Å ²)	124.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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: NA, ANP

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	0.53	0/4669	1.01	28/6328 (0.4%)
1	B	0.53	0/4669	1.02	30/6328 (0.5%)
All	All	0.53	0/9338	1.02	58/12656 (0.5%)

There are no bond length outliers.

All (58) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	422	GLN	OE1-CD-NE2	-9.80	112.80	122.60
1	B	422	GLN	OE1-CD-NE2	-9.79	112.81	122.60
1	B	61	ILE	N-CA-C	-8.87	104.84	113.53
1	A	507	ALA	N-CA-C	6.99	121.41	113.02
1	B	507	ALA	N-CA-C	6.83	121.22	113.02
1	B	422	GLN	CG-CD-NE2	6.68	126.42	116.40
1	A	476	VAL	N-CA-C	6.66	120.36	111.17
1	A	422	GLN	CG-CD-NE2	6.66	126.39	116.40
1	B	476	VAL	N-CA-C	6.61	120.29	111.17
1	B	409	LEU	N-CA-C	-6.57	98.55	109.46
1	A	557	GLY	N-CA-C	6.54	120.57	110.88
1	B	333	ILE	N-CA-C	6.53	117.52	107.99
1	B	53	ASP	N-CA-C	-6.52	106.28	114.56
1	B	344	HIS	O-C-N	-6.44	115.13	122.86
1	B	234	LEU	CD1-CG-CD2	6.43	124.95	110.80
1	A	333	ILE	N-CA-C	6.42	117.36	107.99
1	A	262	VAL	N-CA-C	-6.39	104.03	111.00
1	B	557	GLY	N-CA-C	6.39	120.34	110.88
1	A	419	LEU	N-CA-C	6.39	118.83	108.41
1	A	409	LEU	N-CA-C	-6.39	98.85	109.46
1	B	98	LYS	N-CA-C	-6.38	104.32	111.28
1	B	419	LEU	N-CA-C	6.35	118.77	108.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	98	LYS	N-CA-C	-6.32	104.39	111.28
1	B	425	ILE	N-CA-C	6.31	118.75	108.97
1	A	425	ILE	N-CA-C	6.29	118.72	108.97
1	B	17	PHE	N-CA-C	-6.20	104.44	111.07
1	A	166	ALA	N-CA-C	-6.16	104.83	112.90
1	B	47	ASN	N-CA-C	-6.16	104.83	112.90
1	B	234	LEU	CB-CA-C	-6.14	101.50	110.96
1	A	17	PHE	N-CA-C	-6.13	104.51	111.07
1	A	51	THR	N-CA-C	-6.09	102.07	110.35
1	B	57	HIS	N-CA-C	-6.01	105.86	113.43
1	B	70	PHE	N-CA-C	5.96	118.57	111.71
1	A	70	PHE	N-CA-C	5.94	118.54	111.71
1	B	279	THR	N-CA-C	-5.87	104.80	111.14
1	A	234	LEU	CD1-CG-CD2	5.79	123.53	110.80
1	A	59	LEU	N-CA-C	-5.67	105.02	111.14
1	B	275	ILE	N-CA-C	5.59	117.11	108.44
1	A	164	THR	N-CA-C	-5.58	105.73	112.54
1	B	531	ILE	N-CA-C	5.53	115.96	107.77
1	A	50	LEU	N-CA-C	5.50	117.38	108.41
1	A	531	ILE	N-CA-C	5.46	115.86	107.77
1	B	390	PHE	N-CA-C	-5.45	106.47	113.23
1	A	390	PHE	N-CA-C	-5.43	106.50	113.23
1	B	199	VAL	N-CA-C	-5.39	105.28	110.72
1	A	199	VAL	N-CA-C	-5.26	105.41	110.72
1	A	529	THR	N-CA-C	5.24	117.45	108.90
1	B	62	ALA	N-CA-C	-5.21	106.07	112.90
1	A	496	PRO	CA-C-N	5.17	124.67	119.19
1	A	496	PRO	C-N-CA	5.17	124.67	119.19
1	B	529	THR	N-CA-C	5.14	117.29	108.90
1	B	496	PRO	CA-C-N	5.12	124.62	119.19
1	B	496	PRO	C-N-CA	5.12	124.62	119.19
1	A	344	HIS	O-C-N	-5.09	116.75	122.86
1	B	458	ASP	N-CA-C	5.08	116.50	110.97
1	A	458	ASP	N-CA-C	5.07	116.50	110.97
1	B	333	ILE	CB-CA-C	-5.04	104.07	110.98
1	A	333	ILE	CB-CA-C	-5.02	104.10	110.98

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	4584	0	4713	352	0
1	B	4584	0	4714	363	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
3	A	31	0	12	8	0
3	B	31	0	12	9	0
4	A	10	0	0	3	0
4	B	10	0	0	3	0
All	All	9254	0	9451	652	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 (652) 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:15:ARG:H	1:A:15:ARG:HD2	1.05	1.19
1:A:52:THR:HA	1:A:55:LYS:HE2	1.18	1.17
1:A:94:TYR:CD1	1:B:234:LEU:HD21	1.79	1.16
1:A:234:LEU:HD21	1:B:94:TYR:CD1	1.84	1.13
1:A:94:TYR:CD1	1:B:234:LEU:CD2	2.36	1.08
1:B:15:ARG:H	1:B:15:ARG:HD2	1.05	1.07
1:A:234:LEU:CD2	1:B:94:TYR:CD1	2.38	1.07
1:B:276:THR:HG22	1:B:278:GLY:H	1.23	1.02
1:B:44:VAL:HG13	1:B:55:LYS:HB2	1.42	1.01
1:A:94:TYR:CG	1:B:234:LEU:HD21	1.95	1.00
1:B:156:MET:HB3	1:B:164:THR:HG22	1.45	0.98
1:A:234:LEU:HD21	1:B:94:TYR:CG	2.00	0.95
1:A:234:LEU:HD21	1:B:94:TYR:HB2	1.48	0.93
1:A:276:THR:HG22	1:A:277:VAL:H	1.31	0.92
1:A:263:ILE:HG22	1:B:63:ILE:HD11	1.50	0.91
1:A:75:PRO:HB2	1:A:76:PRO:HD3	1.52	0.91
1:A:505:THR:HG21	1:A:513:GLU:OE2	1.70	0.91
1:B:505:THR:HG21	1:B:513:GLU:OE2	1.71	0.91
1:A:335:ILE:HD13	1:A:400:ILE:HG21	1.54	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:ARG:HD2	1:A:15:ARG:N	1.87	0.89
1:B:75:PRO:HB2	1:B:76:PRO:HD3	1.53	0.88
1:B:335:ILE:HD13	1:B:400:ILE:HG21	1.54	0.88
1:A:234:LEU:HD21	1:B:94:TYR:CB	2.04	0.87
1:B:15:ARG:HD2	1:B:15:ARG:N	1.87	0.86
1:B:51:THR:HB	1:B:54:GLU:HG2	1.59	0.84
1:A:455:ASN:HD22	1:A:515:ILE:HG21	1.42	0.84
1:B:455:ASN:HD22	1:B:515:ILE:HG21	1.43	0.83
1:A:204:HIS:HD2	1:B:204:HIS:ND1	1.77	0.82
1:A:558:THR:HB	1:A:561:GLU:HG3	1.62	0.82
1:A:162:LYS:H	1:A:162:LYS:HD3	1.44	0.81
1:A:234:LEU:HD23	1:B:94:TYR:CD1	2.15	0.81
1:B:428:SER:HB2	1:B:473:GLU:HA	1.65	0.80
1:A:275:ILE:HG22	1:A:276:THR:H	1.47	0.79
1:B:558:THR:HB	1:B:561:GLU:HG3	1.62	0.79
1:A:94:TYR:HB2	1:B:234:LEU:HD21	1.63	0.79
1:B:209:GLY:O	1:B:212:VAL:HG12	1.84	0.78
1:B:331:GLN:O	1:B:333:ILE:HG13	1.83	0.78
1:A:234:LEU:CD2	1:B:94:TYR:HD1	1.96	0.78
1:A:94:TYR:CB	1:B:234:LEU:HD21	2.13	0.77
1:A:331:GLN:O	1:A:333:ILE:HG13	1.84	0.77
1:A:353:GLU:HG2	1:B:464:PRO:HG3	1.65	0.77
1:A:387:ILE:C	1:A:389:ARG:H	1.93	0.77
1:A:397:GLN:HE21	1:A:399:LEU:HD11	1.50	0.76
1:B:461:MET:HE2	1:B:461:MET:HA	1.67	0.76
1:B:397:GLN:HE21	1:B:399:LEU:HD11	1.50	0.76
1:A:364:ILE:HD13	1:A:530:LEU:HD21	1.68	0.76
1:A:209:GLY:O	1:A:212:VAL:HG12	1.85	0.76
1:A:142:ILE:HD11	1:A:304:LEU:HD11	1.67	0.76
1:B:332:PRO:HD3	1:B:409:LEU:HD12	1.67	0.76
1:B:364:ILE:HD13	1:B:530:LEU:HD21	1.67	0.76
1:A:332:PRO:HD3	1:A:409:LEU:HD12	1.68	0.75
1:B:142:ILE:HD11	1:B:304:LEU:HD11	1.68	0.75
1:B:162:LYS:H	1:B:162:LYS:HD3	1.52	0.75
1:A:461:MET:HE2	1:A:461:MET:HA	1.68	0.74
1:B:276:THR:HG22	1:B:278:GLY:N	2.00	0.74
1:B:387:ILE:C	1:B:389:ARG:H	1.92	0.74
1:B:381:SER:OG	4:B:808:HOH:O	2.06	0.74
1:A:428:SER:HB2	1:A:473:GLU:HA	1.68	0.74
1:B:410:THR:HG22	1:B:411:GLY:N	2.02	0.73
1:A:94:TYR:HD1	1:B:234:LEU:CD2	2.02	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:410:THR:HG22	1:A:411:GLY:N	2.03	0.73
1:B:534:HIS:O	1:B:536:LEU:HD23	1.88	0.72
1:A:534:HIS:O	1:A:536:LEU:HD23	1.89	0.72
1:B:262:VAL:HG11	1:B:287:LEU:HD21	1.71	0.72
1:A:204:HIS:CD2	1:B:204:HIS:ND1	2.57	0.72
1:A:160:ASP:O	1:A:164:THR:HG23	1.90	0.71
1:B:459:PHE:CE1	1:B:482:GLN:HG2	2.24	0.71
1:A:473:GLU:O	1:A:476:VAL:HG23	1.90	0.71
1:B:387:ILE:HB	1:B:388:PRO:HD3	1.73	0.71
1:A:94:TYR:CD1	1:B:234:LEU:HD23	2.24	0.71
1:A:387:ILE:HB	1:A:388:PRO:HD3	1.73	0.70
1:A:459:PHE:CE1	1:A:482:GLN:HG2	2.26	0.70
1:B:356:ILE:CD1	3:B:700:ANP:H1'	2.22	0.69
1:B:473:GLU:O	1:B:476:VAL:HG23	1.92	0.69
1:A:338:GLY:HA3	1:A:528:THR:OG1	1.93	0.68
1:B:431:VAL:HG11	1:B:460:ILE:HD13	1.75	0.68
1:B:338:GLY:HA3	1:B:528:THR:OG1	1.92	0.68
1:A:276:THR:HG22	1:A:277:VAL:N	2.07	0.68
1:B:42:ASP:HA	1:B:46:ASN:HB2	1.74	0.67
1:A:495:ASN:CG	1:A:527:ARG:HH22	2.03	0.67
1:A:52:THR:CA	1:A:55:LYS:HE2	2.10	0.67
1:A:47:ASN:HD22	1:A:50:LEU:HG	1.58	0.67
1:A:330:ALA:O	1:A:331:GLN:HG2	1.96	0.66
1:B:51:THR:CB	1:B:54:GLU:HG2	2.25	0.66
1:B:258:GLY:HA3	1:B:291:PHE:CE2	2.31	0.66
1:A:106:ALA:HB3	1:A:322:TYR:HE2	1.61	0.66
1:B:495:ASN:CG	1:B:527:ARG:HH22	2.03	0.66
1:A:116:GLN:HA	1:B:473:GLU:OE1	1.96	0.66
1:A:258:GLY:HA3	1:A:291:PHE:CE2	2.31	0.65
1:B:25:ILE:HG22	1:B:25:ILE:O	1.96	0.65
1:A:377:GLY:C	3:A:701:ANP:O1A	2.40	0.65
1:B:106:ALA:HB3	1:B:322:TYR:HE2	1.61	0.65
1:A:37:ILE:CG1	1:B:263:ILE:HD11	2.27	0.65
1:A:464:PRO:HG3	1:B:353:GLU:HG2	1.79	0.65
1:B:387:ILE:C	1:B:389:ARG:N	2.53	0.65
1:A:431:VAL:HG11	1:A:460:ILE:HD13	1.77	0.64
1:A:25:ILE:O	1:A:25:ILE:HG22	1.96	0.64
1:A:384:ILE:HD12	1:A:532:VAL:CG2	2.27	0.64
1:A:15:ARG:H	1:A:15:ARG:CD	1.95	0.64
1:B:15:ARG:H	1:B:15:ARG:CD	1.95	0.64
1:B:384:ILE:HD12	1:B:532:VAL:CG2	2.28	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ILE:HG12	1:B:263:ILE:HD11	1.80	0.64
1:A:275:ILE:HG22	1:A:276:THR:N	2.13	0.64
1:B:330:ALA:O	1:B:331:GLN:HG2	1.97	0.64
1:B:472:GLY:O	1:B:475:GLY:N	2.31	0.64
1:B:491:ILE:HD13	1:B:499:LEU:HD22	1.79	0.64
1:B:160:ASP:OD2	1:B:163:LEU:HB2	1.97	0.64
1:B:485:ARG:HG2	1:B:516:ILE:HD11	1.80	0.63
1:A:170:ILE:HG13	1:A:258:GLY:HA2	1.80	0.63
1:A:549:GLU:HB2	1:A:554:VAL:HG21	1.79	0.63
1:B:181:PHE:O	1:B:182:PHE:C	2.42	0.63
1:B:549:GLU:HB2	1:B:554:VAL:HG21	1.79	0.63
1:A:118:GLY:HA3	1:A:201:GLY:HA2	1.80	0.63
1:B:162:LYS:HE2	1:B:275:ILE:HD11	1.80	0.63
1:A:485:ARG:HG2	1:A:516:ILE:HD11	1.80	0.63
1:A:387:ILE:C	1:A:389:ARG:N	2.54	0.63
1:A:472:GLY:O	1:A:475:GLY:N	2.31	0.62
1:B:210:ILE:O	1:B:211:SER:C	2.41	0.62
1:B:118:GLY:HA3	1:B:201:GLY:HA2	1.80	0.62
1:A:337:GLN:O	1:A:401:ASP:OD2	2.17	0.62
1:B:156:MET:HE3	1:B:283:PHE:CZ	2.34	0.62
1:B:170:ILE:HG13	1:B:258:GLY:HA2	1.80	0.62
1:B:267:ALA:C	1:B:269:LEU:H	2.07	0.62
1:B:506:SER:O	1:B:535:ARG:NH2	2.32	0.62
1:A:491:ILE:HD13	1:A:499:LEU:HD22	1.80	0.62
1:A:506:SER:O	1:A:535:ARG:NH2	2.32	0.62
1:A:256:ASP:HB3	1:B:70:PHE:HD2	1.64	0.62
1:A:181:PHE:O	1:A:182:PHE:C	2.42	0.62
1:A:450:ALA:O	1:A:453:MET:HB2	2.00	0.62
1:B:358:LYS:HD2	1:B:552:HIS:NE2	2.14	0.62
1:A:202:PHE:CE2	1:A:206:ARG:HG3	2.35	0.61
1:A:269:LEU:HB3	1:A:274:SER:CB	2.30	0.61
1:B:357:LEU:HD22	1:B:360:ILE:HD11	1.83	0.61
1:B:337:GLN:O	1:B:401:ASP:OD2	2.18	0.61
1:B:450:ALA:O	1:B:453:MET:HB2	2.00	0.61
1:A:381:SER:CB	4:A:818:HOH:O	2.48	0.61
1:A:455:ASN:ND2	1:A:515:ILE:HG21	2.14	0.61
1:B:185:LEU:HB2	1:B:305:THR:HG21	1.82	0.61
1:A:70:PHE:HD2	1:B:256:ASP:HB3	1.66	0.60
1:A:185:LEU:HB2	1:A:305:THR:HG21	1.82	0.60
1:A:357:LEU:HD22	1:A:360:ILE:HD11	1.83	0.60
1:A:358:LYS:HD2	1:A:552:HIS:NE2	2.15	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:PHE:CE2	1:B:206:ARG:HG3	2.35	0.60
1:B:405:ILE:HG23	1:B:413:LEU:HD21	1.84	0.60
1:B:455:ASN:ND2	1:B:515:ILE:HG21	2.15	0.60
1:B:425:ILE:O	1:B:426:LEU:HD23	2.02	0.59
1:A:210:ILE:O	1:A:211:SER:C	2.43	0.59
1:A:558:THR:HG22	1:A:560:ARG:H	1.68	0.59
1:A:425:ILE:O	1:A:426:LEU:HD23	2.02	0.59
1:B:106:ALA:CB	1:B:322:TYR:HE2	2.15	0.59
1:B:443:THR:HB	1:B:446:GLU:HG3	1.84	0.59
1:A:405:ILE:HG23	1:A:413:LEU:HD21	1.84	0.59
1:A:71:VAL:HG12	1:A:71:VAL:O	2.02	0.59
1:B:24:ILE:C	1:B:26:LYS:H	2.11	0.59
1:A:536:LEU:HD23	1:A:536:LEU:H	1.68	0.58
1:B:71:VAL:HG12	1:B:71:VAL:O	2.01	0.58
1:A:217:ALA:HA	1:A:219:GLU:OE1	2.03	0.58
1:A:349:TYR:HE1	1:A:356:ILE:HD12	1.68	0.58
1:A:574:SER:O	1:A:578:LEU:HB2	2.03	0.58
1:A:47:ASN:HD22	1:A:50:LEU:CG	2.17	0.58
1:A:398:ILE:HB	1:A:405:ILE:HD12	1.86	0.58
1:B:558:THR:HG22	1:B:560:ARG:H	1.67	0.58
1:B:405:ILE:HG23	1:B:413:LEU:CD2	2.34	0.58
1:A:106:ALA:CB	1:A:322:TYR:HE2	2.15	0.58
1:A:443:THR:HB	1:A:446:GLU:HG3	1.84	0.58
1:B:387:ILE:O	1:B:389:ARG:N	2.36	0.58
1:B:398:ILE:HB	1:B:405:ILE:HD12	1.85	0.58
1:A:387:ILE:O	1:A:389:ARG:N	2.37	0.57
1:B:217:ALA:HA	1:B:219:GLU:OE1	2.03	0.57
1:A:24:ILE:C	1:A:26:LYS:H	2.11	0.57
1:B:356:ILE:HD12	3:B:700:ANP:HI'	1.86	0.57
1:A:399:LEU:HD23	1:A:404:ASN:HA	1.87	0.57
1:A:405:ILE:HG23	1:A:413:LEU:CD2	2.35	0.57
1:A:418:GLY:HA3	1:A:496:PRO:HG3	1.87	0.57
1:B:137:THR:O	1:B:142:ILE:HG13	2.03	0.57
1:B:384:ILE:HG22	1:B:385:ASN:N	2.20	0.57
1:A:137:THR:O	1:A:142:ILE:HG13	2.04	0.57
1:B:536:LEU:HD23	1:B:536:LEU:H	1.68	0.57
1:B:19:THR:HG21	1:B:140:MET:HE3	1.87	0.57
1:B:56:VAL:O	1:B:56:VAL:HG12	2.05	0.56
1:B:324:ILE:HD11	1:B:390:PHE:C	2.30	0.56
1:B:371:ALA:CB	1:B:539:ILE:HG13	2.35	0.56
1:B:444:ASP:O	1:B:448:VAL:HG23	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:324:ILE:HD11	1:A:390:PHE:C	2.31	0.56
1:A:371:ALA:CB	1:A:539:ILE:HG13	2.35	0.56
1:A:453:MET:HB3	1:A:492:PHE:CE2	2.40	0.56
1:B:275:ILE:HG22	1:B:276:THR:N	2.20	0.56
1:B:349:TYR:HE1	1:B:356:ILE:HD12	1.70	0.56
1:B:418:GLY:HA3	1:B:496:PRO:HG3	1.87	0.56
1:A:156:MET:HE2	1:A:283:PHE:CZ	2.41	0.56
1:A:309:ALA:O	1:A:312:ASP:HB2	2.05	0.56
1:B:63:ILE:HG22	1:B:63:ILE:O	2.05	0.56
1:B:453:MET:HB3	1:B:492:PHE:CE2	2.41	0.56
1:A:384:ILE:HD13	1:A:500:ILE:CG2	2.36	0.56
1:A:260:ILE:HG21	1:B:67:LEU:HD21	1.86	0.56
1:A:444:ASP:O	1:A:448:VAL:HG23	2.04	0.56
1:A:491:ILE:HG22	1:A:492:PHE:N	2.21	0.56
1:B:155:ILE:HG21	1:B:286:TYR:CE2	2.41	0.56
1:B:399:LEU:HD23	1:B:404:ASN:HA	1.87	0.56
1:B:309:ALA:O	1:B:312:ASP:HB2	2.05	0.56
1:B:384:ILE:HD13	1:B:500:ILE:CG2	2.36	0.56
1:A:26:LYS:O	1:A:30:PRO:HD2	2.06	0.55
1:B:47:ASN:HD22	1:B:50:LEU:HD21	1.71	0.55
1:A:345:VAL:HG13	1:A:393:VAL:CG2	2.35	0.55
1:A:162:LYS:HD3	1:A:162:LYS:N	2.18	0.55
1:B:453:MET:HE2	1:B:453:MET:HA	1.88	0.55
1:A:269:LEU:HB3	1:A:274:SER:HB3	1.89	0.55
1:B:345:VAL:HG13	1:B:393:VAL:CG2	2.36	0.55
1:A:156:MET:HB3	1:A:283:PHE:CE1	2.41	0.55
1:B:16:ILE:O	1:B:20:ILE:HG13	2.06	0.55
1:A:92:ILE:HD12	1:A:135:ILE:HD13	1.89	0.55
1:A:177:THR:HB	1:A:251:ILE:HD13	1.89	0.55
1:B:177:THR:HB	1:B:251:ILE:HD13	1.88	0.55
1:A:210:ILE:HG22	1:A:214:LYS:HG2	1.88	0.55
1:A:276:THR:CG2	1:A:277:VAL:H	2.12	0.55
1:B:60:THR:HG22	1:B:60:THR:O	2.07	0.55
1:A:16:ILE:O	1:A:20:ILE:HG13	2.07	0.55
1:B:357:LEU:HB3	1:B:360:ILE:HD11	1.89	0.55
1:A:206:ARG:NH1	1:B:427:PHE:CE1	2.76	0.55
1:A:479:SER:OG	1:A:480:GLY:N	2.40	0.55
1:A:75:PRO:HB2	1:A:76:PRO:CD	2.34	0.54
1:A:453:MET:HE2	1:A:453:MET:HA	1.88	0.54
1:B:26:LYS:O	1:B:30:PRO:HD2	2.06	0.54
1:B:142:ILE:CD1	1:B:304:LEU:HD11	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:52:THR:HG22	1:B:52:THR:O	2.08	0.54
1:B:210:ILE:HG22	1:B:214:LYS:HG2	1.88	0.54
1:A:159:LEU:HD23	1:A:283:PHE:HD1	1.73	0.54
1:A:384:ILE:HG22	1:A:385:ASN:N	2.21	0.54
1:A:389:ARG:HD2	1:A:405:ILE:HG22	1.89	0.54
1:A:473:GLU:C	1:A:475:GLY:H	2.14	0.54
1:A:456:ALA:O	1:A:457:HIS:C	2.51	0.54
1:A:142:ILE:CD1	1:A:304:LEU:HD11	2.36	0.54
1:A:536:LEU:HD23	1:A:536:LEU:N	2.23	0.54
1:B:92:ILE:HD12	1:B:135:ILE:HD13	1.90	0.54
1:A:19:THR:HG21	1:A:140:MET:HE3	1.87	0.54
1:B:389:ARG:HD2	1:B:405:ILE:HG22	1.89	0.54
1:A:156:MET:HB3	1:A:164:THR:HG22	1.88	0.54
1:A:479:SER:HB2	3:B:700:ANP:O3A	2.08	0.54
1:B:277:VAL:HG12	1:B:277:VAL:O	2.08	0.54
1:A:12:TYR:HA	1:A:15:ARG:HD3	1.89	0.54
1:A:353:GLU:CG	1:B:464:PRO:HG3	2.36	0.54
1:B:549:GLU:HB2	1:B:554:VAL:CG2	2.38	0.53
1:A:2:ILE:HD11	1:A:308:PHE:HE2	1.72	0.53
1:A:157:PHE:HA	1:A:164:THR:HG21	1.90	0.53
1:B:491:ILE:HG22	1:B:492:PHE:N	2.21	0.53
1:B:456:ALA:O	1:B:457:HIS:C	2.51	0.53
1:B:12:TYR:HA	1:B:15:ARG:HD3	1.90	0.53
1:B:357:LEU:HB3	1:B:360:ILE:CD1	2.38	0.53
1:B:156:MET:HB3	1:B:164:THR:CG2	2.30	0.53
1:B:160:ASP:O	1:B:164:THR:HG23	2.08	0.53
1:B:377:GLY:C	3:B:700:ANP:O1A	2.52	0.53
1:B:2:ILE:HD11	1:B:308:PHE:HE2	1.73	0.53
1:B:473:GLU:C	1:B:475:GLY:H	2.17	0.53
1:B:479:SER:OG	1:B:480:GLY:N	2.40	0.53
1:A:67:LEU:HD21	1:B:260:ILE:HG21	1.89	0.52
1:B:536:LEU:HD23	1:B:536:LEU:N	2.23	0.52
1:B:260:ILE:C	1:B:262:VAL:H	2.17	0.52
1:A:357:LEU:HB3	1:A:360:ILE:CD1	2.39	0.52
1:A:357:LEU:HB3	1:A:360:ILE:HD11	1.91	0.52
1:A:464:PRO:HB2	1:A:465:GLN:NE2	2.24	0.52
1:A:549:GLU:HB2	1:A:554:VAL:CG2	2.39	0.52
1:A:345:VAL:HG13	1:A:393:VAL:HG23	1.91	0.52
1:A:335:ILE:CD1	1:A:400:ILE:HG21	2.35	0.52
1:A:33:ILE:HB	1:A:34:PRO:CD	2.40	0.52
1:B:33:ILE:HB	1:B:34:PRO:CD	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:41:ILE:HG22	1:A:42:ASP:N	2.24	0.52
1:A:349:TYR:CE1	1:A:356:ILE:HD12	2.44	0.52
1:A:495:ASN:ND2	1:A:527:ARG:HH22	2.08	0.52
1:A:234:LEU:CD2	1:B:94:TYR:HB2	2.29	0.51
1:B:163:LEU:HD23	1:B:283:PHE:CG	2.46	0.51
1:B:459:PHE:CZ	1:B:482:GLN:HG2	2.45	0.51
1:A:65:ILE:HG22	1:A:66:ALA:N	2.25	0.51
1:A:337:GLN:O	1:A:339:ARG:N	2.43	0.51
1:B:196:LEU:HB2	1:B:233:PHE:CE1	2.44	0.51
1:B:335:ILE:CD1	1:B:400:ILE:HG21	2.35	0.51
1:B:337:GLN:O	1:B:339:ARG:N	2.43	0.51
1:B:495:ASN:ND2	1:B:527:ARG:HH22	2.08	0.51
1:A:196:LEU:HB2	1:A:233:PHE:CE1	2.45	0.51
1:A:209:GLY:HA2	1:B:425:ILE:HD13	1.92	0.51
1:A:418:GLY:CA	1:A:496:PRO:HG3	2.41	0.51
1:B:464:PRO:HB2	1:B:465:GLN:NE2	2.26	0.51
1:A:173:PHE:H	1:A:173:PHE:HD1	1.59	0.51
3:A:701:ANP:O3A	1:B:479:SER:HB2	2.10	0.51
1:B:345:VAL:HG13	1:B:393:VAL:HG23	1.92	0.51
1:A:459:PHE:CZ	1:A:482:GLN:HG2	2.45	0.51
1:A:482:GLN:O	1:A:483:LYS:C	2.54	0.51
1:B:92:ILE:CD1	1:B:135:ILE:HD13	2.41	0.51
1:B:443:THR:C	1:B:445:GLU:N	2.67	0.51
1:A:200:GLN:HG2	1:B:125:ILE:CD1	2.41	0.51
1:A:159:LEU:O	1:A:160:ASP:HB2	2.10	0.51
1:A:304:LEU:O	1:A:308:PHE:HD1	1.94	0.51
1:B:349:TYR:CE1	1:B:356:ILE:HD12	2.46	0.51
1:A:328:VAL:HG23	1:A:329:GLY:N	2.26	0.50
1:A:364:ILE:HD13	1:A:530:LEU:CD2	2.40	0.50
1:B:328:VAL:HG23	1:B:329:GLY:N	2.26	0.50
1:B:575:ILE:HG22	1:B:575:ILE:O	2.10	0.50
1:A:92:ILE:CD1	1:A:135:ILE:HD13	2.41	0.50
1:A:356:ILE:CD1	3:A:701:ANP:HI'	2.42	0.50
1:A:427:PHE:CE1	1:B:206:ARG:NH1	2.79	0.50
1:B:364:ILE:HD13	1:B:530:LEU:CD2	2.39	0.50
1:A:125:ILE:CD1	1:B:200:GLN:HG2	2.40	0.50
1:A:153:LEU:HD11	1:A:168:LEU:HD21	1.94	0.50
1:A:177:THR:CG2	1:A:251:ILE:HD13	2.42	0.50
1:B:177:THR:CG2	1:B:251:ILE:HD13	2.42	0.50
1:A:384:ILE:HD12	1:A:532:VAL:HG23	1.94	0.50
1:B:65:ILE:HG22	1:B:66:ALA:N	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:MET:C	1:B:164:THR:HG21	2.36	0.50
1:B:173:PHE:HD1	1:B:173:PHE:H	1.58	0.50
1:B:418:GLY:CA	1:B:496:PRO:HG3	2.42	0.50
1:A:1:MET:O	1:A:4:ARG:HB2	2.12	0.50
1:B:260:ILE:C	1:B:262:VAL:N	2.68	0.50
1:A:153:LEU:HD21	1:A:168:LEU:HD21	1.93	0.50
1:B:75:PRO:HB2	1:B:76:PRO:CD	2.35	0.50
1:B:342:ILE:HG23	1:B:345:VAL:HG21	1.94	0.50
1:A:94:TYR:HB2	1:B:234:LEU:CD2	2.37	0.50
1:A:260:ILE:HG21	1:B:67:LEU:CD2	2.42	0.49
1:B:384:ILE:HD12	1:B:532:VAL:HG23	1.94	0.49
1:A:505:THR:O	1:A:506:SER:C	2.55	0.49
1:B:153:LEU:HD11	1:B:168:LEU:HD21	1.95	0.49
1:B:558:THR:O	1:B:559:HIS:C	2.54	0.49
1:A:45:ILE:HG21	1:B:277:VAL:HG11	1.95	0.49
1:A:51:THR:HB	1:A:54:GLU:HG2	1.94	0.49
1:A:269:LEU:HB3	1:A:274:SER:OG	2.11	0.49
1:B:153:LEU:HD21	1:B:168:LEU:HD21	1.93	0.49
1:B:379:GLY:N	3:B:700:ANP:O1A	2.46	0.49
1:B:276:THR:C	1:B:278:GLY:H	2.20	0.49
1:B:1:MET:O	1:B:4:ARG:HB2	2.12	0.49
1:B:212:VAL:HG13	1:B:213:VAL:N	2.27	0.49
1:A:47:ASN:ND2	1:A:50:LEU:HG	2.27	0.49
1:A:575:ILE:O	1:A:575:ILE:HG22	2.11	0.49
1:A:443:THR:C	1:A:445:GLU:N	2.68	0.49
1:B:91:LYS:O	1:B:94:TYR:HB3	2.13	0.49
1:B:267:ALA:C	1:B:269:LEU:N	2.68	0.49
1:B:482:GLN:O	1:B:483:LYS:C	2.53	0.49
1:A:558:THR:O	1:A:559:HIS:C	2.54	0.49
1:B:304:LEU:O	1:B:308:PHE:HD1	1.94	0.49
1:A:167:ALA:O	1:A:169:PHE:N	2.46	0.48
1:B:10:LYS:C	1:B:12:TYR:H	2.21	0.48
1:B:156:MET:HE3	1:B:283:PHE:HZ	1.77	0.48
1:A:106:ALA:CB	1:A:322:TYR:CE2	2.96	0.48
1:A:443:THR:HG22	1:A:445:GLU:OE1	2.14	0.48
1:B:74:ARG:HB3	1:B:75:PRO:HD3	1.95	0.48
1:A:1:MET:HE1	1:A:186:ARG:NH2	2.28	0.48
1:A:428:SER:N	1:B:205:GLU:OE1	2.41	0.48
1:B:570:GLU:OE1	1:B:570:GLU:C	2.56	0.48
1:B:101:TYR:OH	1:B:105:GLN:NE2	2.46	0.48
1:B:106:ALA:O	1:B:322:TYR:HD2	1.96	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:LYS:O	1:A:94:TYR:HB3	2.13	0.48
1:A:342:ILE:HG23	1:A:345:VAL:HG21	1.94	0.48
1:A:145:ASP:O	1:A:149:ILE:HG13	2.14	0.48
1:B:89:SER:HA	1:B:92:ILE:HD12	1.95	0.48
1:B:171:PHE:CE1	1:B:294:LEU:HD11	2.49	0.48
1:B:271:ILE:C	1:B:273:GLY:H	2.22	0.48
1:A:10:LYS:C	1:A:12:TYR:H	2.21	0.48
1:B:1:MET:HE1	1:B:186:ARG:NH2	2.28	0.48
1:B:106:ALA:CB	1:B:322:TYR:CE2	2.96	0.48
1:B:381:SER:CB	4:B:808:HOH:O	2.59	0.48
1:B:505:THR:O	1:B:506:SER:C	2.56	0.48
1:A:74:ARG:HB3	1:A:75:PRO:HD3	1.96	0.48
1:A:461:MET:HA	1:A:461:MET:CE	2.42	0.48
1:A:570:GLU:C	1:A:570:GLU:OE1	2.56	0.48
1:B:544:LYS:HE3	1:B:556:THR:HG23	1.96	0.48
1:A:212:VAL:HG13	1:A:213:VAL:N	2.27	0.47
1:B:145:ASP:O	1:B:149:ILE:HG13	2.14	0.47
1:A:89:SER:HA	1:A:92:ILE:HD12	1.95	0.47
1:A:106:ALA:O	1:A:322:TYR:HD2	1.97	0.47
1:A:125:ILE:HD13	1:B:200:GLN:HG2	1.96	0.47
1:B:47:ASN:ND2	1:B:50:LEU:HD21	2.29	0.47
1:A:101:TYR:OH	1:A:105:GLN:NE2	2.46	0.47
1:A:163:LEU:HG	1:A:283:PHE:CE2	2.50	0.47
1:A:479:SER:OG	3:B:700:ANP:N3B	2.47	0.47
1:A:86:GLN:O	1:A:87:TRP:C	2.57	0.47
1:A:171:PHE:CE1	1:A:294:LEU:HD11	2.49	0.47
1:A:375:MET:HE2	1:B:511:GLU:OE1	2.14	0.47
1:A:544:LYS:HE3	1:A:556:THR:HG23	1.96	0.47
1:A:221:ASN:O	1:A:224:LYS:HB2	2.14	0.47
1:A:549:GLU:O	1:A:550:ASN:C	2.58	0.47
1:B:443:THR:HG22	1:B:445:GLU:OE1	2.14	0.47
1:A:253:THR:OG1	1:B:75:PRO:HG3	2.15	0.47
1:A:381:SER:OG	4:A:818:HOH:O	2.20	0.47
1:A:536:LEU:HG	1:B:510:LEU:HD11	1.97	0.47
1:B:324:ILE:HD13	1:B:389:ARG:O	2.15	0.47
1:A:104:LEU:C	1:A:106:ALA:H	2.23	0.47
1:A:104:LEU:HB3	1:A:112:TYR:OH	2.14	0.47
1:A:422:GLN:NE2	1:A:503:GLU:OE1	2.48	0.47
1:A:473:GLU:C	1:A:475:GLY:N	2.71	0.47
1:B:188:LEU:HD23	1:B:188:LEU:HA	1.76	0.47
1:B:456:ALA:O	1:B:460:ILE:HG13	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:206:ARG:NH1	1:B:427:PHE:CD1	2.82	0.47
1:B:163:LEU:O	1:B:166:ALA:HB3	2.14	0.47
1:B:234:LEU:O	1:B:235:THR:C	2.58	0.47
1:B:448:VAL:O	1:B:452:LYS:HG3	2.15	0.47
1:A:329:GLY:O	1:A:330:ALA:C	2.58	0.47
1:B:104:LEU:HB3	1:B:112:TYR:OH	2.15	0.47
1:B:329:GLY:O	1:B:330:ALA:C	2.58	0.47
1:A:324:ILE:HD13	1:A:389:ARG:O	2.15	0.47
1:A:456:ALA:O	1:A:460:ILE:HG13	2.15	0.47
1:B:104:LEU:C	1:B:106:ALA:H	2.23	0.47
1:B:110:ARG:O	1:B:111:PHE:C	2.57	0.47
1:B:145:ASP:OD1	1:B:296:ARG:HD2	2.15	0.47
1:B:422:GLN:NE2	1:B:503:GLU:OE1	2.47	0.47
1:A:145:ASP:OD1	1:A:296:ARG:HD2	2.15	0.46
1:A:409:LEU:O	1:A:410:THR:C	2.58	0.46
1:B:238:LEU:O	1:B:239:LYS:C	2.59	0.46
1:A:205:GLU:OE1	1:B:428:SER:N	2.39	0.46
1:B:266:GLY:O	1:B:280:LEU:HD22	2.15	0.46
1:A:188:LEU:HD23	1:A:188:LEU:HA	1.77	0.46
1:A:66:ALA:HB1	1:B:260:ILE:HD11	1.96	0.46
1:A:448:VAL:O	1:A:452:LYS:HG3	2.15	0.46
1:B:409:LEU:O	1:B:410:THR:C	2.58	0.46
1:A:170:ILE:HG13	1:A:258:GLY:CA	2.44	0.46
1:A:425:ILE:HD13	1:B:209:GLY:HA2	1.96	0.46
1:B:33:ILE:HB	1:B:34:PRO:HD3	1.98	0.46
1:B:185:LEU:CB	1:B:305:THR:HG21	2.46	0.46
1:B:383:LEU:O	1:B:386:LEU:HB2	2.16	0.46
1:B:429:ASP:O	1:B:471:VAL:HG22	2.16	0.46
1:A:2:ILE:HD11	1:A:308:PHE:CE2	2.50	0.46
1:A:61:ILE:O	1:A:65:ILE:HB	2.16	0.46
1:A:364:ILE:HG12	1:A:370:VAL:HG21	1.98	0.46
1:A:425:ILE:HG22	1:A:426:LEU:N	2.30	0.46
1:A:485:ARG:HG3	1:A:508:LEU:HD21	1.97	0.46
1:A:357:LEU:HD11	1:A:383:LEU:CA	2.46	0.46
1:B:221:ASN:O	1:B:224:LYS:HB2	2.15	0.46
1:B:420:VAL:O	1:B:420:VAL:HG12	2.16	0.46
1:B:461:MET:HA	1:B:461:MET:CE	2.41	0.46
1:A:304:LEU:O	1:A:305:THR:C	2.59	0.46
1:A:427:PHE:CD1	1:B:206:ARG:NH1	2.84	0.46
1:A:439:ARG:NH2	1:A:446:GLU:CD	2.74	0.46
1:B:275:ILE:CG2	1:B:276:THR:N	2.79	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:425:ILE:HG22	1:B:426:LEU:N	2.31	0.46
1:B:170:ILE:HG13	1:B:258:GLY:CA	2.45	0.46
1:A:238:LEU:O	1:A:239:LYS:C	2.59	0.45
1:A:260:ILE:HD11	1:B:66:ALA:HB1	1.98	0.45
1:A:464:PRO:O	1:A:465:GLN:HB2	2.16	0.45
1:A:472:GLY:O	1:A:473:GLU:C	2.58	0.45
3:A:701:ANP:H2'	1:B:477:LYS:O	2.16	0.45
1:B:162:LYS:H	1:B:162:LYS:CD	2.23	0.45
1:B:485:ARG:HG3	1:B:508:LEU:HD21	1.98	0.45
1:B:2:ILE:HD11	1:B:308:PHE:CE2	2.51	0.45
1:A:510:LEU:HD11	1:B:536:LEU:HG	1.98	0.45
1:A:41:ILE:HA	1:A:45:ILE:HD12	1.99	0.45
1:A:27:PHE:C	1:A:30:PRO:HD2	2.41	0.45
1:A:234:LEU:O	1:A:235:THR:C	2.59	0.45
1:A:383:LEU:O	1:A:386:LEU:HB2	2.17	0.45
1:B:304:LEU:O	1:B:305:THR:C	2.60	0.45
1:B:364:ILE:HG12	1:B:370:VAL:HG21	1.97	0.45
1:B:380:LYS:HB2	1:B:380:LYS:HE3	1.49	0.45
1:B:508:LEU:HD13	1:B:516:ILE:HD12	1.99	0.45
1:A:173:PHE:CD1	1:A:173:PHE:N	2.84	0.45
1:A:289:LEU:HD23	1:A:289:LEU:HA	1.83	0.45
1:A:381:SER:HB2	4:A:818:HOH:O	2.14	0.45
1:B:86:GLN:O	1:B:87:TRP:C	2.58	0.45
1:A:271:ILE:HD13	1:B:56:VAL:HG22	1.98	0.45
1:A:429:ASP:O	1:A:471:VAL:HG22	2.17	0.45
1:B:570:GLU:O	1:B:571:HIS:C	2.60	0.45
1:A:33:ILE:HB	1:A:34:PRO:HD3	1.98	0.45
1:A:37:ILE:HG13	1:B:263:ILE:HD11	1.98	0.45
1:A:422:GLN:NE2	1:B:507:ALA:CB	2.80	0.45
1:B:27:PHE:C	1:B:30:PRO:HD2	2.41	0.45
1:B:108:SER:O	1:B:109:ALA:C	2.60	0.45
1:B:173:PHE:CD1	1:B:173:PHE:N	2.84	0.45
1:B:212:VAL:CG1	1:B:213:VAL:N	2.79	0.45
1:B:439:ARG:NH2	1:B:446:GLU:CD	2.74	0.45
1:A:110:ARG:O	1:A:111:PHE:C	2.58	0.45
1:A:212:VAL:CG1	1:A:213:VAL:N	2.79	0.45
1:B:104:LEU:C	1:B:106:ALA:N	2.73	0.45
1:B:266:GLY:HA3	1:B:280:LEU:HD11	1.98	0.45
1:B:267:ALA:O	1:B:269:LEU:N	2.50	0.45
1:B:384:ILE:HD13	1:B:500:ILE:HG23	1.99	0.45
1:A:167:ALA:C	1:A:169:PHE:N	2.74	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:169:PHE:HD2	1:A:261:ILE:HD13	1.82	0.45
1:B:156:MET:C	1:B:164:THR:CG2	2.90	0.45
1:B:473:GLU:C	1:B:475:GLY:N	2.75	0.45
1:A:24:ILE:O	1:A:26:LYS:N	2.51	0.44
1:A:539:ILE:HD12	1:A:539:ILE:HA	1.67	0.44
1:B:59:LEU:O	1:B:59:LEU:HG	2.17	0.44
1:B:357:LEU:HD11	1:B:383:LEU:CA	2.46	0.44
1:B:27:PHE:H	1:B:27:PHE:HD1	1.64	0.44
1:B:169:PHE:HD2	1:B:261:ILE:HD13	1.82	0.44
1:B:472:GLY:O	1:B:473:GLU:C	2.59	0.44
1:B:549:GLU:O	1:B:550:ASN:C	2.59	0.44
1:B:332:PRO:HD3	1:B:409:LEU:CD1	2.43	0.44
1:A:104:LEU:C	1:A:106:ALA:N	2.73	0.44
1:A:167:ALA:C	1:A:169:PHE:H	2.24	0.44
1:A:202:PHE:CE1	1:A:206:ARG:NE	2.86	0.44
1:B:294:LEU:O	1:B:298:VAL:HG23	2.16	0.44
1:A:384:ILE:HD13	1:A:500:ILE:HG23	1.98	0.44
1:A:466:GLY:O	1:A:468:ASP:N	2.50	0.44
1:A:555:GLU:OE1	1:A:568:ALA:HB3	2.17	0.44
1:B:292:GLY:O	1:B:296:ARG:HG3	2.17	0.44
1:B:489:ALA:O	1:B:490:ARG:C	2.61	0.44
1:A:67:LEU:CD2	1:B:260:ILE:HG21	2.47	0.44
1:A:420:VAL:O	1:A:420:VAL:HG12	2.16	0.44
1:A:571:HIS:O	1:A:575:ILE:HG13	2.18	0.44
1:B:106:ALA:HB3	1:B:322:TYR:CE2	2.48	0.44
1:B:252:ASN:O	1:B:253:THR:C	2.61	0.44
1:B:202:PHE:CE1	1:B:206:ARG:NE	2.86	0.44
1:B:349:TYR:OH	1:B:382:THR:HG23	2.18	0.44
1:B:571:HIS:O	1:B:575:ILE:HG13	2.18	0.44
1:A:108:SER:O	1:A:109:ALA:C	2.61	0.44
1:A:275:ILE:HG21	1:A:279:THR:OG1	2.18	0.44
1:A:332:PRO:HD3	1:A:409:LEU:CD1	2.44	0.44
1:A:466:GLY:C	1:A:468:ASP:N	2.75	0.44
1:B:27:PHE:CD1	1:B:27:PHE:N	2.86	0.44
1:B:202:PHE:CZ	1:B:206:ARG:HG3	2.53	0.44
1:A:58:HIS:HA	1:A:61:ILE:HG12	2.00	0.44
1:A:82:GLN:O	1:A:83:TYR:C	2.60	0.44
1:A:292:GLY:O	1:A:296:ARG:HG3	2.18	0.44
1:A:294:LEU:O	1:A:298:VAL:HG23	2.16	0.44
1:A:169:PHE:CD2	1:A:261:ILE:HD13	2.53	0.43
1:B:82:GLN:O	1:B:83:TYR:C	2.60	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:169:PHE:CD2	1:B:261:ILE:HD13	2.53	0.43
1:B:466:GLY:O	1:B:468:ASP:N	2.50	0.43
1:A:171:PHE:HB2	1:A:172:PRO:HD3	2.00	0.43
1:A:349:TYR:OH	1:A:382:THR:HG23	2.18	0.43
1:A:489:ALA:O	1:A:490:ARG:C	2.61	0.43
1:B:203:LEU:O	1:B:204:HIS:C	2.59	0.43
1:B:276:THR:HB	1:B:279:THR:OG1	2.18	0.43
1:B:466:GLY:C	1:B:468:ASP:H	2.26	0.43
1:A:466:GLY:C	1:A:468:ASP:H	2.26	0.43
1:A:477:LYS:HG2	3:B:700:ANP:N6	2.32	0.43
1:A:190:ARG:HG3	1:A:190:ARG:HH11	1.83	0.43
1:A:508:LEU:HD13	1:A:516:ILE:HD12	2.00	0.43
1:B:51:THR:HG22	1:B:52:THR:N	2.33	0.43
1:B:100:LEU:O	1:B:103:HIS:HB3	2.18	0.43
1:B:244:ASN:OD1	1:B:302:THR:HG23	2.19	0.43
1:B:509:ASP:OD2	1:B:511:GLU:HB3	2.18	0.43
1:A:27:PHE:H	1:A:27:PHE:HD1	1.64	0.43
1:B:24:ILE:C	1:B:26:LYS:N	2.76	0.43
1:A:200:GLN:HG2	1:B:125:ILE:HD13	2.00	0.43
1:A:203:LEU:O	1:A:204:HIS:C	2.60	0.43
1:A:509:ASP:OD2	1:A:511:GLU:HB3	2.18	0.43
1:B:153:LEU:HD23	1:B:153:LEU:HA	1.83	0.43
1:B:379:GLY:O	1:B:380:LYS:C	2.61	0.43
1:A:24:ILE:C	1:A:26:LYS:N	2.75	0.43
1:A:202:PHE:CZ	1:A:206:ARG:HG3	2.53	0.43
1:A:267:ALA:HA	1:A:280:LEU:CD2	2.49	0.43
1:A:570:GLU:O	1:A:571:HIS:C	2.60	0.43
1:B:24:ILE:O	1:B:26:LYS:N	2.51	0.43
1:B:466:GLY:C	1:B:468:ASP:N	2.75	0.43
1:A:379:GLY:O	1:A:380:LYS:C	2.61	0.43
1:B:54:GLU:O	1:B:57:HIS:HB3	2.19	0.43
1:B:357:LEU:HD11	1:B:383:LEU:HA	2.01	0.43
1:B:488:ILE:O	1:B:489:ALA:C	2.62	0.43
1:A:75:PRO:HG3	1:B:253:THR:OG1	2.19	0.43
1:A:100:LEU:O	1:A:103:HIS:HB3	2.18	0.43
1:A:153:LEU:HD23	1:A:153:LEU:HA	1.86	0.43
1:B:34:PRO:HA	1:B:37:ILE:HD12	2.01	0.43
1:B:171:PHE:HB2	1:B:172:PRO:HD3	1.99	0.43
1:B:443:THR:C	1:B:445:GLU:H	2.26	0.43
1:B:555:GLU:OE1	1:B:568:ALA:HB3	2.19	0.43
1:A:377:GLY:N	3:A:701:ANP:O1B	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:190:ARG:HG3	1:B:190:ARG:HH11	1.83	0.43
1:A:2:ILE:O	1:A:6:LEU:HG	2.19	0.42
1:A:29:ILE:N	1:A:30:PRO:HD2	2.34	0.42
1:A:244:ASN:OD1	1:A:302:THR:HG23	2.19	0.42
1:A:453:MET:HB3	1:A:492:PHE:CD2	2.54	0.42
1:B:71:VAL:O	1:B:71:VAL:CG1	2.67	0.42
1:A:357:LEU:HD11	1:A:383:LEU:HA	2.01	0.42
1:A:518:GLU:O	1:A:519:ALA:C	2.62	0.42
1:A:159:LEU:HD23	1:A:283:PHE:CD1	2.53	0.42
1:B:269:LEU:HB3	1:B:274:SER:OG	2.19	0.42
1:B:422:GLN:NE2	1:B:503:GLU:CD	2.77	0.42
1:B:453:MET:HB3	1:B:492:PHE:CD2	2.54	0.42
1:A:185:LEU:CB	1:A:305:THR:HG21	2.47	0.42
1:A:502:ASP:HA	1:A:532:VAL:HB	2.02	0.42
3:A:701:ANP:N3B	1:B:479:SER:OG	2.53	0.42
1:A:34:PRO:HA	1:A:37:ILE:HD12	2.02	0.42
1:A:273:GLY:O	1:A:274:SER:C	2.62	0.42
1:A:507:ALA:CB	1:B:422:GLN:NE2	2.83	0.42
1:B:384:ILE:CD1	1:B:500:ILE:HG23	2.50	0.42
1:A:384:ILE:CD1	1:A:532:VAL:HG23	2.49	0.42
1:B:289:LEU:HD23	1:B:289:LEU:HA	1.83	0.42
1:A:422:GLN:HE22	1:B:507:ALA:HB1	1.85	0.42
1:B:163:LEU:HG	1:B:283:PHE:CE2	2.55	0.42
1:B:262:VAL:HG12	1:B:263:ILE:N	2.34	0.42
1:B:365:GLU:N	1:B:368:GLU:OE1	2.47	0.42
1:A:284:VAL:HG11	1:B:37:ILE:HG23	2.01	0.42
1:A:290:LEU:HD23	1:A:290:LEU:HA	1.81	0.42
1:A:422:GLN:NE2	1:B:507:ALA:HB2	2.35	0.42
1:A:464:PRO:HG3	1:B:353:GLU:CG	2.48	0.42
1:A:163:LEU:O	1:A:166:ALA:HB3	2.20	0.42
1:A:199:VAL:CG2	1:A:200:GLN:N	2.83	0.42
1:B:206:ARG:O	1:B:209:GLY:N	2.52	0.42
1:B:356:ILE:O	1:B:551:GLY:HA3	2.20	0.42
1:A:141:ASN:O	1:A:142:ILE:C	2.63	0.42
1:A:443:THR:C	1:A:445:GLU:H	2.26	0.42
1:B:108:SER:N	4:B:816:HOH:O	2.17	0.42
1:B:194:GLN:O	1:B:197:ALA:HB3	2.20	0.42
1:A:71:VAL:O	1:A:71:VAL:CG1	2.67	0.41
1:A:422:GLN:NE2	1:A:503:GLU:CD	2.78	0.41
3:A:701:ANP:C5	1:B:477:LYS:HA	2.50	0.41
1:A:121:ILE:HD13	1:B:204:HIS:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:224:LYS:O	1:B:225:ASN:C	2.63	0.41
1:A:480:GLY:HA3	3:B:700:ANP:O2G	2.20	0.41
1:A:511:GLU:OE1	1:B:375:MET:HE2	2.19	0.41
1:A:480:GLY:CA	3:B:700:ANP:O2G	2.69	0.41
1:B:167:ALA:O	1:B:169:PHE:N	2.53	0.41
1:B:518:GLU:O	1:B:519:ALA:C	2.63	0.41
1:A:10:LYS:HB3	1:A:11:PRO:CD	2.50	0.41
1:A:206:ARG:O	1:A:209:GLY:N	2.52	0.41
1:A:252:ASN:O	1:A:253:THR:C	2.62	0.41
1:A:437:LEU:HD12	1:A:490:ARG:NH2	2.35	0.41
1:A:488:ILE:O	1:A:489:ALA:C	2.62	0.41
1:B:29:ILE:N	1:B:30:PRO:HD2	2.35	0.41
1:B:260:ILE:O	1:B:262:VAL:N	2.54	0.41
1:B:437:LEU:HD12	1:B:490:ARG:NH2	2.35	0.41
1:A:106:ALA:HB3	1:A:322:TYR:CE2	2.48	0.41
1:A:202:PHE:O	1:A:203:LEU:C	2.63	0.41
1:B:93:LEU:O	1:B:94:TYR:C	2.64	0.41
1:B:502:ASP:HA	1:B:532:VAL:HB	2.02	0.41
1:A:74:ARG:O	1:A:75:PRO:C	2.63	0.41
1:A:479:SER:O	1:A:483:LYS:HG3	2.20	0.41
1:B:259:PRO:HD3	1:B:291:PHE:CD2	2.56	0.41
1:B:479:SER:O	1:B:483:LYS:HG3	2.20	0.41
1:A:189:THR:HG21	1:A:306:GLN:HA	2.02	0.41
1:A:242:ARG:HG2	1:B:83:TYR:CE1	2.56	0.41
1:A:259:PRO:HD3	1:A:291:PHE:CD2	2.56	0.41
1:A:266:GLY:HA3	1:A:280:LEU:HD11	2.01	0.41
1:A:371:ALA:HB1	1:A:539:ILE:CG1	2.51	0.41
1:A:380:LYS:HB2	1:A:380:LYS:HE3	1.50	0.41
1:B:2:ILE:O	1:B:6:LEU:HG	2.20	0.41
1:B:189:THR:HG21	1:B:306:GLN:HA	2.02	0.41
1:B:384:ILE:CD1	1:B:532:VAL:HG23	2.50	0.41
1:A:27:PHE:CD1	1:A:27:PHE:N	2.86	0.41
1:A:156:MET:HB3	1:A:283:PHE:HE1	1.85	0.41
1:A:384:ILE:CD1	1:A:500:ILE:HG23	2.50	0.41
1:B:141:ASN:O	1:B:142:ILE:C	2.63	0.41
1:B:371:ALA:HB1	1:B:539:ILE:CG1	2.51	0.41
1:A:10:LYS:O	1:A:12:TYR:N	2.54	0.41
1:A:260:ILE:O	1:A:263:ILE:N	2.54	0.41
1:A:291:PHE:CD1	1:A:291:PHE:N	2.89	0.41
1:B:25:ILE:O	1:B:25:ILE:CG2	2.67	0.41
1:A:356:ILE:HD12	3:A:701:ANP:HI'	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:ILE:O	1:A:551:GLY:HA3	2.21	0.40
1:B:206:ARG:O	1:B:207:VAL:C	2.65	0.40
1:A:59:LEU:HD21	1:B:267:ALA:HB3	2.04	0.40
1:B:9:VAL:O	1:B:10:LYS:C	2.64	0.40
1:B:160:ASP:OD1	1:B:275:ILE:HD11	2.20	0.40
1:B:443:THR:CB	1:B:446:GLU:HG3	2.50	0.40
1:B:202:PHE:O	1:B:203:LEU:C	2.63	0.40
1:B:265:VAL:O	1:B:269:LEU:HG	2.21	0.40
1:B:331:GLN:O	1:B:333:ILE:N	2.54	0.40
1:B:404:ASN:O	1:B:405:ILE:C	2.65	0.40
1:A:160:ASP:OD1	1:A:163:LEU:N	2.55	0.40
1:A:181:PHE:CE2	1:A:246:TYR:HD2	2.39	0.40
1:A:200:GLN:HE21	1:A:200:GLN:HB3	1.63	0.40
1:B:74:ARG:O	1:B:75:PRO:C	2.64	0.40
1:B:181:PHE:CE2	1:B:246:TYR:HD2	2.40	0.40
1:A:194:GLN:O	1:A:197:ALA:HB3	2.22	0.40
1:B:84:LEU:O	1:B:85:ALA:C	2.65	0.40
1:B:290:LEU:HD23	1:B:290:LEU:HA	1.81	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	576/578 (100%)	463 (80%)	95 (16%)	18 (3%)	3	18
1	B	576/578 (100%)	458 (80%)	102 (18%)	16 (3%)	4	19
All	All	1152/1156 (100%)	921 (80%)	197 (17%)	34 (3%)	3	18

All (34) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	25	ILE
1	A	338	GLY
1	A	506	SER
1	B	25	ILE
1	B	182	PHE
1	B	338	GLY
1	B	506	SER
1	A	41	ILE
1	A	160	ASP
1	A	168	LEU
1	A	182	PHE
1	A	466	GLY
1	B	466	GLY
1	A	467	TYR
1	A	537	SER
1	B	168	LEU
1	B	268	TYR
1	B	467	TYR
1	B	537	SER
1	A	49	ALA
1	A	88	THR
1	A	250	ALA
1	A	410	THR
1	B	88	THR
1	B	250	ALA
1	B	410	THR
1	A	332	PRO
1	B	332	PRO
1	A	11	PRO
1	B	11	PRO
1	A	10	LYS
1	A	171	PHE
1	B	10	LYS
1	B	171	PHE

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	499/499 (100%)	468 (94%)	31 (6%)	16	43
1	B	499/499 (100%)	468 (94%)	31 (6%)	16	43
All	All	998/998 (100%)	936 (94%)	62 (6%)	16	43

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	56	VAL
1	A	65	ILE
1	A	82	GLN
1	A	199	VAL
1	A	200	GLN
1	A	241	THR
1	A	244	ASN
1	A	289	LEU
1	A	290	LEU
1	A	295	ARG
1	A	321	ASP
1	A	353	GLU
1	A	356	ILE
1	A	365	GLU
1	A	373	VAL
1	A	384	ILE
1	A	393	VAL
1	A	410	THR
1	A	424	ASN
1	A	429	ASP
1	A	443	THR
1	A	461	MET
1	A	479	SER
1	A	486	LEU
1	A	487	SER
1	A	491	ILE
1	A	496	PRO
1	A	536	LEU
1	A	539	ILE
1	A	556	THR
1	A	570	GLU
1	B	65	ILE
1	B	159	LEU
1	B	199	VAL
1	B	241	THR

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Mol	Chain	Res	Type
1	B	244	ASN
1	B	289	LEU
1	B	290	LEU
1	B	295	ARG
1	B	321	ASP
1	B	353	GLU
1	B	356	ILE
1	B	365	GLU
1	B	373	VAL
1	B	384	ILE
1	B	393	VAL
1	B	410	THR
1	B	424	ASN
1	B	429	ASP
1	B	443	THR
1	B	461	MET
1	B	479	SER
1	B	486	LEU
1	B	487	SER
1	B	491	ILE
1	B	496	PRO
1	B	536	LEU
1	B	539	ILE
1	B	556	THR
1	B	570	GLU
1	B	577	ASN
1	B	578	LEU

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	47	ASN
1	A	86	GLN
1	A	105	GLN
1	A	126	ASN
1	A	200	GLN
1	A	204	HIS
1	A	306	GLN
1	A	397	GLN
1	A	455	ASN
1	A	465	GLN
1	A	550	ASN

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Mol	Chain	Res	Type
1	A	571	HIS
1	B	47	ASN
1	B	48	HIS
1	B	105	GLN
1	B	126	ASN
1	B	200	GLN
1	B	306	GLN
1	B	397	GLN
1	B	455	ASN
1	B	465	GLN
1	B	571	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	ANP	B	700	2	33,33,33	4.75	21 (63%)	45,52,52	2.84	24 (53%)
3	ANP	A	701	2	33,33,33	4.83	23 (69%)	45,52,52	2.81	25 (55%)

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	ANP	B	700	2	-	8/18/38/38	0/3/3/3
3	ANP	A	701	2	-	8/18/38/38	0/3/3/3

All (44) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	701	ANP	PB-O3A	13.81	1.76	1.59
3	B	700	ANP	PB-O3A	13.76	1.76	1.59
3	A	701	ANP	PG-O1G	13.45	1.66	1.46
3	B	700	ANP	PG-O1G	12.47	1.65	1.46
3	B	700	ANP	PB-O1B	9.37	1.60	1.46
3	A	701	ANP	PB-O1B	8.59	1.59	1.46
3	B	700	ANP	PG-O3G	7.64	1.77	1.56
3	A	701	ANP	PG-O3G	7.41	1.76	1.56
3	A	701	ANP	PG-O2G	6.49	1.74	1.56
3	B	700	ANP	PG-O2G	6.34	1.73	1.56
3	B	700	ANP	PB-N3B	5.28	1.77	1.63
3	B	700	ANP	C2-N1	4.96	1.42	1.33
3	A	701	ANP	PA-O3A	-4.87	1.54	1.59
3	A	701	ANP	PG-N3B	4.36	1.74	1.63
3	A	701	ANP	C2-N1	4.32	1.41	1.33
3	A	701	ANP	PA-O2A	4.21	1.74	1.55
3	B	700	ANP	C3'-C4'	4.12	1.63	1.53
3	B	700	ANP	O4'-C4'	-4.01	1.36	1.45
3	A	701	ANP	C3'-C4'	4.00	1.63	1.53
3	A	701	ANP	C6-N1	3.98	1.46	1.35
3	A	701	ANP	PB-N3B	3.88	1.73	1.63
3	A	701	ANP	C6-N6	3.79	1.43	1.34
3	B	700	ANP	C6-N1	3.62	1.45	1.35
3	B	700	ANP	PA-O3A	-3.56	1.55	1.59
3	A	701	ANP	C5-C4	3.51	1.45	1.39
3	A	701	ANP	O4'-C4'	-3.50	1.37	1.45
3	B	700	ANP	PG-N3B	3.48	1.72	1.63
3	B	700	ANP	PA-O2A	3.40	1.71	1.55
3	B	700	ANP	C5-C4	3.25	1.44	1.39
3	B	700	ANP	C6-N6	3.07	1.42	1.34
3	A	701	ANP	O5'-C5'	3.04	1.56	1.44
3	A	701	ANP	C2'-C3'	2.79	1.60	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	700	ANP	C8-N9	2.76	1.42	1.37
3	B	700	ANP	O5'-C5'	2.72	1.54	1.44
3	A	701	ANP	C8-N9	2.55	1.41	1.37
3	A	701	ANP	C4-N9	-2.49	1.32	1.37
3	B	700	ANP	C2'-C3'	2.36	1.59	1.53
3	B	700	ANP	C2'-C1'	2.32	1.60	1.53
3	A	701	ANP	C2-N3	2.32	1.38	1.33
3	B	700	ANP	PA-O1A	2.28	1.58	1.50
3	A	701	ANP	C4-N3	2.18	1.38	1.34
3	B	700	ANP	C4-N3	2.17	1.38	1.34
3	A	701	ANP	C2'-C1'	2.08	1.60	1.53
3	A	701	ANP	O2'-C2'	2.02	1.48	1.43

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	ANP	C4'-O4'-C1'	-7.87	92.08	109.47
3	B	700	ANP	C4'-O4'-C1'	-7.67	92.53	109.47
3	B	700	ANP	O3A-PB-N3B	-6.97	87.24	106.59
3	A	701	ANP	O3A-PB-N3B	-6.86	87.57	106.59
3	B	700	ANP	N3-C2-N1	-5.65	120.03	128.58
3	A	701	ANP	N3-C2-N1	-5.04	120.95	128.58
3	A	701	ANP	O4'-C4'-C5'	4.76	124.60	109.33
3	B	700	ANP	O3'-C3'-C4'	4.66	124.47	111.08
3	B	700	ANP	O4'-C4'-C5'	4.44	123.56	109.33
3	A	701	ANP	O3'-C3'-C4'	4.24	123.27	111.08
3	A	701	ANP	O5'-C5'-C4'	-3.95	95.53	108.99
3	B	700	ANP	C2'-C3'-C4'	-3.71	95.44	102.61
3	B	700	ANP	O5'-C5'-C4'	-3.68	96.46	108.99
3	A	701	ANP	C2'-C3'-C4'	-3.56	95.74	102.61
3	B	700	ANP	N6-C6-N1	3.35	125.85	118.38
3	B	700	ANP	C2-N3-C4	3.29	119.86	111.83
3	A	701	ANP	N6-C6-N1	3.24	125.59	118.38
3	B	700	ANP	O5'-PA-O1A	3.22	121.71	108.94
3	B	700	ANP	O2B-PB-O3A	3.14	115.12	104.64
3	A	701	ANP	O5'-PA-O1A	3.07	121.08	108.94
3	A	701	ANP	C2-N3-C4	3.03	119.24	111.83
3	B	700	ANP	C5-C6-N6	-2.97	115.94	123.29
3	A	701	ANP	C5-C6-N6	-2.95	115.99	123.29
3	A	701	ANP	O2G-PG-O3G	2.89	115.36	107.59
3	B	700	ANP	N3-C4-N9	2.88	132.07	127.17
3	A	701	ANP	N3-C4-N9	2.78	131.90	127.17

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	701	ANP	O2B-PB-O3A	2.78	113.91	104.64
3	B	700	ANP	C5-N7-C8	2.73	107.74	103.45
3	A	701	ANP	C5-C4-N3	-2.60	123.13	126.72
3	B	700	ANP	C5-C4-N3	-2.52	123.25	126.72
3	B	700	ANP	C4-N9-C8	2.50	108.37	105.74
3	B	700	ANP	N9-C8-N7	-2.50	110.39	113.94
3	A	701	ANP	O3'-C3'-C2'	2.47	119.72	111.82
3	A	701	ANP	O2A-PA-O3A	-2.44	100.67	107.27
3	A	701	ANP	O1B-PB-N3B	2.44	115.37	111.77
3	A	701	ANP	O3G-PG-O1G	-2.43	107.36	113.45
3	B	700	ANP	O2'-C2'-C1'	2.36	118.22	110.10
3	B	700	ANP	O3'-C3'-C2'	2.32	119.25	111.82
3	B	700	ANP	O2G-PG-O3G	2.28	113.71	107.59
3	B	700	ANP	C2'-C1'-N9	2.26	118.93	113.30
3	A	701	ANP	C4-N9-C8	2.25	108.10	105.74
3	A	701	ANP	PA-O5'-C5'	-2.22	108.64	121.35
3	A	701	ANP	O4'-C1'-C2'	-2.22	101.87	106.62
3	A	701	ANP	C5-N7-C8	2.19	106.89	103.45
3	B	700	ANP	O4'-C1'-C2'	-2.15	102.02	106.62
3	A	701	ANP	O3A-PA-O1A	2.14	117.13	110.70
3	B	700	ANP	PA-O5'-C5'	-2.12	109.21	121.35
3	A	701	ANP	O2'-C2'-C1'	2.10	117.32	110.10
3	B	700	ANP	O3G-PG-O1G	-2.01	108.41	113.45

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	701	ANP	PB-N3B-PG-O1G
3	A	701	ANP	PG-N3B-PB-O1B
3	A	701	ANP	PG-N3B-PB-O3A
3	A	701	ANP	C5'-O5'-PA-O1A
3	A	701	ANP	C5'-O5'-PA-O2A
3	A	701	ANP	C5'-O5'-PA-O3A
3	A	701	ANP	O4'-C4'-C5'-O5'
3	B	700	ANP	PB-N3B-PG-O1G
3	B	700	ANP	PG-N3B-PB-O1B
3	B	700	ANP	PG-N3B-PB-O3A
3	B	700	ANP	C5'-O5'-PA-O1A
3	B	700	ANP	C5'-O5'-PA-O2A
3	B	700	ANP	C5'-O5'-PA-O3A
3	B	700	ANP	O4'-C4'-C5'-O5'

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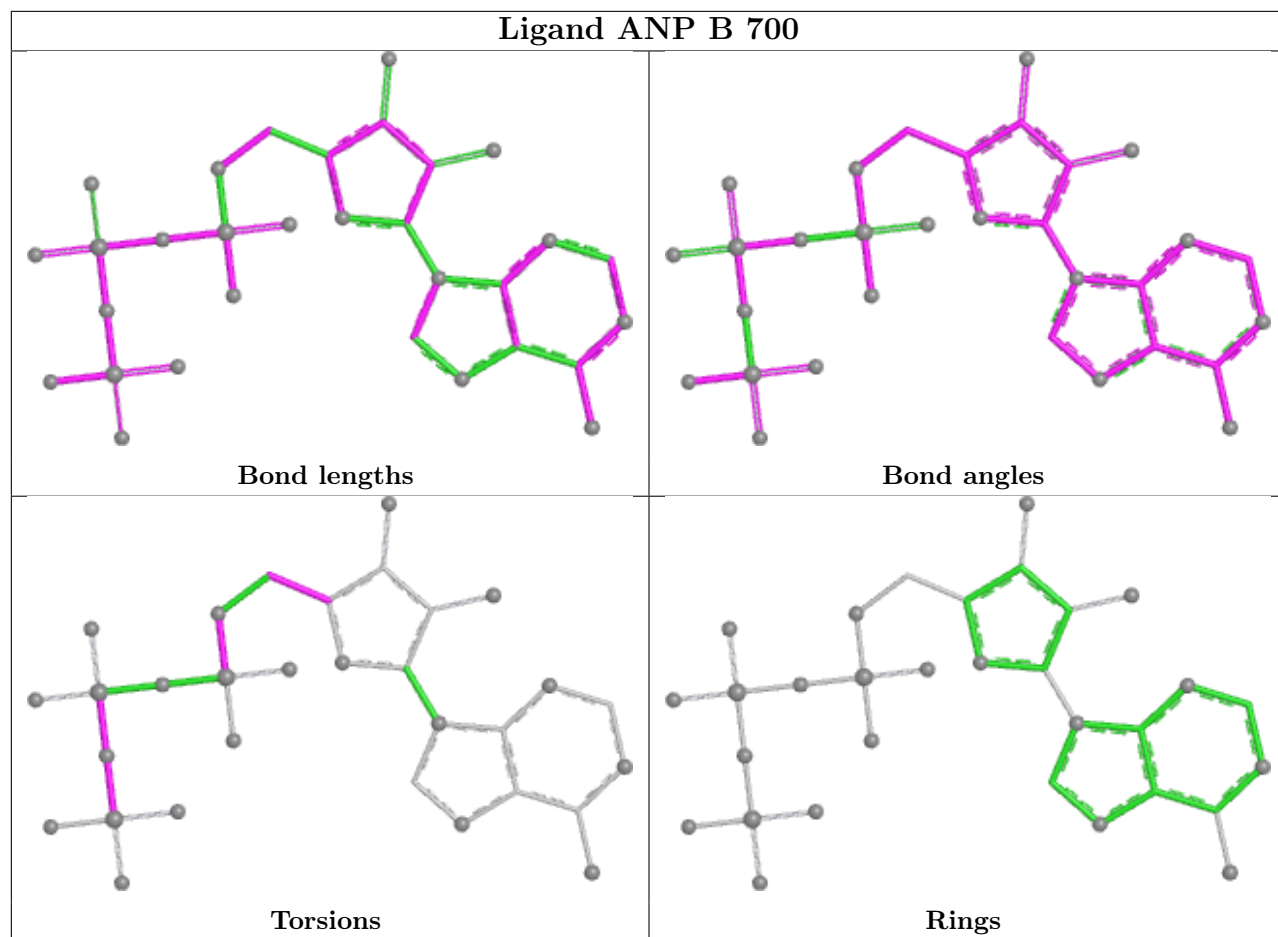
Mol	Chain	Res	Type	Atoms
3	A	701	ANP	C3'-C4'-C5'-O5'
3	B	700	ANP	C3'-C4'-C5'-O5'

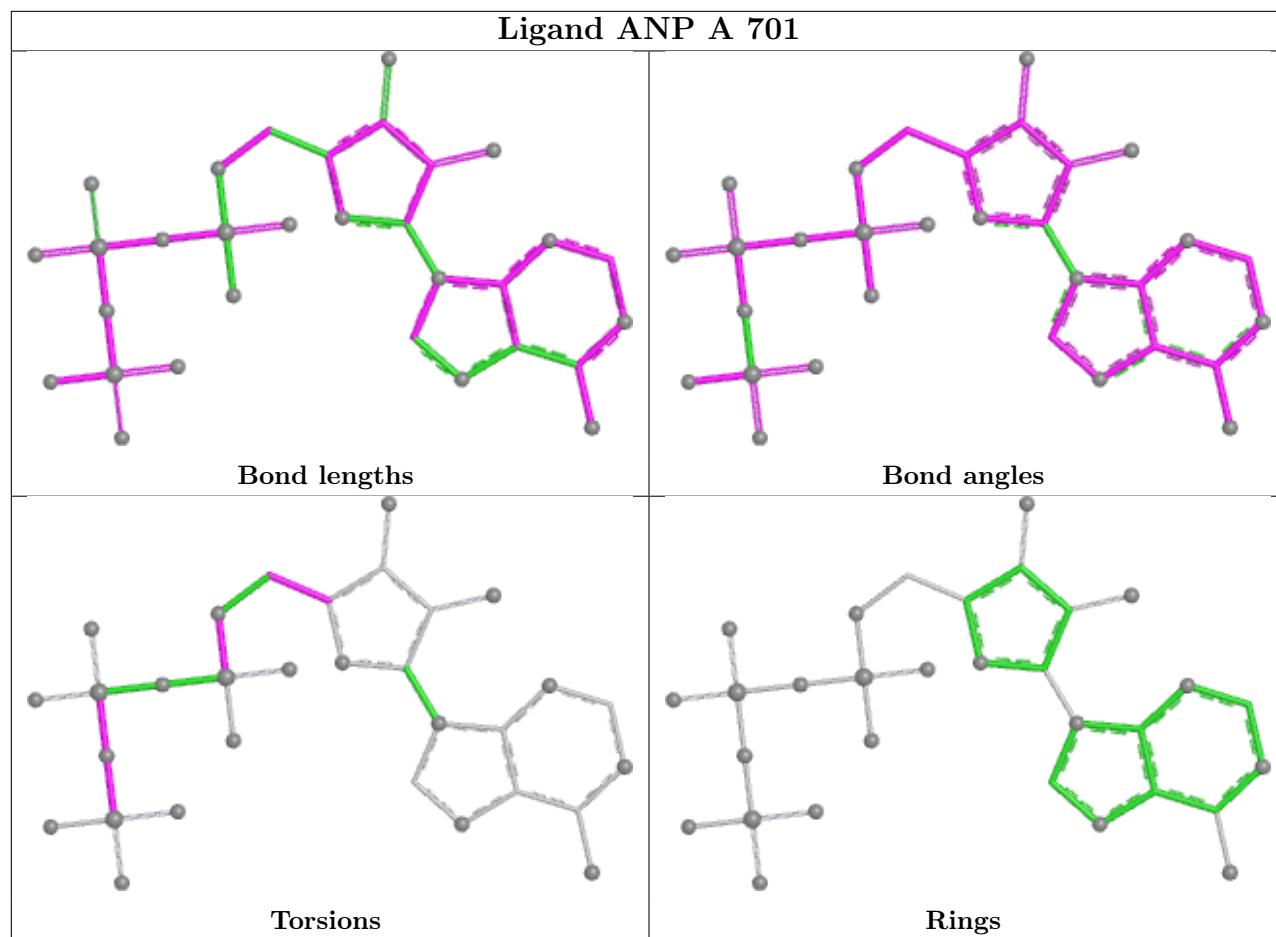
There are no ring outliers.

2 monomers are involved in 17 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	700	ANP	9	0
3	A	701	ANP	8	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	578/578 (100%)	0.21	19 (3%)	49	36	55, 120, 187, 200	0
1	B	578/578 (100%)	0.19	24 (4%)	40	29	52, 117, 194, 200	0
All	All	1156/1156 (100%)	0.20	43 (3%)	45	32	52, 119, 189, 200	0

All (43) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	507	ALA	4.9
1	A	374	GLY	4.6
1	A	277	VAL	4.0
1	B	374	GLY	3.9
1	B	54	GLU	3.8
1	B	47	ASN	3.8
1	A	507	ALA	3.6
1	A	1	MET	3.4
1	A	256	ASP	3.4
1	B	55	LYS	3.3
1	B	481	GLY	3.3
1	B	534	HIS	3.2
1	B	46	ASN	3.2
1	B	556	THR	3.1
1	A	534	HIS	3.0
1	A	422	GLN	3.0
1	A	259	PRO	3.0
1	B	483	LYS	2.8
1	A	90	ASN	2.7
1	A	375	MET	2.7
1	A	556	THR	2.6
1	B	338	GLY	2.6
1	B	37	ILE	2.6
1	A	255	THR	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	192	ARG	2.4
1	B	36	LEU	2.4
1	A	143	TRP	2.4
1	A	282	ALA	2.3
1	B	13	LYS	2.3
1	B	41	ILE	2.3
1	B	44	VAL	2.3
1	A	289	LEU	2.2
1	A	173	PHE	2.2
1	B	1	MET	2.2
1	A	188	LEU	2.2
1	A	565	LYS	2.1
1	B	56	VAL	2.1
1	B	271	ILE	2.1
1	B	478	LEU	2.1
1	B	45	ILE	2.0
1	A	453	MET	2.0
1	B	273	GLY	2.0
1	B	422	GLN	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.

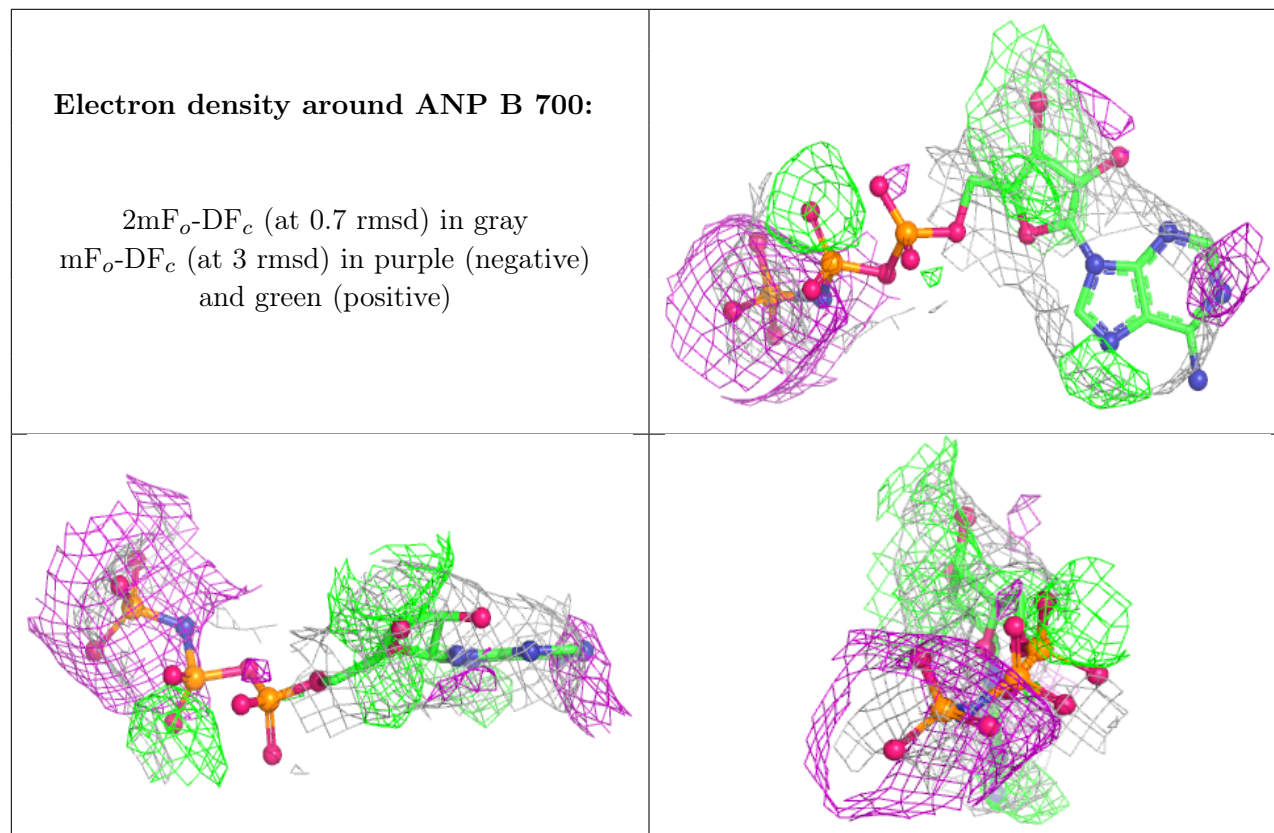
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ANP	B	700	31/31	0.84	0.16	74,74,74,74	0
3	ANP	A	701	31/31	0.86	0.14	80,80,80,80	0
2	NA	A	900	1/1	0.88	0.06	125,125,125,125	0
2	NA	B	901	1/1	0.88	0.12	64,64,64,64	0

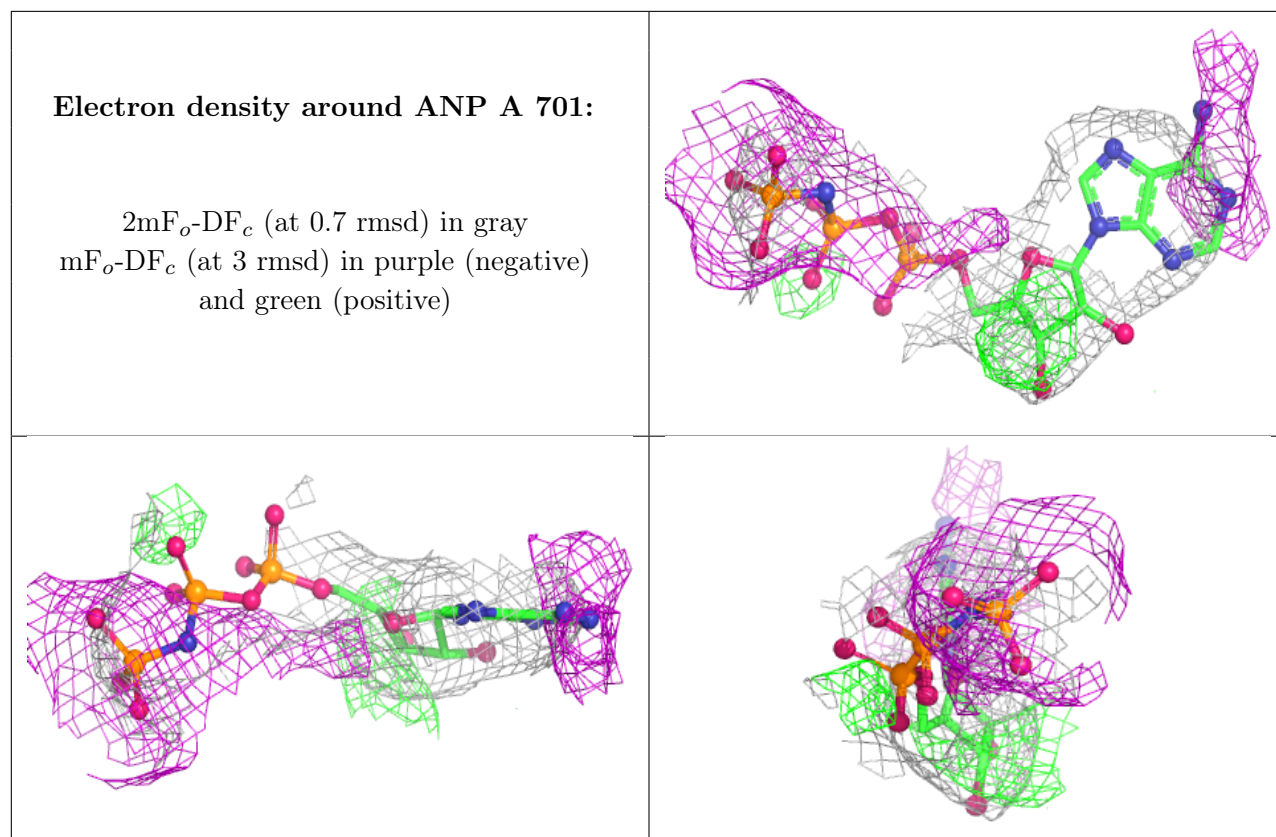
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	NA	B	910	1/1	0.89	0.08	132,132,132,132	0
2	NA	A	911	1/1	0.92	0.12	63,63,63,63	0

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.