



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:19 PM UTC

PDB ID : 5ZQ7 / pdb_00005zq7
Title : SidE-Ubi-NAD
Authors : Wang, Y.; Gao, A.; Gao, P.
Deposited on : 2018-04-17
Resolution : 2.85 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

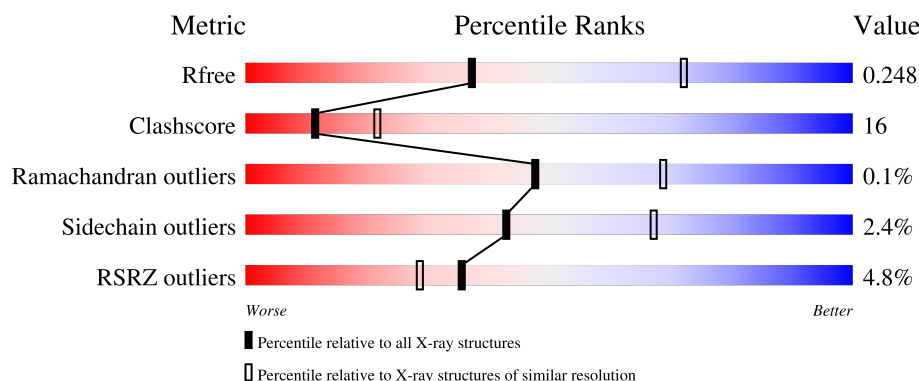
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1520 (2.86-2.82)
Clashscore	190562	1559 (2.86-2.82)
Ramachandran outliers	187476	1517 (2.86-2.82)
Sidechain outliers	187428	1518 (2.86-2.82)
RSRZ outliers	180081	1521 (2.86-2.82)

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	845	4% 73% 23% ..
1	C	845	5% 70% 25% ..
2	B	79	70% 27% .
2	D	79	13% 53% 42% ..

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
4	AMP	C	1102	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14508 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 Side.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	828	Total	C	N	O	S	Se	0	0	0
			6606	4164	1153	1267	6	16			
1	C	824	Total	C	N	O	S	Se	0	0	0
			6578	4149	1149	1258	6	16			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	221	MSE	-	initiating methionine	UNP Q6RCR1
A	1058	LEU	-	expression tag	UNP Q6RCR1
A	1059	GLU	-	expression tag	UNP Q6RCR1
A	1060	HIS	-	expression tag	UNP Q6RCR1
A	1061	HIS	-	expression tag	UNP Q6RCR1
A	1062	HIS	-	expression tag	UNP Q6RCR1
A	1063	HIS	-	expression tag	UNP Q6RCR1
A	1064	HIS	-	expression tag	UNP Q6RCR1
A	1065	HIS	-	expression tag	UNP Q6RCR1
C	221	MSE	-	initiating methionine	UNP Q6RCR1
C	1058	LEU	-	expression tag	UNP Q6RCR1
C	1059	GLU	-	expression tag	UNP Q6RCR1
C	1060	HIS	-	expression tag	UNP Q6RCR1
C	1061	HIS	-	expression tag	UNP Q6RCR1
C	1062	HIS	-	expression tag	UNP Q6RCR1
C	1063	HIS	-	expression tag	UNP Q6RCR1
C	1064	HIS	-	expression tag	UNP Q6RCR1
C	1065	HIS	-	expression tag	UNP Q6RCR1

- Molecule 2 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	76	Total	C	N	O	S	0	0	0
			595	375	102	117	1			

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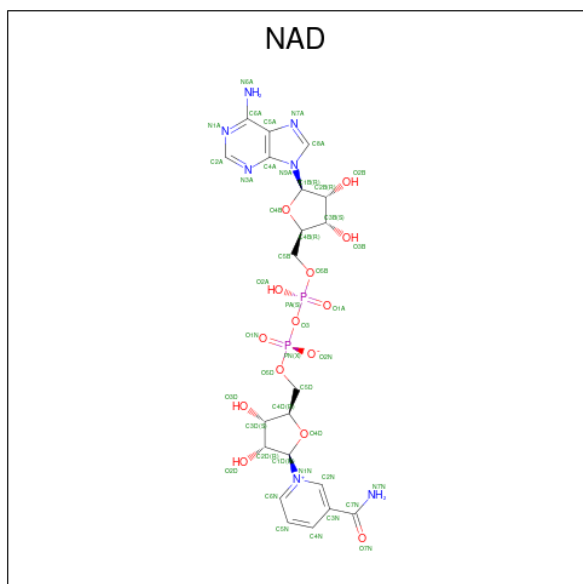
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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	76	Total	C	N	O	S	0	0	0
			595	375	102	117	1			

There are 8 discrepancies between the modelled and reference sequences:

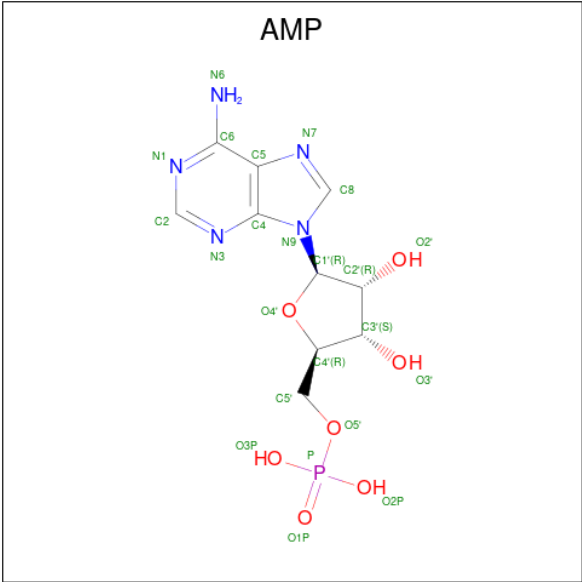
Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	GLY	-	expression tag	UNP P0CG48
B	-1	GLY	-	expression tag	UNP P0CG48
B	0	SER	-	expression tag	UNP P0CG48
B	42	ALA	ARG	engineered mutation	UNP P0CG48
D	-2	GLY	-	expression tag	UNP P0CG48
D	-1	GLY	-	expression tag	UNP P0CG48
D	0	SER	-	expression tag	UNP P0CG48
D	42	ALA	ARG	engineered mutation	UNP P0CG48

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: $C_{10}H_{14}N_5O_7P$).

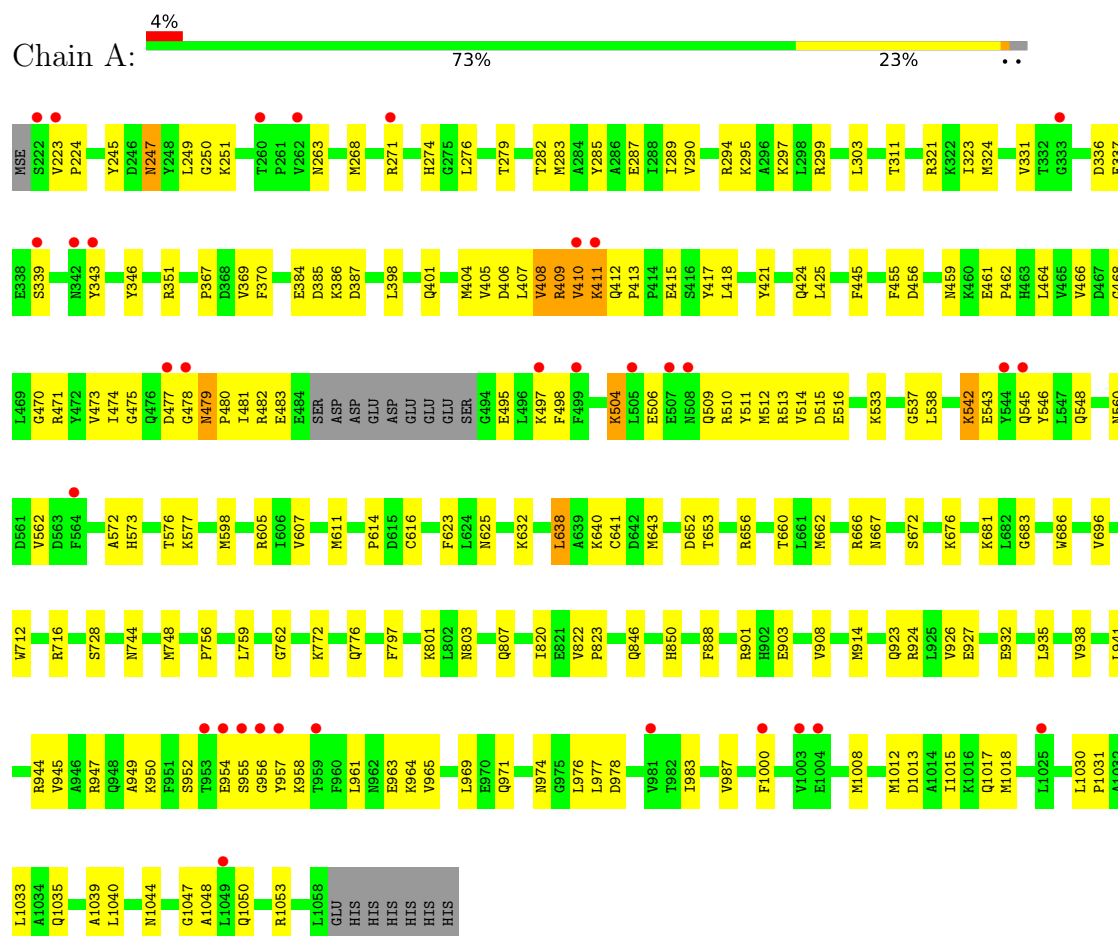


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

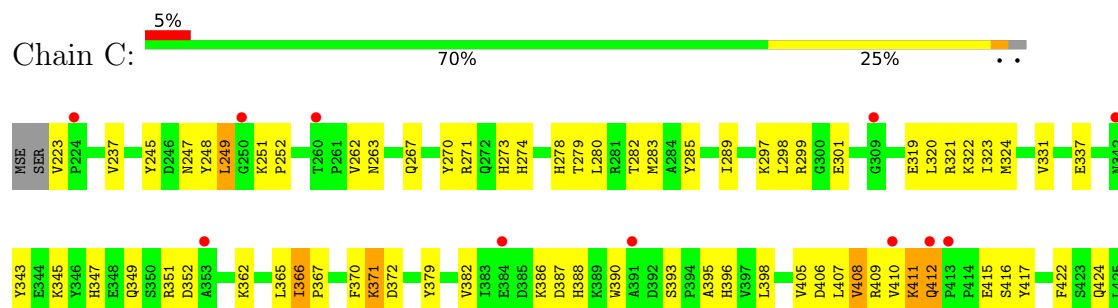
3 Residue-property plots

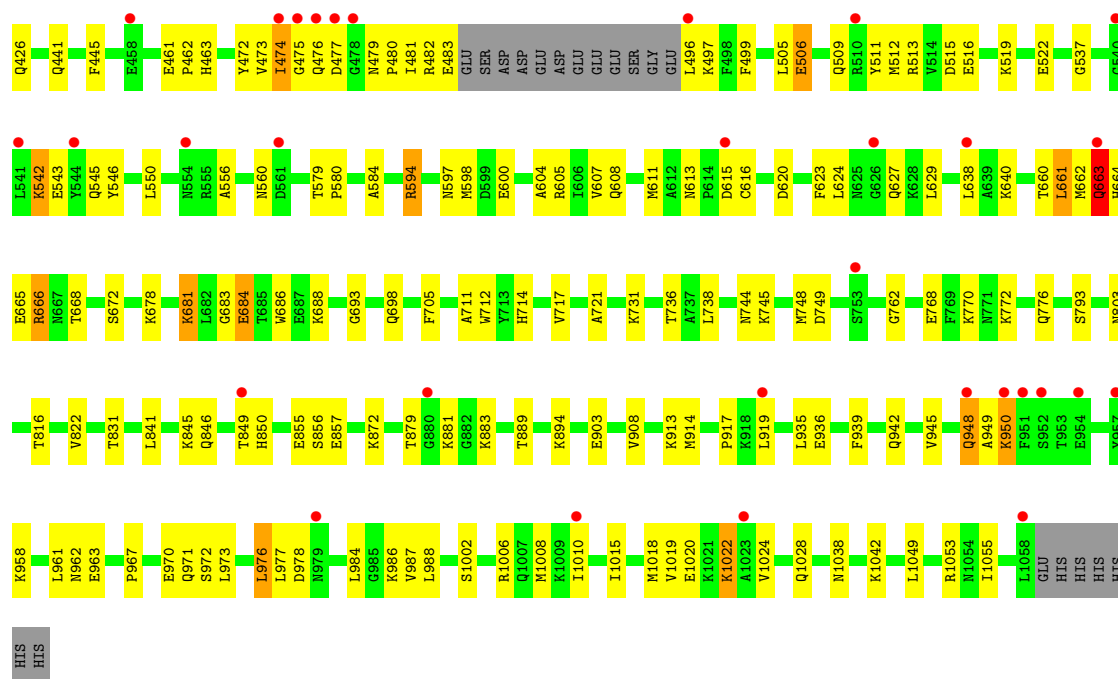
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: SidE



• Molecule 1: SidE

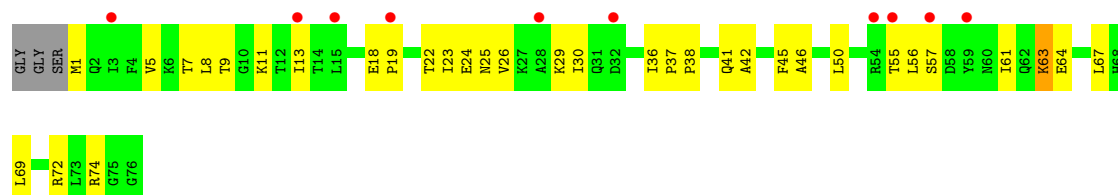




• Molecule 2: Ubiquitin



• Molecule 2: Ubiquitin



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.41Å 129.38Å 192.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.94 – 2.85 48.94 – 2.85	Depositor EDS
% Data completeness (in resolution range)	99.6 (48.94-2.85) 99.8 (48.94-2.85)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.76 (at 2.86Å)	Xtriage
Refinement program	PHENIX (1.11.1 _2575: ???)	Depositor
R, R_{free}	0.192 , 0.239 0.207 , 0.248	Depositor DCC
R_{free} test set	2847 reflections (5.14%)	wwPDB-VP
Wilson B-factor (Å ²)	59.6	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 63.8	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	0.92	EDS
Total number of atoms	14508	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.67% 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: NAD, AMP

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	0.34	3/6720 (0.0%)	0.63	4/9053 (0.0%)
1	C	0.54	3/6692 (0.0%)	0.67	7/9016 (0.1%)
2	B	0.59	1/601 (0.2%)	0.67	1/809 (0.1%)
2	D	0.40	0/601	0.74	0/809
All	All	0.45	7/14614 (0.0%)	0.65	12/19687 (0.1%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	36	ILE	N-CA	11.35	1.55	1.46
1	C	661	LEU	C-O	-5.91	1.17	1.24
1	A	339	SER	CA-C	5.73	1.57	1.52
1	C	249	LEU	CA-C	-5.62	1.45	1.52
1	C	684	GLU	C-O	-5.28	1.18	1.24
1	A	250	GLY	C-O	-5.14	1.17	1.23
1	A	406	ASP	C-O	-5.11	1.17	1.24

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	247	ASN	N-CA-C	8.54	121.82	111.40
1	A	410	VAL	N-CA-C	6.87	117.66	110.72
1	C	962	ASN	CA-C-N	-6.12	110.26	121.52
1	C	962	ASN	C-N-CA	-6.12	110.26	121.52
1	C	620	ASP	N-CA-C	5.71	117.58	111.36
1	C	412	GLN	N-CA-C	-5.49	103.21	110.40
1	C	249	LEU	N-CA-C	-5.24	103.11	110.50
1	A	408	VAL	N-CA-C	5.24	115.96	110.62
1	C	663	GLN	CB-CA-C	-5.19	102.74	110.88
1	C	506	GLU	N-CA-C	5.18	116.62	110.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	408	VAL	CB-CA-C	-5.13	105.21	112.14
2	B	36	ILE	O-C-N	5.00	124.52	121.37

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	6606	0	6542	189	0
1	C	6578	0	6522	239	0
2	B	595	0	621	13	0
2	D	595	0	621	33	0
3	A	44	0	26	0	0
3	C	44	0	26	3	0
4	A	23	0	12	1	0
4	C	23	0	12	7	0
All	All	14508	0	14382	464	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 16.

All (464) 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:411:LYS:HB3	1:A:417:TYR:CE2	1.38	1.58
1:C:475:GLY:CA	1:C:509:GLN:HG2	1.43	1.42
1:C:473:VAL:HG23	1:C:481:ILE:CD1	1.47	1.42
1:C:475:GLY:HA2	1:C:509:GLN:CG	1.59	1.32
1:A:411:LYS:HB2	1:A:417:TYR:CD2	1.66	1.29
1:A:411:LYS:CB	1:A:417:TYR:CE2	2.14	1.28
1:C:949:ALA:HB2	1:C:961:LEU:CD1	1.67	1.23
1:A:411:LYS:CB	1:A:417:TYR:CD2	2.24	1.20
1:A:247:ASN:O	1:A:251:LYS:HD2	1.40	1.18
1:A:954:GLU:OE1	1:A:1000:PHE:HA	1.41	1.17

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:473:VAL:CG2	1:C:481:ILE:HD13	1.76	1.14
1:C:949:ALA:HB2	1:C:961:LEU:HD12	1.29	1.13
1:C:949:ALA:CB	1:C:961:LEU:HD12	1.80	1.12
1:C:472:TYR:CE2	1:C:496:LEU:HD23	1.87	1.10
1:C:424:GLN:NE2	4:C:1102:AMP:HN62	1.50	1.09
1:C:1006:ARG:O	1:C:1010:ILE:HD12	1.52	1.07
1:C:973:LEU:HD13	1:C:977:LEU:HD12	1.38	1.06
1:A:411:LYS:HD3	1:A:417:TYR:CZ	1.89	1.05
1:C:424:GLN:HE21	4:C:1102:AMP:N6	1.54	1.05
1:C:473:VAL:HG23	1:C:481:ILE:HD13	1.06	1.04
1:A:412:GLN:HG3	1:A:413:PRO:HA	1.40	1.04
1:C:415:GLU:OE2	1:C:415:GLU:N	1.89	1.04
1:C:473:VAL:HG23	1:C:481:ILE:HD12	1.36	1.02
1:C:474:ILE:HG22	1:C:480:PRO:HA	1.40	1.02
1:C:474:ILE:HG22	1:C:480:PRO:CA	1.90	1.00
1:C:973:LEU:HD13	1:C:977:LEU:CD1	1.92	1.00
1:A:483:GLU:HG2	1:A:497:LYS:HB2	1.45	0.99
1:C:405:VAL:O	1:C:408:VAL:HG12	1.62	0.98
1:C:949:ALA:HB2	1:C:961:LEU:HD11	1.44	0.98
1:A:954:GLU:OE2	1:A:1000:PHE:HB3	1.61	0.98
1:C:409:ARG:HG3	1:C:410:VAL:H	1.26	0.98
1:C:411:LYS:HB3	1:C:417:TYR:CE2	2.01	0.95
1:C:474:ILE:CG2	1:C:480:PRO:HA	1.98	0.94
4:C:1102:AMP:H8	4:C:1102:AMP:H5'2	1.32	0.94
1:C:473:VAL:CG2	1:C:481:ILE:CD1	2.40	0.93
1:A:410:VAL:HG13	1:A:411:LYS:HG2	1.50	0.93
1:A:411:LYS:HB3	1:A:417:TYR:HE2	1.28	0.92
1:A:504:LYS:HE2	1:A:504:LYS:HA	1.52	0.91
1:A:504:LYS:HA	1:A:504:LYS:CE	2.01	0.90
1:A:409:ARG:HG2	1:A:445:PHE:CZ	2.07	0.89
1:C:474:ILE:HG22	1:C:479:ASN:C	1.97	0.89
1:C:362:LYS:O	1:C:366:ILE:HG22	1.74	0.88
2:D:1:MET:HG3	2:D:63:LYS:HB3	1.57	0.87
4:C:1102:AMP:H5'2	4:C:1102:AMP:C8	2.09	0.87
1:C:542:LYS:HA	1:C:542:LYS:CE	2.03	0.87
1:C:1006:ARG:O	1:C:1010:ILE:CD1	2.23	0.87
1:A:954:GLU:HB2	1:A:957:TYR:HB2	1.57	0.86
1:C:408:VAL:CG1	1:C:441:GLN:HE22	1.88	0.86
1:C:408:VAL:HG13	1:C:441:GLN:HE22	1.41	0.85
1:C:474:ILE:HG22	1:C:479:ASN:O	1.75	0.85
1:A:411:LYS:CD	1:A:417:TYR:CZ	2.59	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:954:GLU:CD	1:A:1000:PHE:HA	2.02	0.84
1:A:405:VAL:O	1:A:408:VAL:HG23	1.77	0.84
1:C:223:VAL:HG22	1:C:297:LYS:HD3	1.60	0.83
1:C:949:ALA:HA	1:C:958:LYS:HZ1	1.42	0.82
1:A:410:VAL:CG1	1:A:411:LYS:HG2	2.09	0.82
2:D:5:VAL:HG12	2:D:67:LEU:HB2	1.60	0.82
1:C:945:VAL:O	1:C:949:ALA:CB	2.28	0.82
1:C:474:ILE:HG22	1:C:480:PRO:N	1.94	0.81
1:C:248:TYR:O	1:C:251:LYS:HB2	1.81	0.81
1:C:386:LYS:HD2	1:C:386:LYS:O	1.81	0.80
1:C:424:GLN:HE21	4:C:1102:AMP:HN62	0.80	0.79
1:A:274:HIS:HB3	1:A:331:VAL:HG11	1.64	0.78
1:C:475:GLY:CA	1:C:509:GLN:CG	2.37	0.77
1:C:409:ARG:HG3	1:C:410:VAL:N	1.99	0.77
1:C:542:LYS:HA	1:C:542:LYS:HE2	1.64	0.77
1:C:973:LEU:CD1	1:C:977:LEU:CD1	2.61	0.77
2:D:7:THR:HG22	2:D:9:THR:H	1.49	0.77
1:C:973:LEU:CD1	1:C:977:LEU:HD11	2.14	0.77
1:C:473:VAL:C	1:C:481:ILE:HD12	2.10	0.76
1:C:613:ASN:HD21	1:C:615:ASP:HB2	1.49	0.76
1:C:408:VAL:CG1	1:C:441:GLN:NE2	2.48	0.76
1:C:475:GLY:HA3	1:C:509:GLN:HG2	1.62	0.76
1:A:482:ARG:HG3	1:A:495:GLU:H	1.49	0.76
1:C:762:GLY:H	3:C:1101:NAD:H72N	1.34	0.76
1:A:641:CYS:HB2	1:A:643:MSE:HE3	1.67	0.76
1:C:279:THR:HG22	1:C:283:MSE:HE2	1.65	0.75
1:C:472:TYR:CZ	1:C:496:LEU:HD23	2.21	0.75
1:C:474:ILE:N	1:C:481:ILE:HD12	2.02	0.75
1:A:1053:ARG:HA	1:C:1053:ARG:HA	1.68	0.75
1:C:366:ILE:HG13	1:C:367:PRO:HA	1.69	0.75
1:C:409:ARG:HB3	1:C:445:PHE:CE2	2.22	0.74
1:A:274:HIS:ND1	1:A:337:GLU:OE2	2.20	0.74
1:A:478:GLY:C	1:A:479:ASN:ND2	2.45	0.74
1:A:475:GLY:HA2	1:A:509:GLN:HG2	1.70	0.74
2:D:19:PRO:HB3	2:D:57:SER:HB2	1.69	0.74
1:C:850:HIS:ND1	1:C:856:SER:HA	2.03	0.73
1:A:744:ASN:O	1:A:748:MSE:HG3	1.88	0.72
1:C:949:ALA:CA	1:C:958:LYS:HZ1	2.03	0.72
1:A:409:ARG:HG2	1:A:445:PHE:HZ	1.55	0.71
1:C:945:VAL:O	1:C:949:ALA:HB3	1.92	0.70
1:A:404:MSE:O	1:A:407:LEU:HB2	1.91	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1053:ARG:HH11	1:C:1055:ILE:HB	1.56	0.69
1:C:472:TYR:CE2	1:C:496:LEU:CD2	2.73	0.69
1:C:409:ARG:HB3	1:C:445:PHE:CZ	2.27	0.69
1:C:475:GLY:HA2	1:C:509:GLN:HG2	0.70	0.69
1:C:505:LEU:HD22	1:C:506:GLU:HG2	1.73	0.69
2:B:7:THR:HG22	2:B:9:THR:H	1.59	0.69
1:C:879:THR:HG21	1:C:883:LYS:HE2	1.75	0.69
2:D:22:THR:HA	2:D:55:THR:HA	1.75	0.68
1:A:513:ARG:HB2	1:A:515:ASP:OD1	1.93	0.68
1:A:954:GLU:OE2	1:A:1000:PHE:CB	2.39	0.68
2:D:23:ILE:HD13	2:D:50:LEU:HB3	1.74	0.68
1:C:949:ALA:CB	1:C:961:LEU:CD1	2.48	0.68
2:D:45:PHE:HB2	2:D:67:LEU:HD22	1.76	0.67
1:C:474:ILE:CG2	1:C:480:PRO:CA	2.66	0.67
1:C:664:HIS:O	1:C:664:HIS:ND1	2.27	0.67
1:C:973:LEU:HD11	1:C:977:LEU:HD11	1.75	0.67
1:C:411:LYS:HB3	1:C:417:TYR:CD2	2.29	0.67
1:C:949:ALA:HB1	1:C:961:LEU:HD12	1.72	0.67
1:A:411:LYS:HD3	1:A:417:TYR:OH	1.95	0.66
1:A:477:ASP:OD2	1:A:479:ASN:ND2	2.28	0.65
1:A:1030:LEU:HD13	1:C:919:LEU:HD21	1.78	0.65
1:C:917:PRO:HB2	1:C:919:LEU:HG	1.76	0.65
1:C:474:ILE:CG2	1:C:479:ASN:O	2.45	0.65
1:A:424:GLN:HE21	4:A:1102:AMP:HN62	1.45	0.64
1:C:408:VAL:O	1:C:408:VAL:HG22	1.95	0.64
1:C:366:ILE:HD11	1:C:372:ASP:HA	1.77	0.64
1:C:482:ARG:HD3	1:C:496:LEU:N	2.12	0.64
1:C:594:ARG:NH2	1:C:600:GLU:OE2	2.30	0.64
1:A:224:PRO:O	1:A:294:ARG:NH2	2.29	0.63
1:A:455:PHE:O	1:A:533:LYS:HG2	1.97	0.63
1:C:945:VAL:O	1:C:949:ALA:HB2	1.97	0.63
2:D:30:ILE:HG22	2:D:36:ILE:HG21	1.79	0.63
1:C:472:TYR:CD2	1:C:496:LEU:HD23	2.31	0.63
1:C:745:LYS:NZ	1:C:749:ASP:OD2	2.31	0.63
1:C:351:ARG:NH1	1:C:352:ASP:OD1	2.32	0.63
1:C:424:GLN:NE2	4:C:1102:AMP:N6	2.26	0.63
1:C:319:GLU:O	1:C:323:ILE:HG12	1.98	0.62
1:A:947:ARG:O	1:A:950:LYS:HG2	1.98	0.62
1:A:977:LEU:HD21	1:C:598:MSE:HE1	1.82	0.62
1:C:386:LYS:HD2	1:C:386:LYS:C	2.25	0.62
1:A:776:GLN:HB3	1:A:803:ASN:HB3	1.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1013:ASP:O	1:A:1017:GLN:HG3	1.99	0.61
1:C:472:TYR:CD2	1:C:496:LEU:CD2	2.83	0.61
2:D:63:LYS:O	2:D:64:GLU:HB2	2.00	0.61
2:D:41:GLN:HB3	2:D:69:LEU:HD11	1.83	0.61
1:A:504:LYS:HE2	1:A:504:LYS:CA	2.26	0.61
2:B:22:THR:HG23	2:B:25:ASN:H	1.65	0.61
1:C:627:GLN:HG3	1:C:913:LYS:HB2	1.81	0.61
1:A:598:MSE:HE3	1:A:908:VAL:HG21	1.83	0.60
1:C:512:MSE:HG3	1:C:516:GLU:HG3	1.83	0.60
1:C:343:TYR:HE2	1:C:388:HIS:NE2	2.00	0.60
1:A:506:GLU:HB2	1:A:509:GLN:OE1	2.01	0.60
1:C:411:LYS:CB	1:C:417:TYR:CD2	2.85	0.60
1:C:988:LEU:HD11	1:C:1020:GLU:HB2	1.84	0.60
1:A:483:GLU:CG	1:A:497:LYS:HB2	2.27	0.59
1:A:935:LEU:HD11	1:A:976:LEU:HB3	1.84	0.59
1:C:515:ASP:O	1:C:519:LYS:HG3	2.02	0.59
1:A:290:VAL:O	1:A:294:ARG:HG3	2.03	0.59
1:A:411:LYS:HD3	1:A:417:TYR:CE2	2.38	0.59
1:A:407:LEU:O	1:A:410:VAL:HG12	2.03	0.59
1:A:483:GLU:HG2	1:A:497:LYS:CB	2.27	0.59
1:C:762:GLY:N	3:C:1101:NAD:H72N	2.01	0.59
1:C:973:LEU:O	1:C:977:LEU:HD12	2.03	0.59
1:A:632:LYS:O	1:A:632:LYS:HG3	2.02	0.58
1:A:473:VAL:HG23	1:A:481:ILE:HD12	1.84	0.58
1:C:542:LYS:HB2	1:C:545:GLN:OE1	2.03	0.58
1:C:409:ARG:CG	1:C:410:VAL:H	2.09	0.58
1:C:248:TYR:O	1:C:271:ARG:NH2	2.36	0.58
1:C:660:THR:O	1:C:663:GLN:HB2	2.02	0.58
1:A:285:TYR:O	1:A:289:ILE:HG13	2.04	0.57
1:A:945:VAL:O	1:A:949:ALA:HB2	2.05	0.57
1:A:474:ILE:HD13	1:A:510:ARG:HH21	1.70	0.57
1:A:223:VAL:HG22	1:A:297:LYS:HD3	1.87	0.57
1:C:672:SER:HB2	1:C:712:TRP:HA	1.87	0.57
1:A:409:ARG:HB3	1:A:445:PHE:CE2	2.39	0.57
1:A:625:ASN:HB2	1:A:914:MSE:HG2	1.86	0.57
1:A:672:SER:HB2	1:A:712:TRP:HA	1.87	0.57
1:C:665:GLU:OE1	1:C:731:LYS:NZ	2.36	0.57
1:C:881:LYS:HB2	1:C:883:LYS:NZ	2.20	0.57
1:A:605:ARG:HH21	1:A:605:ARG:HG3	1.69	0.56
1:C:939:PHE:HD1	1:C:942:GLN:OE1	1.89	0.56
1:A:456:ASP:HA	1:A:533:LYS:HG2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:483:GLU:OE1	1:A:483:GLU:HA	2.05	0.56
1:C:1049:LEU:O	1:C:1053:ARG:HG3	2.06	0.56
1:A:923:GLN:HA	1:A:926:VAL:HG12	1.87	0.56
1:A:954:GLU:O	1:A:956:GLY:HA2	2.06	0.55
2:D:46:ALA:HB1	1:C:881:LYS:HE3	1.88	0.55
1:C:662:MSE:HG3	1:C:686:TRP:CD1	2.42	0.55
1:A:653:THR:HG22	1:A:656:ARG:HH21	1.71	0.55
1:C:367:PRO:HA	1:C:370:PHE:O	2.06	0.55
1:C:613:ASN:ND2	1:C:615:ASP:HB2	2.20	0.55
1:C:976:LEU:HD21	1:C:1019:VAL:HG22	1.88	0.55
1:A:411:LYS:HD2	1:A:417:TYR:CE1	2.42	0.55
1:A:954:GLU:CB	1:A:957:TYR:HB2	2.32	0.55
1:C:776:GLN:HB3	1:C:803:ASN:HB3	1.89	0.55
1:C:984:LEU:HA	1:C:987:VAL:HG12	1.89	0.55
1:A:343:TYR:OH	1:A:385:ASP:OD2	2.23	0.54
1:A:247:ASN:O	1:A:251:LYS:CD	2.34	0.54
2:D:56:LEU:CD1	2:D:61:ILE:HB	2.37	0.54
1:C:717:VAL:HG13	1:C:736:THR:HG23	1.88	0.54
1:A:1015:ILE:HA	1:A:1018:MSE:HE3	1.89	0.54
1:A:1031:PRO:O	1:A:1035:GLN:HG3	2.08	0.54
2:D:22:THR:HG23	2:D:25:ASN:H	1.72	0.54
1:A:478:GLY:C	1:A:479:ASN:HD22	2.16	0.54
1:A:251:LYS:O	1:A:271:ARG:NH1	2.41	0.54
1:A:482:ARG:HG3	1:A:495:GLU:N	2.19	0.54
1:C:616:CYS:HB2	1:C:623:PHE:O	2.07	0.54
1:A:662:MSE:HG3	1:A:686:TRP:CG	2.43	0.53
1:C:542:LYS:HE2	1:C:542:LYS:CA	2.36	0.53
1:A:974:ASN:HA	1:A:977:LEU:HD12	1.90	0.53
2:B:18:GLU:HG2	2:B:19:PRO:HD2	1.90	0.53
1:C:598:MSE:HG3	1:C:908:VAL:HG21	1.89	0.53
1:A:470:GLY:HA3	1:A:498:PHE:CE1	2.44	0.53
1:C:279:THR:O	1:C:283:MSE:HG3	2.08	0.53
1:C:280:LEU:HA	1:C:283:MSE:HE3	1.90	0.53
1:C:949:ALA:C	1:C:958:LYS:HZ1	2.17	0.53
1:A:459:ASN:O	1:A:514:VAL:HG23	2.09	0.52
1:A:963:GLU:HG3	1:A:964:LYS:HD2	1.91	0.52
2:B:22:THR:CG2	2:B:25:ASN:H	2.22	0.52
1:C:278:HIS:O	1:C:282:THR:HG23	2.09	0.52
1:C:343:TYR:CE2	1:C:388:HIS:NE2	2.76	0.52
1:C:939:PHE:HA	1:C:942:GLN:HG2	1.91	0.52
1:C:345:LYS:O	1:C:349:GLN:HG3	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:846:GLN:HG3	1:A:850:HIS:NE2	2.24	0.52
1:C:945:VAL:HG13	1:C:961:LEU:HD11	1.90	0.52
2:B:5:VAL:HG21	2:B:30:ILE:HD11	1.91	0.52
1:C:407:LEU:C	1:C:409:ARG:H	2.15	0.52
1:A:287:GLU:HB2	1:A:324:MSE:HE1	1.91	0.52
1:A:983:ILE:O	1:A:987:VAL:HG13	2.09	0.52
1:C:405:VAL:O	1:C:408:VAL:CG1	2.47	0.52
1:A:418:LEU:HD12	1:A:418:LEU:O	2.09	0.52
1:A:415:GLU:H	1:A:415:GLU:CD	2.17	0.52
2:D:72:ARG:NH2	1:C:855:GLU:OE1	2.38	0.52
1:C:505:LEU:HB3	1:C:509:GLN:OE1	2.09	0.51
1:C:948:GLN:HB3	1:C:1008:MSE:HE1	1.92	0.51
1:C:320:LEU:O	1:C:324:MSE:HG3	2.10	0.51
1:C:935:LEU:HD21	1:C:977:LEU:HG	1.92	0.51
1:C:323:ILE:HD12	1:C:395:ALA:HA	1.91	0.51
1:C:223:VAL:HG21	1:C:298:LEU:HG	1.92	0.51
1:C:280:LEU:HD23	1:C:283:MSE:HE3	1.92	0.51
1:C:711:ALA:HA	1:C:714:HIS:CE1	2.45	0.51
2:D:8:LEU:HD11	1:C:822:VAL:HG22	1.92	0.51
2:D:22:THR:HG22	2:D:25:ASN:OD1	2.10	0.51
1:C:462:PRO:HA	1:C:513:ARG:HA	1.93	0.51
1:A:411:LYS:CD	1:A:417:TYR:CE1	2.94	0.51
1:A:641:CYS:CB	1:A:643:MSE:HE3	2.36	0.51
1:A:820:ILE:O	1:A:823:PRO:HD2	2.11	0.51
1:A:412:GLN:HG3	1:A:413:PRO:CA	2.28	0.50
1:A:822:VAL:HB	1:A:823:PRO:HD3	1.94	0.50
1:A:249:LEU:O	1:A:271:ARG:HD2	2.11	0.50
2:D:56:LEU:HD11	2:D:61:ILE:HB	1.91	0.50
1:C:262:VAL:HG12	1:C:263:ASN:H	1.76	0.50
1:C:237:VAL:HG21	1:C:324:MSE:HE3	1.93	0.50
1:C:409:ARG:HB3	1:C:445:PHE:HE2	1.75	0.50
1:C:474:ILE:HA	1:C:480:PRO:HA	1.93	0.50
1:A:969:LEU:HD11	1:A:1012:MSE:HE1	1.94	0.50
1:A:797:PHE:CE1	1:A:801:LYS:HD2	2.46	0.50
1:A:954:GLU:CD	1:A:1000:PHE:CA	2.82	0.50
1:C:285:TYR:O	1:C:289:ILE:HG13	2.11	0.50
1:A:479:ASN:ND2	1:A:479:ASN:N	2.59	0.50
1:A:938:VAL:HG22	1:A:1015:ILE:HD12	1.92	0.50
1:A:956:GLY:O	1:A:1000:PHE:HE1	1.94	0.50
1:C:416:SER:OG	1:C:463:HIS:ND1	2.37	0.49
1:C:607:VAL:O	1:C:611:MSE:HG2	2.11	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:263:ASN:OD1	1:A:268:MSE:HG2	2.11	0.49
1:A:473:VAL:HG12	1:A:511:TYR:HD1	1.76	0.49
1:C:237:VAL:HG23	1:C:321:ARG:HG3	1.93	0.49
1:A:367:PRO:HA	1:A:370:PHE:O	2.12	0.49
1:A:949:ALA:O	1:A:958:LYS:HD3	2.13	0.49
1:A:961:LEU:HA	1:A:965:VAL:HG22	1.93	0.49
1:C:846:GLN:HG3	1:C:850:HIS:NE2	2.26	0.49
2:D:25:ASN:O	2:D:29:LYS:HD3	2.12	0.49
1:C:768:GLU:CD	1:C:768:GLU:H	2.18	0.49
1:C:1024:VAL:HA	1:C:1028:GLN:HE21	1.76	0.49
1:C:252:PRO:HG3	1:C:270:TYR:CE1	2.47	0.49
1:C:537:GLY:HA2	1:C:546:TYR:CZ	2.47	0.49
1:C:1010:ILE:HD12	1:C:1010:ILE:H	1.78	0.49
1:A:401:GLN:O	1:A:405:VAL:HG23	2.12	0.49
1:A:545:GLN:HA	1:A:548:GLN:HB2	1.95	0.49
1:C:1002:SER:O	1:C:1006:ARG:HG2	2.13	0.49
1:A:954:GLU:OE2	1:A:1000:PHE:CA	2.61	0.49
1:C:624:LEU:HD23	1:C:914:MSE:SE	2.63	0.49
1:C:772:LYS:O	1:C:776:GLN:HG3	2.13	0.49
1:C:976:LEU:HD13	1:C:984:LEU:HD21	1.94	0.48
1:A:573:HIS:CE1	1:A:577:LYS:HE2	2.48	0.48
1:C:857:GLU:OE1	3:C:1101:NAD:O2D	2.31	0.48
1:C:274:HIS:HB3	1:C:331:VAL:HG21	1.95	0.48
1:C:624:LEU:CD2	1:C:914:MSE:SE	3.12	0.48
1:A:666:ARG:HA	1:A:683:GLY:HA3	1.95	0.48
2:D:19:PRO:CB	2:D:57:SER:HB2	2.41	0.48
2:D:22:THR:CG2	2:D:24:GLU:HB2	2.44	0.48
2:B:15:LEU:HD23	2:B:33:LYS:NZ	2.29	0.48
1:C:366:ILE:HG13	1:C:367:PRO:CA	2.41	0.48
1:C:881:LYS:HB2	1:C:883:LYS:HZ2	1.77	0.48
1:A:409:ARG:CG	1:A:445:PHE:CZ	2.90	0.48
1:C:666:ARG:HA	1:C:683:GLY:HA3	1.95	0.48
1:C:745:LYS:HA	1:C:748:MSE:HE3	1.94	0.48
1:A:652:ASP:HB3	1:A:696:VAL:HG11	1.95	0.47
1:A:245:TYR:OH	1:A:560:ASN:OD1	2.24	0.47
1:A:418:LEU:HD23	1:A:455:PHE:CD2	2.49	0.47
1:C:475:GLY:HA3	1:C:509:GLN:HE21	1.79	0.47
1:A:410:VAL:CG1	1:A:411:LYS:CE	2.91	0.47
1:A:479:ASN:HD22	1:A:479:ASN:N	2.12	0.47
1:A:978:ASP:OD1	1:C:605:ARG:NH2	2.46	0.47
1:A:1040:LEU:HG	1:A:1048:ALA:CB	2.45	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:542:LYS:HE2	1:A:542:LYS:HA	1.97	0.47
2:B:25:ASN:O	2:B:29:LYS:HG3	2.14	0.47
1:C:386:LYS:C	1:C:386:LYS:CD	2.88	0.47
1:C:497:LYS:HG3	1:C:499:PHE:CE1	2.49	0.47
1:A:954:GLU:O	1:A:957:TYR:N	2.47	0.47
1:A:1040:LEU:HG	1:A:1048:ALA:HB2	1.97	0.47
1:C:474:ILE:C	1:C:481:ILE:HD11	2.39	0.47
2:D:36:ILE:HG23	2:D:41:GLN:NE2	2.29	0.47
1:A:515:ASP:OD1	1:A:516:GLU:N	2.48	0.47
1:C:279:THR:O	1:C:282:THR:OG1	2.22	0.47
1:A:482:ARG:CG	1:A:495:GLU:H	2.21	0.47
1:A:410:VAL:CG1	1:A:411:LYS:HE2	2.45	0.46
1:C:474:ILE:HG23	1:C:480:PRO:HA	1.93	0.46
1:C:948:GLN:HG3	1:C:948:GLN:O	2.15	0.46
1:A:468:GLY:O	1:A:498:PHE:HZ	1.99	0.46
1:A:542:LYS:HA	1:A:542:LYS:CE	2.46	0.46
1:A:407:LEU:HD23	1:A:407:LEU:HA	1.80	0.46
2:B:1:MET:HE2	2:B:17:VAL:HG23	1.96	0.46
1:A:957:TYR:O	1:A:961:LEU:HG	2.15	0.46
1:C:351:ARG:HG2	1:C:351:ARG:HH11	1.80	0.46
2:B:23:ILE:O	2:B:27:LYS:HG3	2.15	0.46
1:C:390:TRP:CZ2	4:C:1102:AMP:H2'	2.51	0.46
1:C:461:GLU:HG3	1:C:462:PRO:HD2	1.98	0.46
1:A:640:LYS:NZ	1:A:903:GLU:OE2	2.48	0.46
1:C:247:ASN:C	1:C:248:TYR:CD2	2.93	0.46
1:C:664:HIS:ND1	1:C:664:HIS:C	2.72	0.46
1:C:343:TYR:HE1	1:C:347:HIS:CE1	2.34	0.46
1:C:407:LEU:C	1:C:409:ARG:N	2.74	0.46
1:C:474:ILE:HD12	1:C:475:GLY:N	2.30	0.46
1:A:249:LEU:O	1:A:271:ARG:CD	2.63	0.46
1:A:756:PRO:HG2	1:A:759:LEU:HD21	1.97	0.46
1:A:954:GLU:HB2	1:A:957:TYR:CB	2.35	0.46
1:C:410:VAL:HG13	1:C:411:LYS:N	2.30	0.46
1:C:816:THR:O	1:C:857:GLU:HA	2.16	0.46
1:A:474:ILE:N	1:A:510:ARG:O	2.41	0.46
1:C:744:ASN:HB3	1:C:748:MSE:HE2	1.98	0.46
1:C:748:MSE:HA	1:C:845:LYS:HD2	1.98	0.46
1:C:473:VAL:HG12	1:C:511:TYR:HD1	1.81	0.46
1:A:480:PRO:HB3	1:A:512:MSE:HE3	1.98	0.45
1:C:604:ALA:O	1:C:608:GLN:HG3	2.16	0.45
1:A:407:LEU:CD1	1:A:421:TYR:OH	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:693:GLY:O	1:C:698:GLN:HG2	2.16	0.45
1:C:945:VAL:HG13	1:C:961:LEU:CD1	2.47	0.45
1:A:762:GLY:HA3	1:A:823:PRO:HB3	1.99	0.45
2:B:22:THR:O	2:B:26:VAL:HG23	2.17	0.45
1:C:343:TYR:HE2	1:C:388:HIS:CE1	2.34	0.45
1:C:474:ILE:CA	1:C:481:ILE:HD12	2.46	0.45
1:A:405:VAL:O	1:A:408:VAL:CG2	2.59	0.45
1:C:422:PHE:O	1:C:426:GLN:HB2	2.16	0.45
1:A:417:TYR:CD1	1:A:466:VAL:HG21	2.51	0.45
1:C:474:ILE:CB	1:C:479:ASN:O	2.65	0.45
1:A:473:VAL:HG23	1:A:481:ILE:CD1	2.47	0.45
2:B:37:PRO:HG2	2:B:40:GLN:HG3	1.99	0.45
1:C:629:LEU:HD11	1:C:914:MSE:HE1	1.99	0.45
1:A:944:ARG:HG2	1:A:1008:MSE:HE1	1.98	0.44
1:C:770:LYS:HD2	1:C:831:THR:OG1	2.18	0.44
1:A:245:TYR:HA	1:A:249:LEU:HB2	1.99	0.44
1:C:872:LYS:HE2	1:C:889:THR:OG1	2.17	0.44
1:A:386:LYS:HD3	1:A:387:ASP:CG	2.42	0.44
1:A:924:ARG:HA	1:A:927:GLU:HG2	2.00	0.44
1:C:273:HIS:HB2	1:C:337:GLU:OE1	2.17	0.44
1:A:279:THR:O	1:A:283:MSE:HG3	2.17	0.44
1:A:676:LYS:HD3	1:A:676:LYS:N	2.32	0.44
1:A:772:LYS:O	1:A:776:GLN:HG3	2.18	0.44
1:C:245:TYR:CE1	1:C:560:ASN:HA	2.53	0.44
1:C:472:TYR:CD2	1:C:496:LEU:HD21	2.53	0.44
1:C:950:LYS:HD3	1:C:950:LYS:HA	1.59	0.44
1:A:932:GLU:OE2	1:C:913:LYS:HD3	2.17	0.44
1:C:482:ARG:HD2	1:C:483:GLU:N	2.32	0.44
1:A:323:ILE:HD13	1:A:398:LEU:HD12	2.00	0.44
1:A:409:ARG:H	1:A:409:ARG:HG3	1.53	0.44
1:C:607:VAL:HG22	1:C:738:LEU:HD23	1.99	0.44
1:A:614:PRO:HG2	1:A:660:THR:HG22	2.00	0.44
1:C:480:PRO:HB3	1:C:512:MSE:HE3	2.00	0.43
1:A:506:GLU:HB2	1:A:509:GLN:CD	2.43	0.43
1:A:662:MSE:HG3	1:A:686:TRP:CD1	2.53	0.43
1:C:1022:LYS:N	1:C:1022:LYS:HD2	2.33	0.43
1:A:515:ASP:OD1	1:A:516:GLU:HG3	2.18	0.43
1:A:607:VAL:O	1:A:611:MSE:HG2	2.18	0.43
1:A:616:CYS:HB2	1:A:623:PHE:O	2.19	0.43
2:D:1:MET:HE1	2:D:56:LEU:HD21	2.00	0.43
2:D:42:ALA:O	2:D:69:LEU:HD12	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:522:GLU:H	1:C:522:GLU:HG3	1.61	0.43
1:C:537:GLY:HA2	1:C:546:TYR:CE2	2.53	0.43
2:B:37:PRO:HA	2:B:38:PRO:HD3	1.93	0.43
1:C:1018:MSE:HE2	1:C:1018:MSE:HB3	1.93	0.43
1:A:474:ILE:HD12	1:A:512:MSE:HA	2.00	0.43
1:A:497:LYS:HD2	1:A:498:PHE:H	1.82	0.43
1:A:941:LEU:HD12	1:A:941:LEU:HA	1.81	0.43
1:A:955:SER:HA	1:A:956:GLY:HA2	1.72	0.43
1:A:1039:ALA:O	1:A:1044:ASN:N	2.52	0.43
1:A:249:LEU:HA	1:A:271:ARG:HD3	1.99	0.43
2:B:23:ILE:HG12	2:B:54:ARG:O	2.18	0.43
1:C:474:ILE:C	1:C:481:ILE:CD1	2.92	0.43
1:C:371:LYS:HA	1:C:371:LYS:HD3	1.61	0.43
1:C:411:LYS:HB2	1:C:417:TYR:CD2	2.54	0.43
1:C:963:GLU:O	1:C:967:PRO:HG2	2.18	0.43
1:A:462:PRO:HA	1:A:513:ARG:HA	2.01	0.43
1:A:638:LEU:HD12	1:A:638:LEU:HA	1.91	0.42
1:A:276:LEU:HD11	1:A:562:VAL:HG22	2.01	0.42
1:A:295:LYS:O	1:A:299:ARG:HG3	2.20	0.42
2:D:37:PRO:HA	2:D:38:PRO:HD3	1.93	0.42
1:C:267:GLN:HB3	1:C:556:ALA:CB	2.48	0.42
1:C:638:LEU:HD13	1:C:721:ALA:HA	2.01	0.42
1:A:279:THR:O	1:A:282:THR:OG1	2.36	0.42
1:A:1047:GLY:HA2	1:A:1050:GLN:HB3	2.01	0.42
1:C:365:LEU:HD23	1:C:365:LEU:HA	1.85	0.42
1:C:579:THR:OG1	1:C:580:PRO:HD3	2.18	0.42
1:A:413:PRO:HB3	1:A:461:GLU:OE1	2.19	0.42
1:A:667:ASN:HD22	1:A:681:LYS:NZ	2.18	0.42
1:A:716:ARG:NH1	1:A:728:SER:OG	2.46	0.42
1:C:505:LEU:HD23	1:C:505:LEU:HA	1.62	0.42
1:C:668:THR:HG23	1:C:731:LYS:HD3	2.01	0.42
2:D:74:ARG:O	1:C:849:THR:HG23	2.20	0.42
1:A:538:LEU:HD23	1:A:538:LEU:HA	1.91	0.42
1:C:393:SER:OG	1:C:396:HIS:ND1	2.49	0.42
1:C:986:LYS:HA	1:C:986:LYS:HD3	1.53	0.42
1:A:407:LEU:HD13	1:A:421:TYR:OH	2.20	0.42
2:D:11:LYS:HE3	2:D:11:LYS:HB3	1.90	0.42
2:D:41:GLN:CB	2:D:69:LEU:HD11	2.49	0.42
1:C:406:ASP:O	1:C:409:ARG:HG2	2.19	0.42
1:C:1038:ASN:O	1:C:1042:LYS:HG3	2.20	0.42
1:A:410:VAL:HG13	1:A:411:LYS:HE2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:303:LEU:HB2	1:A:311:THR:HG21	2.02	0.41
2:D:36:ILE:HG23	2:D:36:ILE:O	2.20	0.41
1:C:972:SER:O	1:C:976:LEU:HD22	2.21	0.41
1:C:550:LEU:HD23	1:C:550:LEU:HA	1.91	0.41
1:A:572:ALA:O	1:A:576:THR:HG23	2.21	0.41
1:A:971:GLN:HB3	1:A:987:VAL:HG11	2.02	0.41
2:D:7:THR:HG22	2:D:8:LEU:N	2.35	0.41
2:D:26:VAL:O	2:D:30:ILE:HG13	2.21	0.41
1:C:841:LEU:HD13	1:C:894:LYS:HB2	2.03	0.41
1:A:497:LYS:HD2	1:A:497:LYS:HA	1.51	0.41
1:A:542:LYS:HD3	1:A:543:GLU:H	1.86	0.41
2:D:74:ARG:HG2	1:C:705:PHE:HB2	2.02	0.41
1:C:299:ARG:NH1	1:C:301:GLU:OE2	2.54	0.41
1:A:351:ARG:HH11	1:A:384:GLU:CD	2.28	0.41
1:A:473:VAL:HG12	1:A:511:TYR:CD1	2.56	0.41
1:C:382:VAL:HG22	1:C:396:HIS:CD2	2.56	0.41
1:A:336:ASP:OD1	1:A:346:TYR:OH	2.32	0.41
1:A:954:GLU:OE2	1:A:1000:PHE:HA	2.20	0.41
1:C:366:ILE:HA	1:C:367:PRO:HA	1.76	0.41
1:C:398:LEU:HD23	1:C:398:LEU:HA	1.91	0.41
1:C:594:ARG:HH12	1:C:597:ASN:ND2	2.19	0.41
1:A:398:LEU:HD23	1:A:398:LEU:HA	1.86	0.40
1:A:464:LEU:HD13	1:A:471:ARG:NH1	2.35	0.40
1:C:481:ILE:HG21	1:C:499:PHE:HZ	1.85	0.40
1:C:584:ALA:HA	1:C:793:SER:HB3	2.02	0.40
1:C:883:LYS:H	1:C:883:LYS:HG3	1.75	0.40
1:A:807:GLN:NE2	1:A:807:GLN:HA	2.36	0.40
1:C:322:LYS:HD2	1:C:379:TYR:CE2	2.56	0.40
1:C:367:PRO:O	1:C:370:PHE:O	2.40	0.40
1:A:605:ARG:NH2	1:C:978:ASP:OD1	2.54	0.40
1:A:797:PHE:CZ	1:A:801:LYS:HD2	2.56	0.40
1:A:888:PHE:CD1	1:A:888:PHE:N	2.89	0.40
2:D:7:THR:CG2	2:D:8:LEU:N	2.84	0.40
1:C:681:LYS:HE3	1:C:684:GLU:OE2	2.22	0.40
1:C:744:ASN:O	1:C:748:MSE:HG3	2.21	0.40
1:C:903:GLU:O	1:C:903:GLU:HG2	2.20	0.40
2:D:22:THR:HG23	2:D:24:GLU:HB2	2.04	0.40
1:C:640:LYS:NZ	1:C:903:GLU:OE2	2.54	0.40
1:A:321:ARG:HD2	1:A:369:VAL:HG13	2.03	0.40
1:A:537:GLY:HA2	1:A:546:TYR:CZ	2.57	0.40
1:A:772:LYS:HE3	1:A:772:LYS:HB2	1.71	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:664:HIS:C	1:C:664:HIS:HD1	2.28	0.40
1:C:984:LEU:HD23	1:C:1019:VAL:HG13	2.03	0.40
1:C:1015:ILE:HA	1:C:1018:MSE:HE2	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	824/845 (98%)	805 (98%)	19 (2%)	0	100	100
1	C	820/845 (97%)	794 (97%)	25 (3%)	1 (0%)	48	69
2	B	74/79 (94%)	72 (97%)	2 (3%)	0	100	100
2	D	74/79 (94%)	72 (97%)	2 (3%)	0	100	100
All	All	1792/1848 (97%)	1743 (97%)	48 (3%)	1 (0%)	48	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	408	VAL

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	719/719 (100%)	709 (99%)	10 (1%)	59	78
1	C	716/719 (100%)	691 (96%)	25 (4%)	32	57
2	B	67/68 (98%)	67 (100%)	0	100	100
2	D	67/68 (98%)	64 (96%)	3 (4%)	24	48
All	All	1569/1574 (100%)	1531 (98%)	38 (2%)	43	67

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	409	ARG
1	A	411	LYS
1	A	425	LEU
1	A	479	ASN
1	A	504	LYS
1	A	542	LYS
1	A	638	LEU
1	A	901	ARG
1	A	952	SER
1	A	1033	LEU
2	D	13	ILE
2	D	18	GLU
2	D	63	LYS
1	C	249	LEU
1	C	366	ILE
1	C	371	LYS
1	C	387	ASP
1	C	411	LYS
1	C	412	GLN
1	C	474	ILE
1	C	476	GLN
1	C	477	ASP
1	C	542	LYS
1	C	543	GLU
1	C	594	ARG
1	C	661	LEU
1	C	663	GLN
1	C	666	ARG
1	C	678	LYS
1	C	681	LYS
1	C	688	LYS
1	C	936	GLU
1	C	948	GLN

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Mol	Chain	Res	Type
1	C	950	LYS
1	C	970	GLU
1	C	971	GLN
1	C	976	LEU
1	C	1022	LYS

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

Mol	Chain	Res	Type
1	A	247	ASN
1	A	424	GLN
1	A	441	GLN
1	A	476	GLN
1	A	479	ASN
1	A	554	ASN
1	A	625	ASN
1	A	667	ASN
1	A	807	GLN
1	A	974	ASN
1	A	1028	GLN
1	C	273	HIS
1	C	342	ASN
1	C	424	GLN
1	C	441	GLN
1	C	476	GLN
1	C	551	ASN
1	C	560	ASN
1	C	568	GLN
1	C	575	GLN
1	C	613	ASN
1	C	787	HIS
1	C	807	GLN
1	C	948	GLN
1	C	979	ASN
1	C	1007	GLN
1	C	1028	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

4 ligands are modelled in this entry.

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	NAD	A	1101	-	46,48,48	2.26	12 (26%)	64,73,73	1.92	18 (28%)
3	NAD	C	1101	-	46,48,48	2.27	12 (26%)	64,73,73	2.13	19 (29%)
4	AMP	C	1102	-	25,25,25	1.72	4 (16%)	37,38,38	2.25	14 (37%)
4	AMP	A	1102	-	25,25,25	1.90	6 (24%)	37,38,38	2.31	13 (35%)

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	NAD	A	1101	-	-	2/30/62/62	0/5/5/5
3	NAD	C	1101	-	-	5/30/62/62	0/5/5/5
4	AMP	C	1102	-	-	2/10/26/26	0/3/3/3
4	AMP	A	1102	-	-	0/10/26/26	0/3/3/3

All (34) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1101	NAD	C3N-C7N	-7.27	1.39	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	1101	NAD	C2N-N1N	6.92	1.42	1.35
3	A	1101	NAD	O7N-C7N	6.80	1.36	1.24
3	C	1101	NAD	C3N-C7N	-6.62	1.40	1.50
3	C	1101	NAD	O7N-C7N	6.48	1.36	1.24
3	A	1101	NAD	C2N-N1N	5.44	1.41	1.35
4	A	1102	AMP	C5-N7	-4.25	1.31	1.39
4	A	1102	AMP	C4-N9	-4.07	1.29	1.37
3	A	1101	NAD	O4D-C1D	3.82	1.45	1.40
4	A	1102	AMP	C8-N9	-3.76	1.31	1.37
3	C	1101	NAD	C2A-N3A	3.54	1.40	1.33
4	C	1102	AMP	C8-N9	-3.51	1.31	1.37
3	C	1101	NAD	C2A-N1A	3.37	1.39	1.33
4	C	1102	AMP	C5-N7	-3.33	1.33	1.39
4	C	1102	AMP	C4-N9	-3.31	1.30	1.37
3	A	1101	NAD	C2A-N1A	3.30	1.39	1.33
3	A	1101	NAD	C2A-N3A	3.16	1.39	1.33
3	C	1101	NAD	O4D-C1D	3.15	1.45	1.40
3	A	1101	NAD	C5A-N7A	-3.12	1.33	1.39
3	C	1101	NAD	C5A-N7A	-2.97	1.33	1.39
3	A	1101	NAD	C5A-C4A	-2.82	1.34	1.39
3	C	1101	NAD	C5A-C4A	-2.79	1.34	1.39
3	A	1101	NAD	C5A-C6A	-2.74	1.33	1.41
4	C	1102	AMP	C5-C4	2.64	1.43	1.39
3	A	1101	NAD	C6N-N1N	2.55	1.41	1.35
3	A	1101	NAD	PN-O3	2.50	1.62	1.59
4	A	1102	AMP	C5-C4	2.46	1.43	1.39
4	A	1102	AMP	C2'-C3'	-2.42	1.46	1.53
3	C	1101	NAD	C8A-N9A	-2.42	1.33	1.37
3	C	1101	NAD	C5A-C6A	-2.38	1.34	1.41
3	C	1101	NAD	PN-O3	2.34	1.62	1.59
4	A	1102	AMP	P-O2P	-2.31	1.46	1.54
3	C	1101	NAD	PA-O3	2.27	1.61	1.59
3	A	1101	NAD	C8A-N9A	-2.15	1.33	1.37

All (64) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1101	NAD	N3A-C2A-N1A	-7.07	117.88	128.58
3	C	1101	NAD	N3A-C2A-N1A	-6.63	118.54	128.58
4	C	1102	AMP	C5-C4-N3	-6.55	117.69	126.72
4	A	1102	AMP	C5-C4-N3	-5.90	118.59	126.72
3	C	1101	NAD	O5B-PA-O1A	-5.78	86.04	108.94

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1102	AMP	N3-C4-N9	4.98	135.64	127.17
4	A	1102	AMP	N3-C4-N9	4.82	135.37	127.17
4	A	1102	AMP	O3'-C3'-C2'	-4.82	96.37	111.82
3	C	1101	NAD	C5A-C4A-N3A	-4.53	120.47	126.72
3	C	1101	NAD	O2A-PA-O5B	-4.37	87.74	107.57
3	A	1101	NAD	C5A-C4A-N3A	-4.32	120.77	126.72
4	A	1102	AMP	O2'-C2'-C3'	-4.08	98.75	111.82
4	C	1102	AMP	C2-N3-C4	4.05	121.73	111.83
3	C	1101	NAD	N9A-C8A-N7A	-3.98	108.29	113.94
3	C	1101	NAD	O2A-PA-O3	3.76	117.43	107.27
3	A	1101	NAD	N9A-C8A-N7A	-3.74	108.63	113.94
3	A	1101	NAD	C4D-O4D-C1D	-3.64	106.59	109.92
4	A	1102	AMP	C2-N3-C4	3.61	120.64	111.83
3	C	1101	NAD	C6N-N1N-C2N	-3.58	118.83	121.88
3	C	1101	NAD	C4D-O4D-C1D	-3.57	106.66	109.92
4	C	1102	AMP	C4-C5-N7	-3.39	106.71	110.58
3	A	1101	NAD	C2A-N3A-C4A	3.33	119.98	111.83
3	C	1101	NAD	C2A-N3A-C4A	3.26	119.79	111.83
3	C	1101	NAD	C5A-N7A-C8A	3.07	108.28	103.45
3	A	1101	NAD	C6N-N1N-C2N	-3.04	119.29	121.88
4	C	1102	AMP	C3'-C2'-C1'	2.96	107.06	101.46
4	A	1102	AMP	C4-C5-N7	-2.95	107.21	110.58
4	A	1102	AMP	C3'-C2'-C1'	2.90	106.95	101.46
4	C	1102	AMP	O2P-P-O5'	-2.87	99.18	106.67
3	C	1101	NAD	C4A-C5A-N7A	-2.87	107.30	110.58
4	C	1102	AMP	N3-C2-N1	-2.83	124.30	128.58
3	A	1101	NAD	C5A-C6A-N6A	-2.83	116.28	123.29
3	A	1101	NAD	C2B-C3B-C4B	-2.82	97.17	102.61
4	A	1102	AMP	C2'-C1'-N9	-2.79	106.36	113.30
3	A	1101	NAD	C2D-C3D-C4D	-2.69	97.42	102.61
3	A	1101	NAD	C5A-N7A-C8A	2.68	107.67	103.45
3	C	1101	NAD	O3-PA-O1A	2.62	118.59	110.70
4	A	1102	AMP	C4-N9-C8	2.60	108.47	105.74
3	A	1101	NAD	O7N-C7N-C3N	-2.60	116.42	119.60
4	A	1102	AMP	C5'-C4'-C3'	-2.59	105.88	115.21
4	C	1102	AMP	O3P-P-O5'	-2.58	99.94	106.67
3	C	1101	NAD	O4D-C4D-C5D	-2.58	101.06	109.33
3	C	1101	NAD	C6A-C5A-C4A	2.54	120.65	117.18
3	C	1101	NAD	C5A-C4A-N9A	2.53	108.57	105.81
4	C	1102	AMP	C4-N9-C8	2.48	108.34	105.74
3	A	1101	NAD	C5A-C4A-N9A	2.46	108.50	105.81
3	A	1101	NAD	C6A-C5A-C4A	2.45	120.53	117.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	1101	NAD	C5A-C6A-N6A	-2.44	117.25	123.29
3	A	1101	NAD	O7N-C7N-N7N	2.40	126.08	122.62
4	A	1102	AMP	N3-C2-N1	-2.39	124.97	128.58
3	A	1101	NAD	O4B-C4B-C3B	-2.37	100.44	105.15
4	C	1102	AMP	C2'-C1'-N9	-2.37	107.42	113.30
4	C	1102	AMP	O3P-P-O2P	2.37	116.68	107.80
4	C	1102	AMP	C5'-C4'-C3'	-2.32	106.88	115.21
3	A	1101	NAD	C4A-C5A-N7A	-2.29	107.96	110.58
3	C	1101	NAD	C2B-C3B-C4B	-2.27	98.23	102.61
3	C	1101	NAD	N3A-C4A-N9A	2.23	130.95	127.17
3	A	1101	NAD	O4B-C1B-N9A	-2.21	103.84	108.09
3	C	1101	NAD	O2A-PA-O1A	2.18	122.57	112.44
4	C	1102	AMP	C6-C5-N7	2.17	136.26	132.09
4	A	1102	AMP	O3P-P-O5'	-2.16	101.05	106.67
3	A	1101	NAD	N3A-C4A-N9A	2.10	130.74	127.17
4	C	1102	AMP	C2'-C3'-C4'	2.03	106.53	102.61
4	A	1102	AMP	O2P-P-O5'	-2.02	101.41	106.67

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	1101	NAD	C5B-O5B-PA-O1A
3	C	1101	NAD	C5B-O5B-PA-O3
3	C	1101	NAD	O4B-C4B-C5B-O5B
3	C	1101	NAD	C3B-C4B-C5B-O5B
4	C	1102	AMP	C3'-C4'-C5'-O5'
4	C	1102	AMP	O4'-C4'-C5'-O5'
3	A	1101	NAD	C5B-O5B-PA-O1A
3	A	1101	NAD	O4D-C1D-N1N-C6N
3	C	1101	NAD	C3D-C4D-C5D-O5D

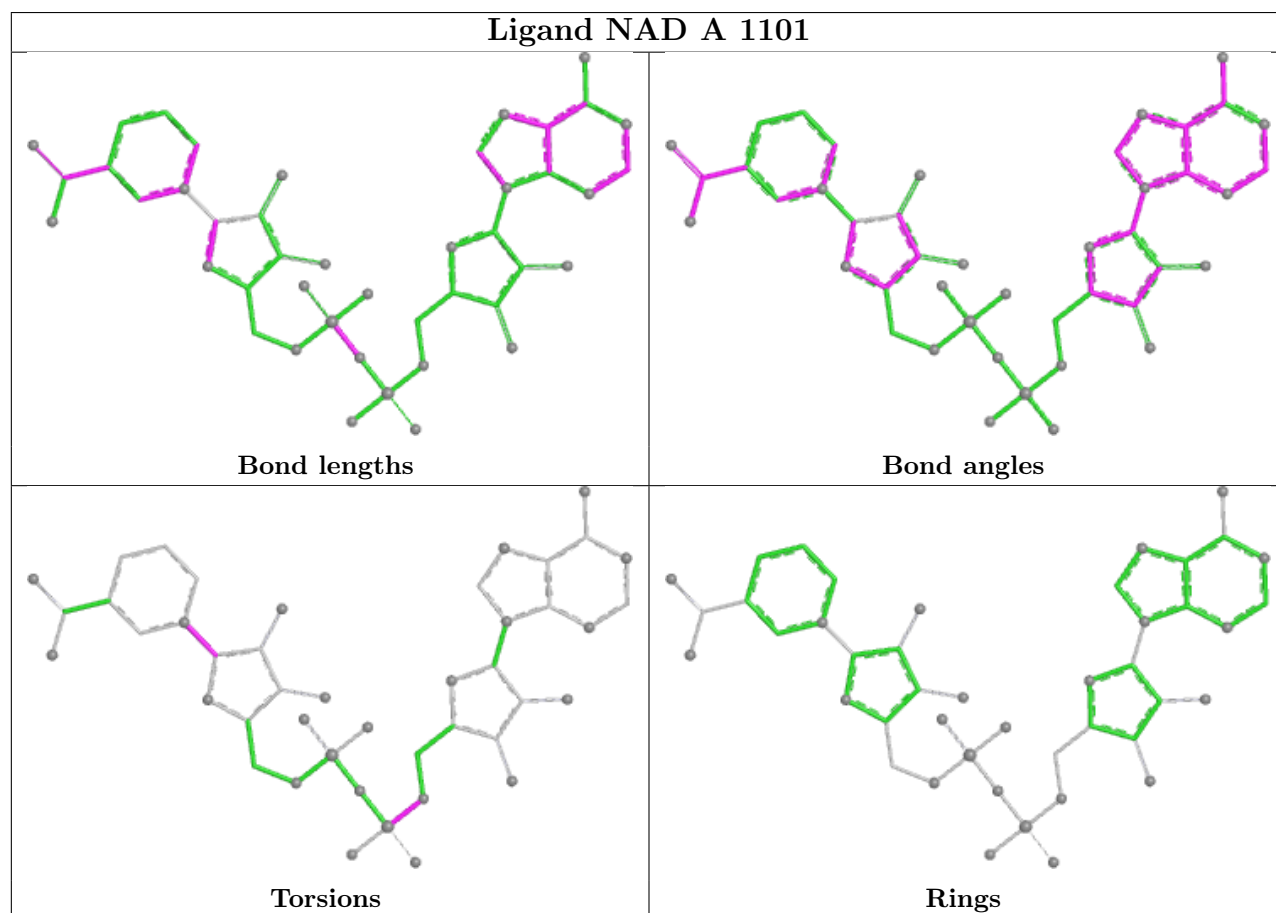
There are no ring outliers.

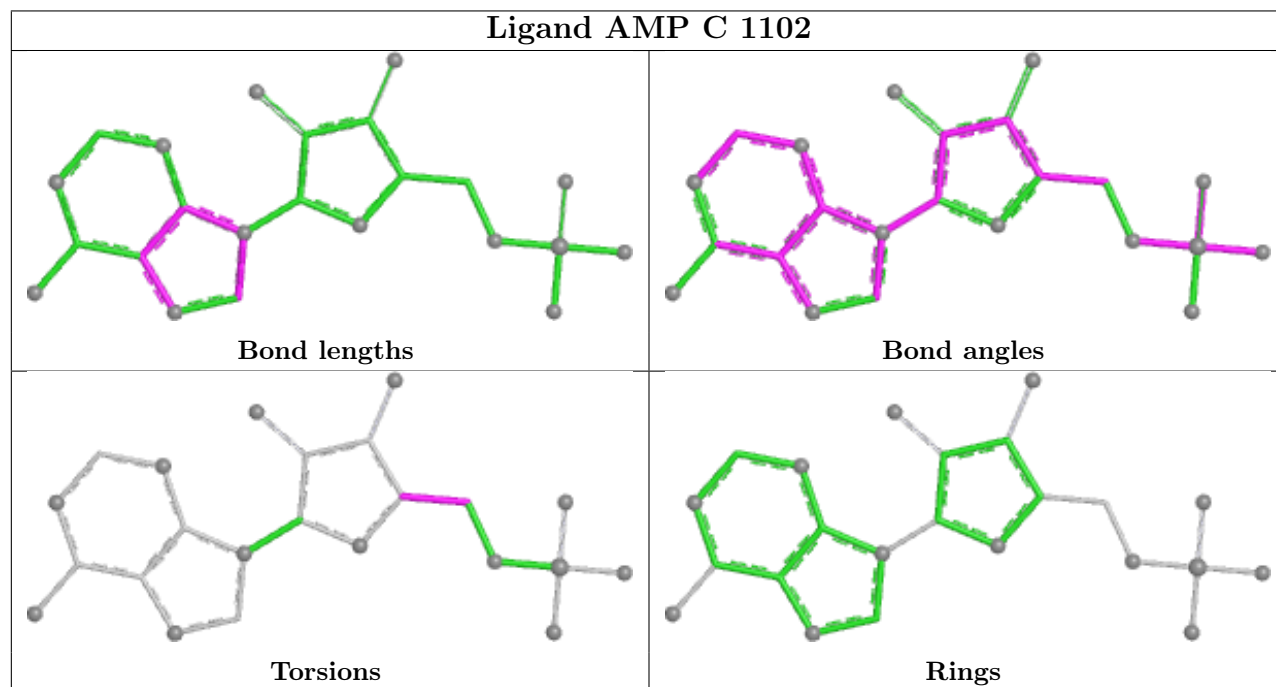
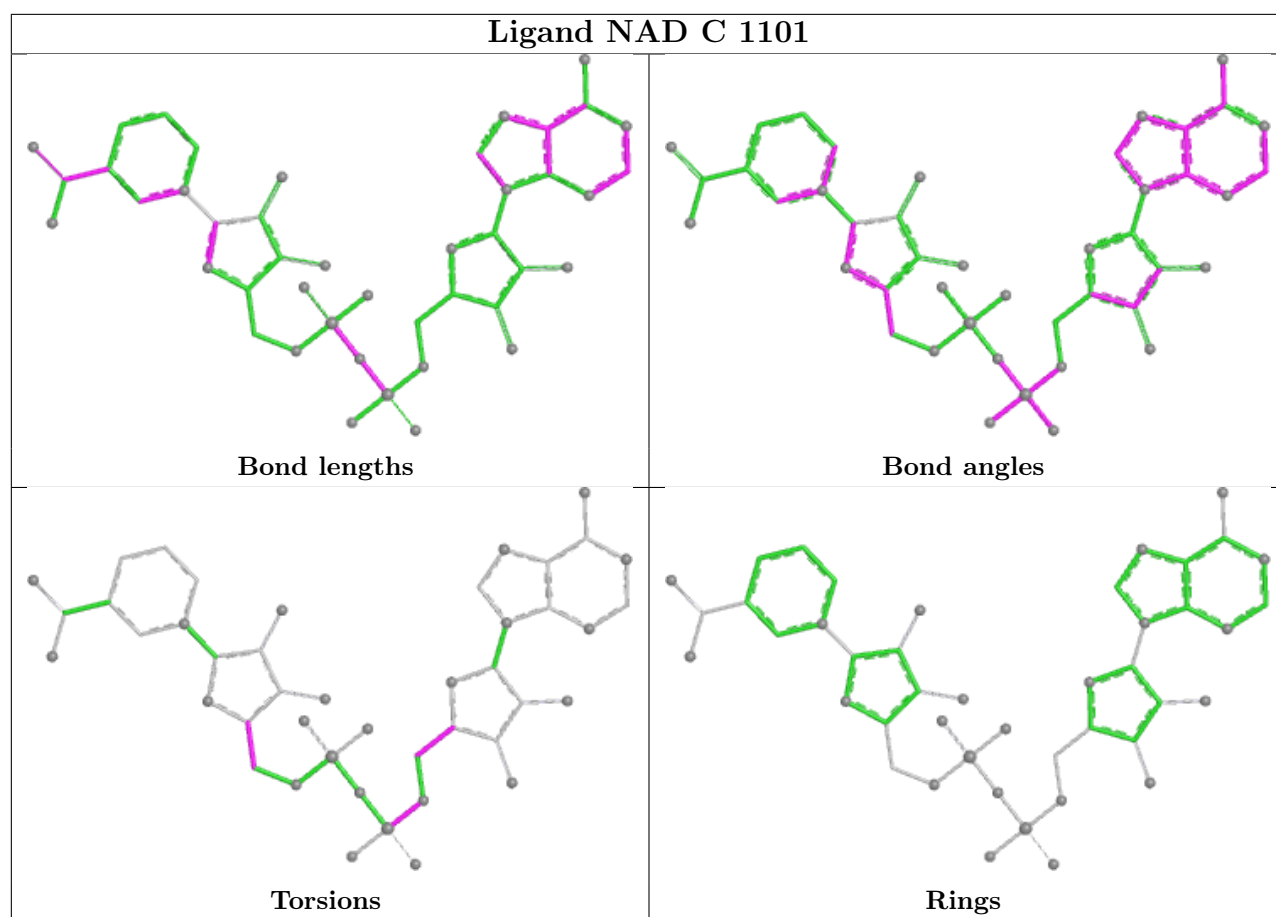
3 monomers are involved in 11 short contacts:

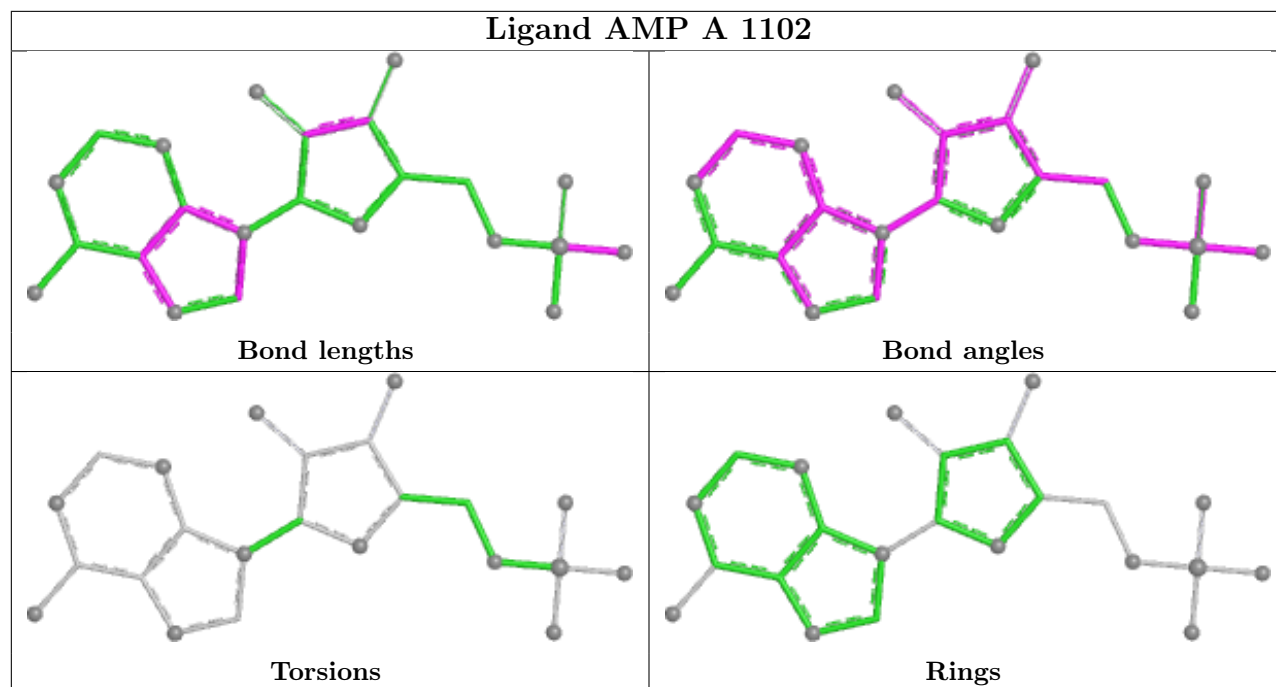
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1101	NAD	3	0
4	C	1102	AMP	7	0
4	A	1102	AMP	1	0

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

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	812/845 (96%)	0.16	33 (4%) 41 33	24, 46, 104, 142	0
1	C	808/845 (95%)	0.34	42 (5%) 33 26	26, 66, 111, 158	0
2	B	76/79 (96%)	0.23	0 100 100	34, 59, 83, 93	0
2	D	76/79 (96%)	1.16	10 (13%) 7 5	61, 119, 144, 157	0
All	All	1772/1848 (95%)	0.29	85 (4%) 35 29	24, 58, 115, 158	0

All (85) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	957	TYR	6.6
1	A	339	SER	4.5
1	A	1000	PHE	4.4
2	D	32	ASP	4.3
1	C	474	ILE	3.9
1	A	955	SER	3.8
1	A	1003	VAL	3.7
1	A	223	VAL	3.7
1	C	458	GLU	3.5
1	C	951	PHE	3.5
1	A	342	ASN	3.5
1	C	250	GLY	3.5
1	A	410	VAL	3.5
1	C	384	GLU	3.4
1	C	410	VAL	3.4
1	C	957	TYR	3.4
1	C	948	GLN	3.2
1	A	956	GLY	3.2
1	C	1058	LEU	3.2
1	C	342	ASN	3.2
1	A	508	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	954	GLU	3.1
1	A	222	SER	3.0
1	C	979	ASN	3.0
1	A	507	GLU	2.8
1	A	953	THR	2.8
1	A	1025	LEU	2.8
1	C	475	GLY	2.8
1	A	478	GLY	2.8
2	D	59	TYR	2.8
2	D	28	ALA	2.7
2	D	13	ILE	2.7
1	C	544	TYR	2.7
1	C	954	GLU	2.7
1	A	477	ASP	2.7
1	A	1049	LEU	2.7
1	C	309	GLY	2.6
1	C	663	GLN	2.6
1	C	753	SER	2.6
1	A	959	THR	2.6
1	C	496	LEU	2.6
2	D	55	THR	2.6
1	C	412	GLN	2.6
1	C	554	ASN	2.6
1	C	615	ASP	2.6
1	A	505	LEU	2.6
1	A	262	VAL	2.6
1	A	499	PHE	2.6
1	C	626	GLY	2.5
1	A	260	THR	2.5
1	A	545	GLN	2.5
1	A	411	LYS	2.5
2	D	57	SER	2.4
1	C	353	ALA	2.4
1	C	510	ARG	2.4
2	D	3	ILE	2.4
2	D	54	ARG	2.4
1	A	544	TYR	2.3
1	C	638	LEU	2.3
1	C	849	THR	2.3
1	C	880	GLY	2.3
1	C	224	PRO	2.3
1	C	478	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	1004	GLU	2.3
1	C	1023	ALA	2.2
1	C	541	LEU	2.2
1	C	950	LYS	2.2
1	C	477	ASP	2.2
2	D	19	PRO	2.2
1	C	540	GLY	2.2
1	A	564	PHE	2.2
1	C	952	SER	2.2
1	C	1010	ILE	2.1
1	A	343	TYR	2.1
1	A	271	ARG	2.1
1	A	497	LYS	2.1
1	A	333	GLY	2.1
1	C	391	ALA	2.1
1	A	981	VAL	2.1
1	C	919	LEU	2.1
2	D	15	LEU	2.1
1	C	476	GLN	2.1
1	C	413	PRO	2.1
1	C	260	THR	2.0
1	C	561	ASP	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
4	AMP	A	1102	23/23	0.72	0.16	20,20,20,20	0

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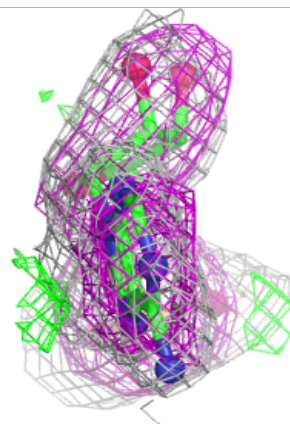
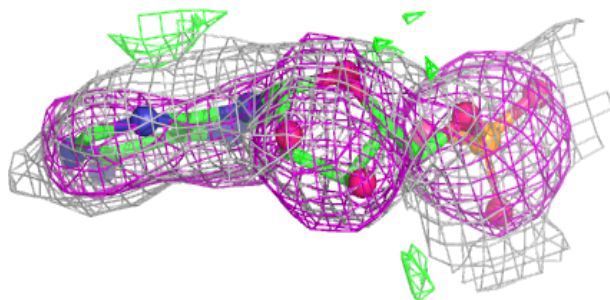
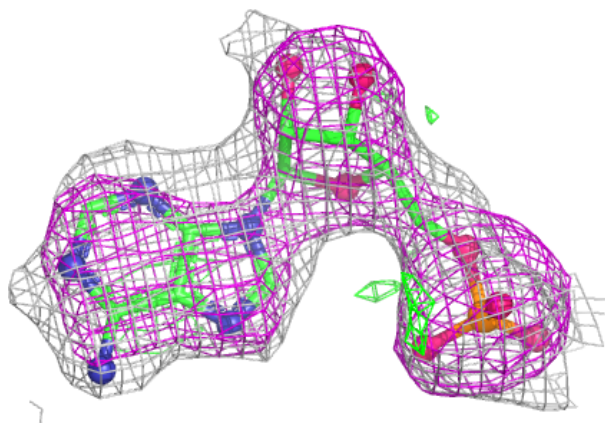
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	AMP	C	1102	23/23	0.72	0.16	20,20,20,20	0
3	NAD	C	1101	44/44	0.94	0.08	28,42,50,51	0
3	NAD	A	1101	44/44	0.97	0.06	21,32,40,48	0

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

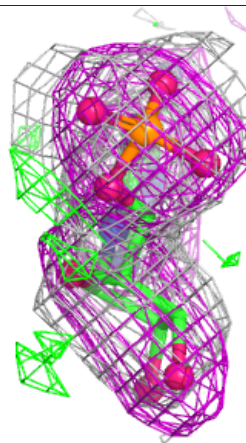
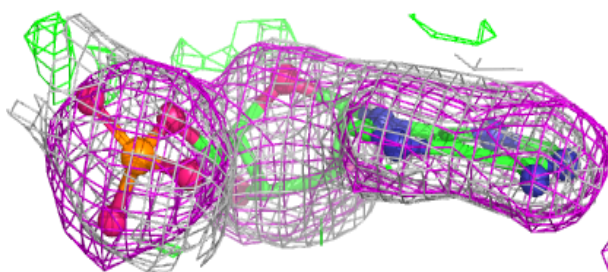
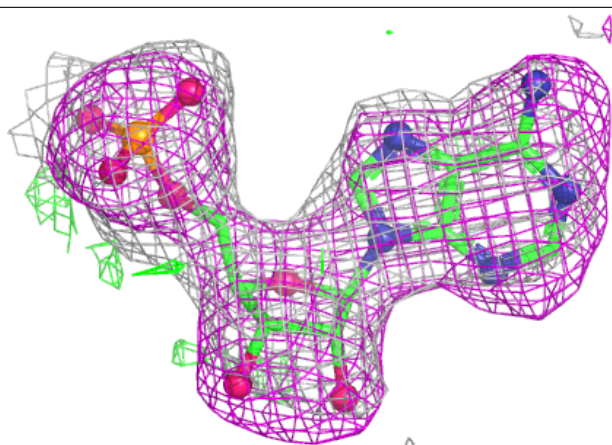
Electron density around AMP A 1102:

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

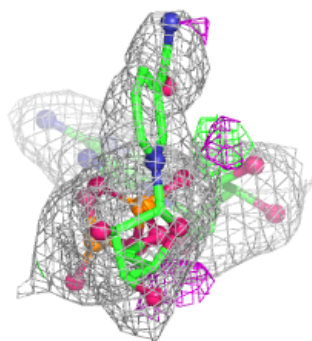
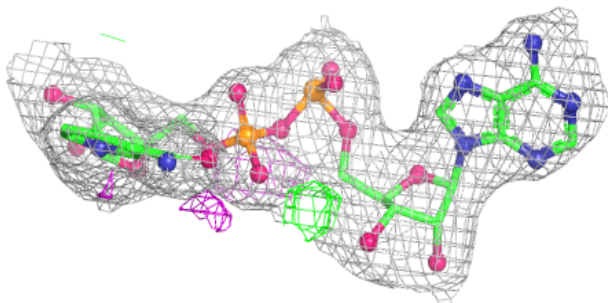
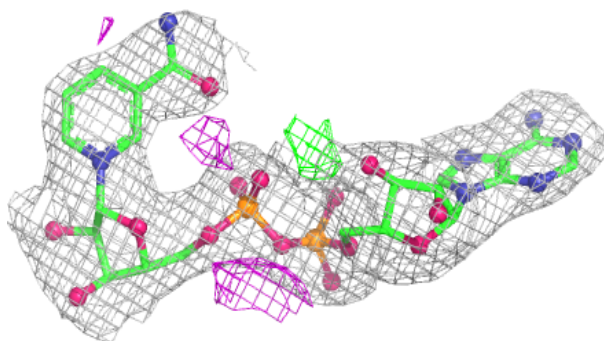


Electron density around AMP C 1102:

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

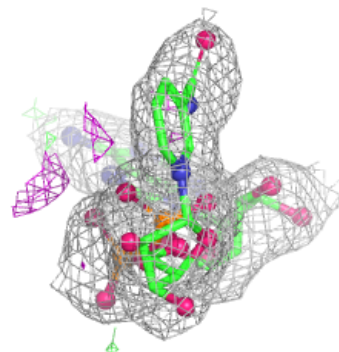
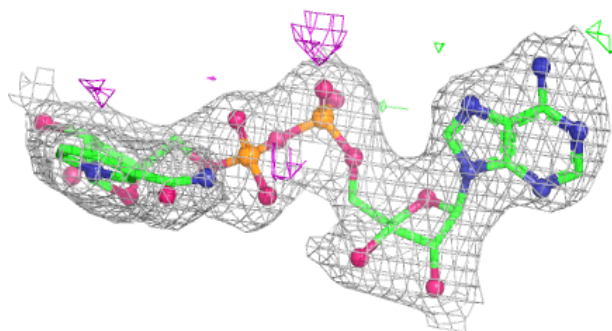
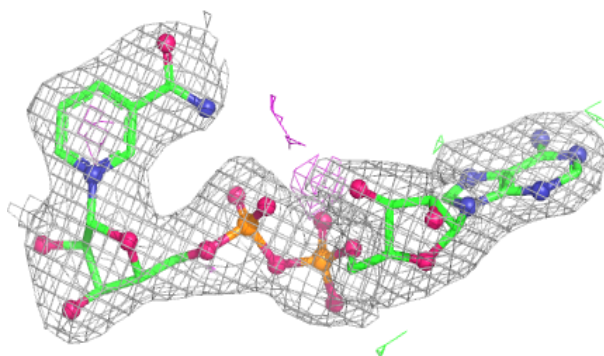
**Electron density around NAD C 1101:**

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



Electron density around NAD A 1101:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.