



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:32 PM UTC

PDB ID : 3ABI / pdb_00003abi
Title : Crystal Structure of L-Lysine Dehydrogenase from Hyperthermophilic Archaeon *Pyrococcus horikoshii*
Authors : Yoneda, K.; Sakuraba, H.; Fukuda, J.; Ohshima, T.
Deposited on : 2009-12-14
Resolution : 2.44 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

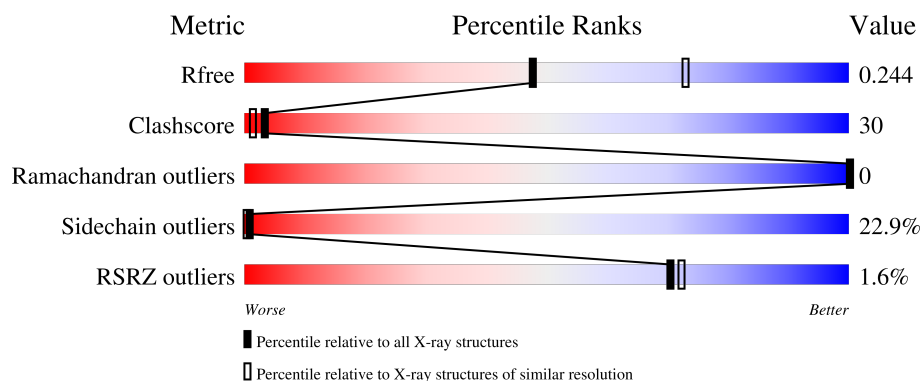
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.44 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	2340 (2.46-2.42)
Clashscore	190562	2400 (2.46-2.42)
Ramachandran outliers	187476	2379 (2.46-2.42)
Sidechain outliers	187428	2379 (2.46-2.42)
RSRZ outliers	180081	2340 (2.46-2.42)

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	365	2% 51% 29% 15% . .
1	B	365	2% 47% 34% 12% . 5%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5796 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 Putative uncharacterized protein PH1688.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	349	Total	C	N	O	S	0	0	0
			2799	1809	456	521	13			
1	B	345	Total	C	N	O	S	0	0	0
			2764	1785	451	515	13			

There are 32 discrepancies between the modelled and reference sequences:

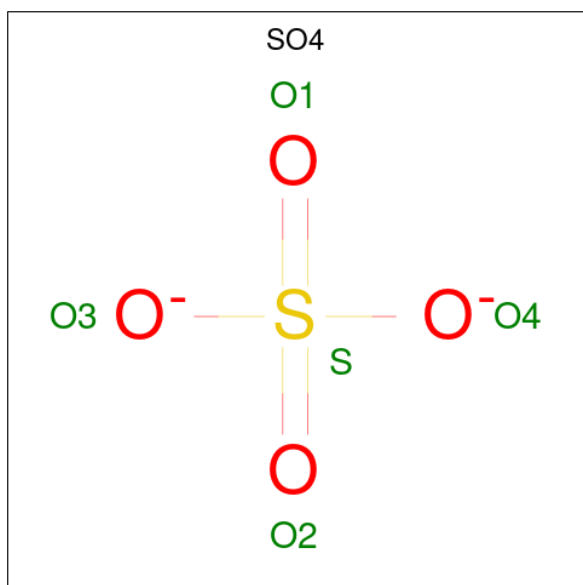
Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	MET	-	expression tag	UNP O59312
A	-14	ASN	-	expression tag	UNP O59312
A	-13	HIS	-	expression tag	UNP O59312
A	-12	LYS	-	expression tag	UNP O59312
A	-11	VAL	-	expression tag	UNP O59312
A	-10	HIS	-	expression tag	UNP O59312
A	-9	HIS	-	expression tag	UNP O59312
A	-8	HIS	-	expression tag	UNP O59312
A	-7	HIS	-	expression tag	UNP O59312
A	-6	HIS	-	expression tag	UNP O59312
A	-5	HIS	-	expression tag	UNP O59312
A	-4	ILE	-	expression tag	UNP O59312
A	-3	GLU	-	expression tag	UNP O59312
A	-2	GLY	-	expression tag	UNP O59312
A	-1	ARG	-	expression tag	UNP O59312
A	0	HIS	-	expression tag	UNP O59312
B	-15	MET	-	expression tag	UNP O59312
B	-14	ASN	-	expression tag	UNP O59312
B	-13	HIS	-	expression tag	UNP O59312
B	-12	LYS	-	expression tag	UNP O59312
B	-11	VAL	-	expression tag	UNP O59312
B	-10	HIS	-	expression tag	UNP O59312
B	-9	HIS	-	expression tag	UNP O59312
B	-8	HIS	-	expression tag	UNP O59312
B	-7	HIS	-	expression tag	UNP O59312

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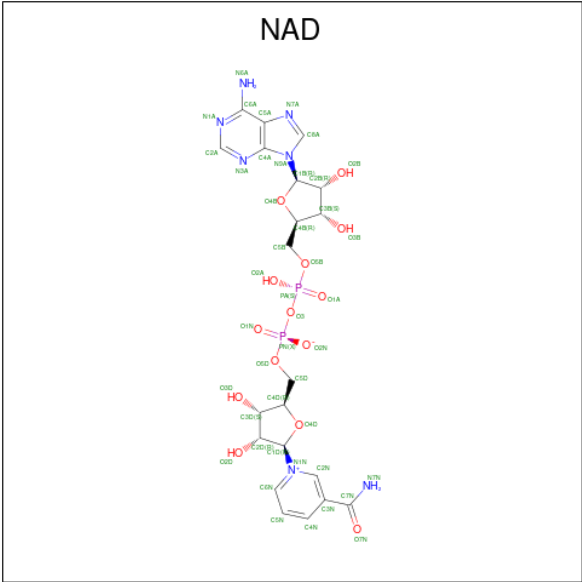
Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	HIS	-	expression tag	UNP O59312
B	-5	HIS	-	expression tag	UNP O59312
B	-4	ILE	-	expression tag	UNP O59312
B	-3	GLU	-	expression tag	UNP O59312
B	-2	GLY	-	expression tag	UNP O59312
B	-1	ARG	-	expression tag	UNP O59312
B	0	HIS	-	expression tag	UNP O59312

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



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

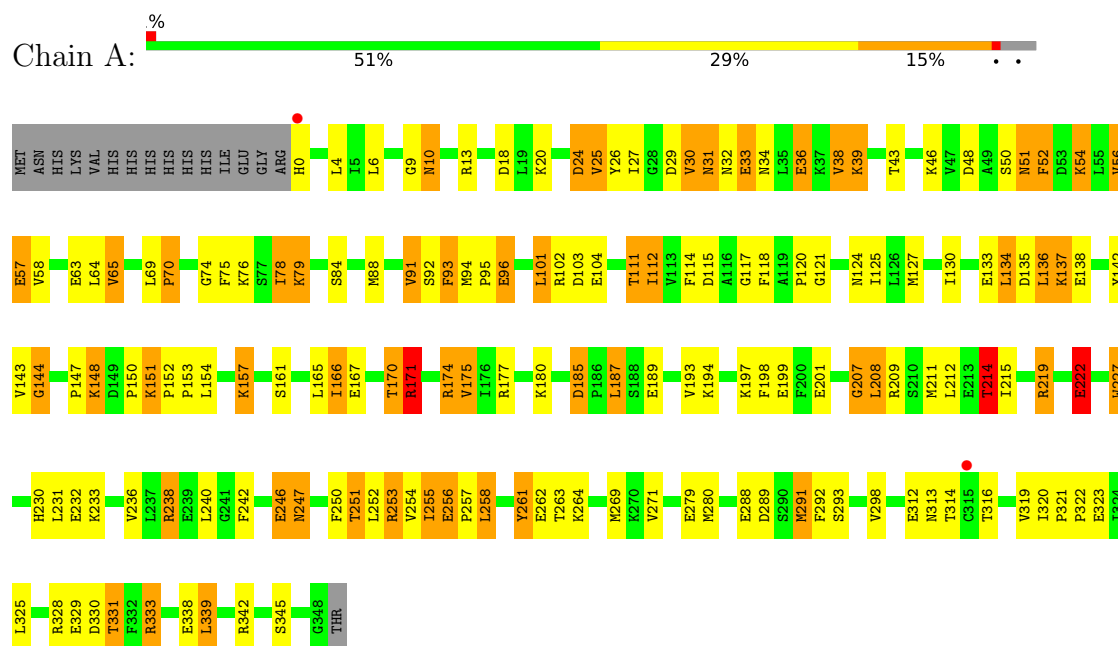
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	66	Total	O	0	0
			66	66		
4	B	69	Total	O	0	0
			69	69		

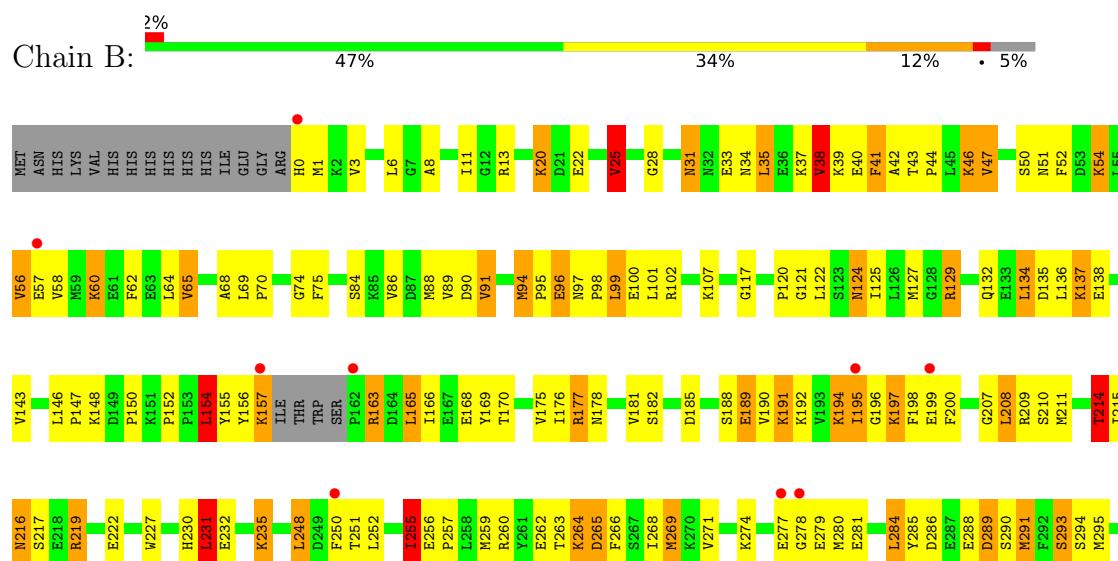
3 Residue-property plots

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: Putative uncharacterized protein PH1688



• Molecule 1: Putative uncharacterized protein PH1688





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	75.29Å 113.01Å 122.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.51 – 2.44 47.51 – 2.44	Depositor EDS
% Data completeness (in resolution range)	(Not available) (47.51-2.44) 99.5 (47.51-2.44)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.21 (at 2.45Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.225 , 0.235 0.223 , 0.244	Depositor DCC
R_{free} test set	1971 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	52.6	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 51.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5796	wwPDB-VP
Average B, all atoms (Å ²)	53.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.94% 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: SO4, NAD

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	1.91	14/2856 (0.5%)	1.21	23/3846 (0.6%)
1	B	1.79	7/2818 (0.2%)	1.20	23/3790 (0.6%)
All	All	1.85	21/5674 (0.4%)	1.21	46/7636 (0.6%)

All (21) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	209	ARG	C-O	-6.14	1.19	1.24
1	B	321	PRO	C-O	-6.07	1.19	1.24
1	A	9	GLY	C-O	-6.01	1.18	1.23
1	A	144	GLY	C-O	-5.76	1.18	1.24
1	A	171	ARG	C-O	-5.64	1.19	1.24
1	A	143	VAL	C-O	-5.62	1.18	1.23
1	A	152	PRO	CA-C	-5.61	1.47	1.52
1	A	142	TYR	C-O	-5.58	1.17	1.24
1	B	86	VAL	C-O	-5.55	1.18	1.24
1	B	90	ASP	C-O	-5.53	1.17	1.24
1	A	207	GLY	C-O	-5.47	1.18	1.24
1	B	207	GLY	C-O	-5.40	1.18	1.24
1	A	321	PRO	C-O	-5.38	1.20	1.24
1	A	256	GLU	C-O	-5.35	1.19	1.24
1	A	222	GLU	C-O	-5.25	1.17	1.24
1	B	143	VAL	C-O	-5.17	1.18	1.24
1	A	112	ILE	CA-CB	-5.14	1.48	1.54
1	B	42	ALA	CA-CB	-5.12	1.45	1.53
1	B	3	VAL	C-O	-5.12	1.19	1.24
1	A	271	VAL	C-O	-5.10	1.18	1.24
1	A	175	VAL	CA-C	-5.03	1.46	1.52

All (46) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	170	THR	N-CA-C	10.43	122.73	111.36
1	B	214	THR	N-CA-C	9.85	122.10	111.36
1	B	74	GLY	N-CA-C	9.15	123.11	112.50
1	B	135	ASP	N-CA-C	-9.02	92.77	108.20
1	A	255	ILE	N-CA-C	8.46	121.67	111.09
1	A	52	PHE	N-CA-C	8.13	119.77	111.07
1	A	74	GLY	N-CA-C	7.81	122.10	112.73
1	A	38	VAL	N-CA-C	7.79	120.54	112.83
1	A	231	LEU	N-CA-C	7.72	119.70	111.28
1	A	214	THR	N-CA-C	7.71	119.76	111.36
1	B	154	LEU	N-CA-C	7.47	119.51	111.36
1	B	38	VAL	N-CA-C	6.87	119.50	112.90
1	B	25	VAL	N-CA-C	6.69	117.93	108.36
1	B	22	GLU	N-CA-C	6.66	119.54	111.82
1	A	198	PHE	N-CA-C	6.55	120.55	110.20
1	B	231	LEU	N-CA-C	6.43	120.38	112.54
1	A	329	GLU	N-CA-C	6.35	118.20	111.28
1	B	197	LYS	N-CA-C	-6.05	106.15	112.93
1	B	94	MET	CA-C-N	5.98	125.37	118.85
1	B	94	MET	C-N-CA	5.98	125.37	118.85
1	A	94	MET	CA-C-N	5.83	125.21	118.85
1	A	94	MET	C-N-CA	5.83	125.21	118.85
1	A	24	ASP	N-CA-C	-5.73	98.40	108.20
1	A	185	ASP	N-CA-C	-5.70	101.32	109.24
1	A	25	VAL	N-CA-C	5.69	116.14	108.17
1	A	254	VAL	N-CA-C	5.67	115.86	110.53
1	B	320	ILE	N-CA-C	5.66	114.18	107.73
1	B	207	GLY	N-CA-C	5.61	120.84	114.67
1	A	70	PRO	N-CA-C	-5.56	102.72	111.34
1	A	298	VAL	N-CA-C	5.55	115.75	110.53
1	A	227	TRP	N-CA-C	-5.40	102.36	110.24
1	A	261	TYR	N-CA-C	-5.34	101.29	109.41
1	B	293	SER	N-CA-C	-5.31	103.88	110.41
1	B	39	LYS	N-CA-C	5.29	118.83	112.38
1	B	185	ASP	N-CA-C	-5.27	103.01	109.65
1	B	232	GLU	N-CA-C	-5.25	105.56	111.28
1	A	320	ILE	N-CA-C	5.25	113.61	107.89
1	B	278	GLY	N-CA-C	5.24	118.16	112.29
1	A	189	GLU	N-CA-C	5.15	117.10	107.99
1	A	230	HIS	N-CA-C	5.12	116.67	111.14
1	B	99	LEU	N-CA-C	-5.12	106.14	112.38
1	A	135	ASP	N-CA-C	-5.10	98.40	107.98
1	B	255	ILE	N-CA-C	5.08	119.47	113.22

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	62	PHE	N-CA-C	5.06	117.85	109.85
1	A	201	GLU	N-CA-C	-5.06	101.15	109.40
1	B	188	SER	N-CA-C	5.06	117.69	111.82

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	2799	0	2840	150	0
1	B	2764	0	2807	196	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
3	A	44	0	26	2	0
3	B	44	0	26	3	0
4	A	66	0	0	3	0
4	B	69	0	0	4	0
All	All	5796	0	5699	344	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 30.

All (344) 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:B:134:LEU:HD22	1:B:280:MET:CE	1.42	1.49
1:B:134:LEU:CD2	1:B:280:MET:HE3	1.68	1.23
1:B:284:LEU:C	1:B:284:LEU:HD12	1.54	1.21
1:B:127:MET:CE	1:B:136:LEU:HD21	1.74	1.16
1:B:195:ILE:HD11	1:B:268:ILE:CD1	1.76	1.16
1:B:195:ILE:CD1	1:B:268:ILE:HD13	1.76	1.13
1:A:333:ARG:HH11	1:A:333:ARG:CG	1.58	1.10
1:B:75:PHE:HD2	1:B:94:MET:HE1	1.12	1.10
1:A:134:LEU:HD13	1:A:280:MET:HE2	1.32	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ARG:HH11	1:A:253:ARG:CG	1.66	1.07
1:A:333:ARG:NH1	1:A:333:ARG:HG3	1.45	1.07
1:A:253:ARG:HH11	1:A:253:ARG:CB	1.66	1.06
1:B:195:ILE:HD11	1:B:268:ILE:HD13	1.10	1.06
1:B:284:LEU:HD12	1:B:284:LEU:O	1.56	1.06
1:B:134:LEU:CD2	1:B:280:MET:CE	2.31	1.04
1:B:284:LEU:C	1:B:284:LEU:CD1	2.30	1.02
1:A:31:ASN:ND2	1:A:34:ASN:H	1.56	1.02
1:B:127:MET:HE1	1:B:136:LEU:HD21	1.38	1.02
1:A:31:ASN:C	1:A:31:ASN:HD22	1.70	1.00
1:A:31:ASN:HD21	1:A:34:ASN:H	1.04	1.00
1:B:165:LEU:HD23	1:B:165:LEU:O	1.61	0.98
1:B:156:TYR:HB3	1:B:259:MET:HE2	1.47	0.94
1:B:75:PHE:HD2	1:B:94:MET:CE	1.82	0.91
1:A:253:ARG:HH11	1:A:253:ARG:HG2	1.34	0.91
1:B:34:ASN:HD22	1:B:37:LYS:HE3	1.34	0.90
1:B:195:ILE:CD1	1:B:268:ILE:CD1	2.42	0.90
1:B:127:MET:CE	1:B:136:LEU:CD2	2.49	0.90
1:B:75:PHE:CD2	1:B:94:MET:HE1	2.03	0.90
1:A:48:ASP:OD2	1:A:50:SER:HB2	1.73	0.89
1:B:165:LEU:C	1:B:165:LEU:CD2	2.45	0.89
1:B:325:LEU:O	1:B:331:THR:HG22	1.72	0.88
1:B:195:ILE:HG12	1:B:195:ILE:O	1.74	0.88
1:A:253:ARG:HH11	1:A:253:ARG:HB3	1.40	0.86
1:A:325:LEU:O	1:A:331:THR:CG2	2.24	0.85
1:A:253:ARG:CB	1:A:253:ARG:NH1	2.39	0.85
1:A:333:ARG:HH11	1:A:333:ARG:HG3	0.73	0.84
1:A:48:ASP:OD2	1:A:50:SER:CB	2.24	0.84
1:A:51:ASN:C	1:A:51:ASN:HD22	1.86	0.83
1:A:26:TYR:CD2	1:A:43:THR:OG1	2.32	0.82
1:B:56:VAL:O	1:B:60:LYS:HD3	1.79	0.82
1:B:190:VAL:HG11	1:B:231:LEU:HD11	1.60	0.81
1:A:31:ASN:ND2	1:A:31:ASN:C	2.30	0.81
1:A:127:MET:HE1	1:A:136:LEU:HD11	1.61	0.81
1:B:69:LEU:O	3:B:1002:NAD:H4D	1.81	0.80
1:A:214:THR:HG22	1:A:215:ILE:HG12	1.63	0.80
1:B:325:LEU:HA	1:B:331:THR:HG21	1.61	0.80
1:B:331:THR:O	1:B:335:ILE:HG13	1.82	0.80
1:B:248:LEU:CD2	1:B:248:LEU:O	2.30	0.80
1:B:134:LEU:HD22	1:B:280:MET:HE3	0.80	0.79
1:B:117:GLY:O	1:B:121:GLY:HA3	1.83	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:LEU:HD23	1:B:165:LEU:C	2.03	0.79
1:B:177:ARG:HG3	1:B:177:ARG:HH11	1.47	0.78
1:B:195:ILE:O	1:B:195:ILE:CG1	2.31	0.78
1:A:75:PHE:CG	1:A:96:GLU:HG3	2.19	0.78
1:A:127:MET:HG3	1:A:211:MET:HE1	1.66	0.78
1:A:10:ASN:ND2	1:A:13:ARG:NH1	2.33	0.77
1:A:253:ARG:HG2	1:A:253:ARG:NH1	1.98	0.77
1:B:269:MET:CE	1:B:271:VAL:CG2	2.63	0.77
1:B:91:VAL:HG22	1:B:91:VAL:O	1.84	0.76
1:B:214:THR:HG21	1:B:323:GLU:HG3	1.66	0.76
1:B:75:PHE:CD2	1:B:94:MET:CE	2.64	0.76
1:B:260:ARG:HG2	1:B:260:ARG:HH21	1.51	0.75
1:B:94:MET:HE3	1:B:96:GLU:HG3	1.67	0.75
1:A:247:ASN:N	1:A:247:ASN:ND2	2.30	0.75
1:A:13:ARG:HG3	1:A:38:VAL:CG1	2.17	0.74
1:B:289:ASP:OD2	1:B:289:ASP:C	2.30	0.74
1:A:194:LYS:HG2	1:A:199:GLU:HG2	1.69	0.74
1:B:248:LEU:O	1:B:248:LEU:HD23	1.87	0.74
1:B:195:ILE:O	1:B:198:PHE:HB2	1.87	0.74
1:B:31:ASN:C	1:B:31:ASN:OD1	2.30	0.74
1:B:165:LEU:O	1:B:165:LEU:CD2	2.35	0.74
1:A:57:GLU:HG3	1:A:58:VAL:N	2.01	0.74
1:B:214:THR:HG22	1:B:215:ILE:HG12	1.69	0.74
1:B:289:ASP:OD2	1:B:291:MET:N	2.21	0.74
1:B:248:LEU:CD2	1:B:248:LEU:C	2.61	0.73
1:B:325:LEU:O	1:B:331:THR:CG2	2.36	0.73
1:B:284:LEU:HD12	1:B:285:TYR:N	2.02	0.73
1:B:325:LEU:CA	1:B:331:THR:HG21	2.18	0.72
1:B:68:ALA:O	3:B:1002:NAD:H51N	1.89	0.72
1:A:185:ASP:OD2	1:A:238:ARG:NH1	2.23	0.72
1:B:269:MET:HE2	1:B:271:VAL:HG23	1.72	0.72
1:B:121:GLY:H	1:B:124:ASN:ND2	1.89	0.71
1:A:147:PRO:HB3	1:A:157:LYS:HB2	1.73	0.70
1:B:211:MET:HA	1:B:214:THR:HG22	1.73	0.70
1:B:338:GLU:OE1	1:B:342:ARG:NH1	2.24	0.70
1:A:10:ASN:ND2	1:A:13:ARG:HH12	1.89	0.70
1:A:124:ASN:HB3	1:A:323:GLU:HB3	1.72	0.70
1:B:251:THR:O	1:B:255:ILE:HG22	1.92	0.70
1:B:91:VAL:O	1:B:91:VAL:CG2	2.39	0.70
1:B:269:MET:CE	1:B:271:VAL:HG23	2.22	0.70
1:A:214:THR:HG21	1:A:323:GLU:HG3	1.74	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:253:ARG:HB3	1:A:253:ARG:NH1	2.07	0.69
1:A:10:ASN:HD21	1:A:13:ARG:HH12	1.40	0.69
1:A:31:ASN:HD21	1:A:34:ASN:N	1.84	0.69
1:B:256:GLU:HB2	1:B:257:PRO:HD3	1.73	0.69
1:A:13:ARG:CG	1:A:38:VAL:CG1	2.71	0.68
1:A:247:ASN:N	1:A:247:ASN:HD22	1.91	0.68
1:B:69:LEU:HB3	1:B:70:PRO:HD2	1.74	0.68
1:A:157:LYS:HG3	1:A:263:THR:CG2	2.23	0.68
1:B:54:LYS:O	1:B:58:VAL:HG23	1.95	0.67
1:B:134:LEU:HD22	1:B:280:MET:HE1	1.63	0.67
1:B:289:ASP:OD2	1:B:290:SER:N	2.28	0.67
1:B:294:SER:O	1:B:298:VAL:HG23	1.93	0.67
1:A:246:GLU:C	1:A:247:ASN:HD22	2.03	0.67
1:A:31:ASN:ND2	1:A:33:GLU:HG2	2.10	0.67
1:B:156:TYR:HB3	1:B:259:MET:CE	2.22	0.66
1:A:13:ARG:HG3	1:A:38:VAL:HG11	1.76	0.66
1:A:207:GLY:HA3	1:A:222:GLU:OE2	1.95	0.66
1:B:134:LEU:HD13	1:B:280:MET:CE	2.26	0.66
1:A:54:LYS:O	1:A:57:GLU:HG2	1.95	0.66
1:B:248:LEU:O	1:B:248:LEU:HD22	1.95	0.65
1:A:177:ARG:NH2	4:A:2013:HOH:O	2.30	0.65
1:B:124:ASN:H	1:B:124:ASN:HD22	1.44	0.65
1:B:230:HIS:HE1	1:B:259:MET:HE1	1.62	0.64
1:B:177:ARG:HG3	1:B:177:ARG:NH1	2.12	0.64
1:A:325:LEU:O	1:A:331:THR:HG22	1.96	0.64
1:B:260:ARG:HG2	1:B:260:ARG:NH2	2.12	0.64
1:B:148:LYS:N	1:B:264:LYS:O	2.25	0.64
1:B:251:THR:O	1:B:255:ILE:CG2	2.46	0.64
1:B:264:LYS:HD3	1:B:288:GLU:HB3	1.80	0.63
1:B:94:MET:HE3	1:B:96:GLU:CG	2.29	0.63
1:A:111:THR:HB	1:A:316:THR:O	1.98	0.63
1:A:153:PRO:O	1:A:233:LYS:HE2	1.98	0.63
1:A:247:ASN:O	1:A:251:THR:HG23	1.99	0.63
1:B:195:ILE:HG12	1:B:198:PHE:HB2	1.81	0.62
1:A:242:PHE:O	1:A:251:THR:HG21	1.98	0.62
1:B:127:MET:HE2	1:B:136:LEU:HD21	1.76	0.62
1:B:195:ILE:CD1	1:B:268:ILE:HD11	2.29	0.62
1:B:332:PHE:O	1:B:336:ILE:HG12	1.99	0.62
1:A:104:GLU:N	1:A:104:GLU:OE2	2.29	0.62
1:A:157:LYS:HG3	1:A:263:THR:HG23	1.81	0.62
1:B:165:LEU:C	1:B:165:LEU:HD22	2.23	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:34:ASN:ND2	1:B:37:LYS:HE3	2.11	0.62
1:A:79:LYS:NZ	4:A:2057:HOH:O	2.33	0.62
1:B:69:LEU:HB3	1:B:70:PRO:CD	2.30	0.61
1:B:264:LYS:HE2	4:B:2041:HOH:O	1.99	0.61
1:A:48:ASP:OD2	1:A:50:SER:N	2.33	0.60
1:A:151:LYS:HE2	1:A:261:TYR:CD1	2.35	0.60
1:A:338:GLU:OE1	1:A:342:ARG:NH2	2.35	0.59
1:B:134:LEU:HD13	1:B:280:MET:HE2	1.84	0.59
1:B:165:LEU:HD21	1:B:169:TYR:CE2	2.38	0.59
1:A:214:THR:HG21	1:A:323:GLU:OE2	2.01	0.59
1:B:340:LYS:HZ3	1:B:345:SER:HG	1.51	0.59
1:B:148:LYS:HB2	1:B:264:LYS:O	2.02	0.59
1:B:138:GLU:OE1	1:B:274:LYS:NZ	2.33	0.58
1:B:198:PHE:HB3	1:B:200:PHE:CE1	2.39	0.58
1:A:46:LYS:NZ	4:A:2051:HOH:O	2.35	0.58
1:B:50:SER:HB3	4:B:2006:HOH:O	2.03	0.58
1:B:340:LYS:NZ	1:B:345:SER:OG	2.32	0.58
1:A:194:LYS:CG	1:A:199:GLU:HG2	2.31	0.58
1:A:208:LEU:HD13	1:A:222:GLU:HB3	1.86	0.58
1:A:325:LEU:O	1:A:331:THR:HG23	2.03	0.58
1:B:146:LEU:HB3	1:B:147:PRO:HD2	1.84	0.57
1:A:289:ASP:C	1:A:289:ASP:OD1	2.47	0.57
1:B:190:VAL:CG1	1:B:231:LEU:HD11	2.32	0.57
1:B:195:ILE:HD12	1:B:268:ILE:CD1	2.31	0.57
1:A:338:GLU:HB3	1:A:342:ARG:HH21	1.69	0.57
1:A:75:PHE:HB2	1:A:96:GLU:CG	2.35	0.57
1:A:289:ASP:OD1	1:A:291:MET:N	2.37	0.57
1:B:208:LEU:HD13	1:B:222:GLU:HB2	1.87	0.57
1:A:288:GLU:HG3	1:A:293:SER:HA	1.85	0.57
1:B:41:PHE:N	1:B:41:PHE:CD1	2.70	0.57
1:B:255:ILE:O	1:B:255:ILE:HG12	2.02	0.56
1:A:32:ASN:OD1	1:A:46:LYS:HE3	2.05	0.56
1:A:114:PHE:O	1:A:322:PRO:HD3	2.04	0.56
1:A:150:PRO:HB3	1:A:227:TRP:CD1	2.40	0.56
1:A:246:GLU:HB2	1:A:247:ASN:ND2	2.21	0.56
1:A:250:PHE:CZ	1:B:250:PHE:HB3	2.40	0.56
1:A:29:ASP:OD1	1:A:30:VAL:N	2.38	0.56
1:B:194:LYS:HA	1:B:198:PHE:O	2.06	0.55
1:A:252:LEU:O	1:A:256:GLU:HB2	2.07	0.55
1:A:91:VAL:HG13	1:A:91:VAL:O	2.04	0.55
1:B:256:GLU:CB	1:B:257:PRO:HD3	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:127:MET:HE3	1:B:136:LEU:CD2	2.34	0.55
1:A:95:PRO:HD2	1:A:96:GLU:OE1	2.06	0.55
1:A:117:GLY:O	1:A:121:GLY:HA3	2.07	0.55
1:B:122:LEU:HA	1:B:125:ILE:HD12	1.89	0.54
1:A:31:ASN:CG	1:A:33:GLU:HG2	2.33	0.54
1:B:138:GLU:HG2	1:B:219:ARG:CB	2.37	0.54
1:B:284:LEU:CD1	1:B:285:TYR:N	2.64	0.54
1:B:124:ASN:HD22	1:B:124:ASN:N	2.06	0.54
1:A:214:THR:CG2	1:A:215:ILE:HG12	2.36	0.54
1:B:175:VAL:HG23	1:B:177:ARG:HG2	1.89	0.53
1:B:129:ARG:NH2	1:B:132:GLN:HB2	2.23	0.53
1:B:325:LEU:HB3	1:B:331:THR:CG2	2.38	0.53
1:A:175:VAL:HG21	1:A:177:ARG:HD2	1.91	0.53
1:A:338:GLU:HB3	1:A:342:ARG:NH2	2.24	0.53
1:B:256:GLU:N	1:B:257:PRO:CD	2.70	0.53
1:A:75:PHE:CB	1:A:96:GLU:HG3	2.39	0.53
1:A:325:LEU:HA	1:A:331:THR:HG21	1.91	0.53
1:B:295:MET:HE2	1:B:295:MET:HA	1.89	0.53
1:B:269:MET:HE1	1:B:271:VAL:CG2	2.37	0.53
1:A:31:ASN:HD21	1:A:33:GLU:HG2	1.74	0.53
1:B:189:GLU:HB2	4:B:2054:HOH:O	2.08	0.53
1:A:312:GLU:O	1:A:313:ASN:HB2	2.08	0.52
1:A:133:GLU:HB2	1:A:280:MET:HE1	1.90	0.52
1:A:194:LYS:HG2	1:A:199:GLU:CG	2.39	0.52
1:B:20:LYS:HD3	1:B:41:PHE:CB	2.40	0.52
1:A:255:ILE:HA	1:A:258:LEU:HD22	1.92	0.52
1:B:8:ALA:O	1:B:13:ARG:NH2	2.43	0.52
1:B:75:PHE:HB2	1:B:96:GLU:HG3	1.92	0.52
1:A:118:PHE:CE2	1:A:269:MET:HE3	2.45	0.51
1:B:279:GLU:HG2	1:B:280:MET:N	2.21	0.51
1:B:165:LEU:CD2	1:B:169:TYR:CE2	2.93	0.51
1:B:51:ASN:C	1:B:51:ASN:HD22	2.17	0.51
1:B:20:LYS:HD3	1:B:41:PHE:HB3	1.93	0.51
1:B:210:SER:O	1:B:214:THR:HB	2.11	0.51
1:B:248:LEU:C	1:B:248:LEU:HD22	2.33	0.51
1:B:230:HIS:HE1	1:B:259:MET:CE	2.23	0.51
1:A:10:ASN:HD21	1:A:13:ARG:NH1	2.04	0.50
1:B:211:MET:HA	1:B:214:THR:CG2	2.41	0.50
1:B:137:LYS:O	1:B:217:SER:OG	2.29	0.50
1:A:54:LYS:O	1:A:57:GLU:CG	2.59	0.50
1:A:93:PHE:HB2	3:A:1001:NAD:O2D	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:PHE:HB3	1:A:251:THR:HG21	1.94	0.50
1:A:69:LEU:HB3	1:A:70:PRO:HD2	1.94	0.49
1:B:31:ASN:OD1	1:B:31:ASN:O	2.30	0.49
1:B:35:LEU:HG	1:B:44:PRO:HB2	1.94	0.49
1:A:250:PHE:CE1	1:B:250:PHE:HB3	2.47	0.49
1:B:97:ASN:O	1:B:100:GLU:HB2	2.12	0.49
1:A:127:MET:CG	1:A:211:MET:HE1	2.39	0.49
1:B:255:ILE:O	1:B:255:ILE:CG1	2.59	0.49
1:B:75:PHE:HB2	1:B:94:MET:HE3	1.95	0.49
1:B:214:THR:CG2	1:B:215:ILE:HG12	2.42	0.49
1:B:256:GLU:N	1:B:257:PRO:HD2	2.27	0.49
1:A:75:PHE:HB2	1:A:96:GLU:HG3	1.95	0.49
1:A:65:VAL:HG22	1:A:88:MET:HG3	1.95	0.48
1:A:214:THR:HG21	1:A:323:GLU:CG	2.43	0.48
1:B:52:PHE:O	1:B:56:VAL:HG13	2.14	0.48
1:A:171:ARG:HH21	1:A:171:ARG:CG	2.27	0.48
1:B:20:LYS:HB3	1:B:20:LYS:HE3	1.41	0.48
1:B:134:LEU:CD1	1:B:280:MET:CE	2.91	0.48
1:A:51:ASN:C	1:A:51:ASN:ND2	2.57	0.48
1:B:94:MET:CE	1:B:96:GLU:HG3	2.41	0.48
1:B:190:VAL:HG11	1:B:231:LEU:CD1	2.37	0.48
1:B:195:ILE:HD12	1:B:268:ILE:HD13	1.81	0.48
1:B:265:ASP:OD2	1:B:288:GLU:HB2	2.14	0.47
1:B:165:LEU:HD21	1:B:169:TYR:HE2	1.79	0.47
1:A:78:ILE:CD1	1:A:88:MET:SD	3.03	0.47
1:A:91:VAL:O	1:A:91:VAL:CG1	2.55	0.47
1:B:120:PRO:HG3	1:B:209:ARG:HD2	1.96	0.47
1:B:210:SER:HG	1:B:323:GLU:CD	2.21	0.47
1:A:27:ILE:HG21	1:A:38:VAL:HG21	1.95	0.47
1:B:134:LEU:HD13	1:B:280:MET:HE1	1.97	0.47
1:B:163:ARG:HB3	1:B:163:ARG:HH21	1.79	0.47
1:B:69:LEU:O	3:B:1002:NAD:C4D	2.59	0.47
1:A:174:ARG:HG3	1:A:212:LEU:HD11	1.97	0.47
1:B:138:GLU:HG2	1:B:219:ARG:HB3	1.97	0.47
1:A:13:ARG:HG2	1:A:38:VAL:CG1	2.44	0.47
1:A:127:MET:CB	1:A:211:MET:CE	2.93	0.46
1:A:256:GLU:N	1:A:257:PRO:CD	2.78	0.46
1:B:252:LEU:HD23	1:B:252:LEU:HA	1.65	0.46
1:A:246:GLU:C	1:A:247:ASN:ND2	2.67	0.46
1:B:65:VAL:O	1:B:88:MET:HA	2.16	0.46
1:B:291:MET:HB2	1:B:291:MET:HE2	1.34	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:265:ASP:OD2	1:B:265:ASP:C	2.59	0.46
1:A:27:ILE:O	1:A:27:ILE:HG23	2.16	0.45
1:B:195:ILE:CD1	1:B:200:PHE:HE1	2.29	0.45
1:B:250:PHE:HD2	1:B:250:PHE:O	1.98	0.45
1:A:92:SER:HA	3:A:1001:NAD:O3D	2.17	0.45
1:A:328:ARG:HG3	1:A:331:THR:CG2	2.46	0.45
1:A:130:ILE:HG23	1:A:280:MET:HE3	1.99	0.45
1:B:214:THR:HG22	1:B:215:ILE:N	2.32	0.45
1:A:291:MET:HE2	1:A:291:MET:HB2	1.65	0.45
1:B:124:ASN:ND2	1:B:124:ASN:N	2.65	0.45
1:B:210:SER:OG	1:B:323:GLU:OE1	2.29	0.45
1:A:194:LYS:HE3	1:A:199:GLU:HG3	1.99	0.44
1:B:138:GLU:HG2	1:B:219:ARG:HB2	1.99	0.44
1:B:28:GLY:HA3	1:B:47:VAL:CG1	2.47	0.44
1:B:340:LYS:HD2	1:B:340:LYS:HA	1.59	0.44
1:B:154:LEU:HB3	1:B:259:MET:HE3	2.00	0.44
1:A:127:MET:HB3	1:A:211:MET:HE3	1.99	0.44
1:A:134:LEU:HD22	1:A:280:MET:HE3	2.00	0.44
1:B:208:LEU:HB2	4:B:2056:HOH:O	2.17	0.44
1:A:78:ILE:HD12	1:A:88:MET:SD	2.58	0.44
1:B:94:MET:HA	1:B:95:PRO:HD3	1.82	0.44
1:B:152:PRO:HG3	1:B:155:TYR:CE1	2.53	0.44
1:B:154:LEU:HD13	1:B:154:LEU:HA	1.69	0.44
1:B:230:HIS:CE1	1:B:259:MET:CE	3.00	0.44
1:B:325:LEU:CB	1:B:331:THR:HG21	2.47	0.43
1:A:144:GLY:HA2	2:A:2001:SO4:O3	2.18	0.43
1:B:98:PRO:C	1:B:100:GLU:N	2.75	0.43
1:A:52:PHE:O	1:A:56:VAL:HG13	2.19	0.43
1:B:194:LYS:HE3	1:B:196:GLY:O	2.17	0.43
1:A:48:ASP:OD2	1:A:48:ASP:C	2.59	0.43
1:A:288:GLU:HG3	1:A:292:PHE:O	2.18	0.43
1:B:134:LEU:CD1	1:B:280:MET:HE2	2.47	0.43
1:B:248:LEU:CD2	1:B:252:LEU:HG	2.49	0.43
1:A:48:ASP:OD2	1:A:50:SER:HB3	2.15	0.43
1:A:148:LYS:HD3	1:A:264:LYS:HB2	2.00	0.43
1:B:214:THR:CG2	1:B:215:ILE:N	2.78	0.43
1:B:235:LYS:HE3	1:B:235:LYS:HB3	1.24	0.43
1:B:137:LYS:H	1:B:137:LYS:HG2	1.51	0.42
1:A:48:ASP:C	1:A:50:SER:N	2.77	0.42
1:A:69:LEU:HB3	1:A:70:PRO:CD	2.50	0.42
1:B:214:THR:HG21	1:B:323:GLU:CG	2.41	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:167:GLU:HA	1:A:170:THR:HG22	2.00	0.42
1:B:157:LYS:HD2	1:B:263:THR:HG22	2.02	0.42
1:A:52:PHE:O	1:A:56:VAL:CG1	2.68	0.42
1:B:150:PRO:HG3	1:B:227:TRP:CD1	2.55	0.42
1:B:330:ASP:OD1	1:B:330:ASP:N	2.50	0.42
1:A:127:MET:CB	1:A:211:MET:HE1	2.49	0.42
1:A:138:GLU:HG2	1:A:219:ARG:HB2	2.02	0.42
1:B:263:THR:OG1	1:B:264:LYS:N	2.52	0.42
1:A:115:ASP:HB3	1:A:120:PRO:HB2	2.02	0.41
1:A:137:LYS:HB3	1:A:137:LYS:HE3	1.61	0.41
1:A:36:GLU:OE1	1:A:39:LYS:HD2	2.19	0.41
1:A:102:ARG:HA	1:A:319:VAL:HG23	2.02	0.41
1:A:187:LEU:HD12	1:A:187:LEU:HA	1.84	0.41
1:A:339:LEU:HD12	1:A:339:LEU:HA	1.96	0.41
1:B:280:MET:HE3	1:B:280:MET:HB2	1.55	0.41
1:A:0:HIS:ND1	1:A:24:ASP:HB2	2.35	0.41
1:A:18:ASP:OD2	1:A:342:ARG:HD3	2.21	0.41
1:A:325:LEU:HA	1:A:325:LEU:HD23	1.84	0.41
1:B:214:THR:HG21	1:B:323:GLU:OE1	2.20	0.41
1:B:138:GLU:HA	1:B:219:ARG:O	2.20	0.41
1:A:101:LEU:HD12	1:A:101:LEU:HA	1.92	0.41
1:B:31:ASN:OD1	1:B:33:GLU:N	2.54	0.41
1:B:38:VAL:HG23	1:B:41:PHE:CZ	2.55	0.41
1:B:95:PRO:HD2	1:B:96:GLU:OE2	2.21	0.41
1:B:264:LYS:HB2	1:B:264:LYS:HE3	1.23	0.41
1:A:4:LEU:O	1:A:65:VAL:HA	2.21	0.41
1:A:127:MET:CB	1:A:211:MET:HE3	2.51	0.41
1:A:134:LEU:CD1	1:A:280:MET:HE2	2.24	0.41
1:B:46:LYS:HB2	1:B:46:LYS:HE3	1.20	0.41
1:B:191:LYS:HE3	1:B:191:LYS:HB3	1.80	0.41
1:B:216:ASN:HD22	1:B:216:ASN:HA	1.63	0.41
1:A:75:PHE:CE2	1:A:101:LEU:HD22	2.56	0.41
1:A:330:ASP:OD1	1:A:331:THR:N	2.52	0.41
1:A:166:ILE:O	1:A:166:ILE:HG22	2.20	0.40
1:A:79:LYS:HG3	1:A:101:LEU:HD21	2.02	0.40
1:A:246:GLU:HB2	1:A:247:ASN:HD21	1.85	0.40
1:B:20:LYS:HD3	1:B:41:PHE:HB2	2.03	0.40
1:A:13:ARG:HG2	1:A:38:VAL:HG12	2.02	0.40
1:A:52:PHE:CD2	1:A:52:PHE:C	2.99	0.40
1:B:56:VAL:HG23	1:B:60:LYS:HE2	2.03	0.40
1:B:163:ARG:HB3	1:B:163:ARG:NH2	2.35	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:166:ILE:HD13	1:B:166:ILE:HA	1.73	0.40
1:B:178:ASN:N	1:B:178:ASN:ND2	2.68	0.40
1:B:196:GLY:C	1:B:198:PHE:H	2.29	0.40
1:B:248:LEU:HD23	1:B:251:THR:HB	2.03	0.40
1:A:134:LEU:HD22	1:A:280:MET:CE	2.51	0.40
1:B:25:VAL:O	1:B:25:VAL:HG22	2.18	0.40
1:B:266:PHE:HB2	1:B:286:ASP:O	2.21	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	347/365 (95%)	342 (99%)	5 (1%)	0	100	100
1	B	341/365 (93%)	337 (99%)	4 (1%)	0	100	100
All	All	688/730 (94%)	679 (99%)	9 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	306/321 (95%)	240 (78%)	66 (22%)	1	0

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	302/321 (94%)	229 (76%)	73 (24%)	1	0
All	All	608/642 (95%)	469 (77%)	139 (23%)	1	0

All (139) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	LEU
1	A	10	ASN
1	A	20	LYS
1	A	25	VAL
1	A	30	VAL
1	A	31	ASN
1	A	33	GLU
1	A	36	GLU
1	A	39	LYS
1	A	51	ASN
1	A	54	LYS
1	A	56	VAL
1	A	57	GLU
1	A	63	GLU
1	A	64	LEU
1	A	65	VAL
1	A	76	LYS
1	A	78	ILE
1	A	79	LYS
1	A	84	SER
1	A	91	VAL
1	A	93	PHE
1	A	96	GLU
1	A	101	LEU
1	A	103	ASP
1	A	111	THR
1	A	112	ILE
1	A	125	ILE
1	A	134	LEU
1	A	136	LEU
1	A	137	LYS
1	A	148	LYS
1	A	151	LYS
1	A	154	LEU
1	A	157	LYS
1	A	161	SER

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Mol	Chain	Res	Type
1	A	165	LEU
1	A	166	ILE
1	A	170	THR
1	A	171	ARG
1	A	174	ARG
1	A	180	LYS
1	A	187	LEU
1	A	193	VAL
1	A	197	LYS
1	A	208	LEU
1	A	214	THR
1	A	219	ARG
1	A	222	GLU
1	A	232	GLU
1	A	236	VAL
1	A	238	ARG
1	A	240	LEU
1	A	246	GLU
1	A	247	ASN
1	A	251	THR
1	A	253	ARG
1	A	258	LEU
1	A	262	GLU
1	A	279	GLU
1	A	291	MET
1	A	314	THR
1	A	331	THR
1	A	333	ARG
1	A	339	LEU
1	A	345	SER
1	B	0	HIS
1	B	1	MET
1	B	6	LEU
1	B	11	ILE
1	B	20	LYS
1	B	25	VAL
1	B	31	ASN
1	B	35	LEU
1	B	38	VAL
1	B	40	GLU
1	B	41	PHE
1	B	43	THR

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Mol	Chain	Res	Type
1	B	46	LYS
1	B	47	VAL
1	B	54	LYS
1	B	56	VAL
1	B	57	GLU
1	B	60	LYS
1	B	64	LEU
1	B	65	VAL
1	B	84	SER
1	B	89	VAL
1	B	91	VAL
1	B	96	GLU
1	B	99	LEU
1	B	101	LEU
1	B	102	ARG
1	B	107	LYS
1	B	124	ASN
1	B	129	ARG
1	B	134	LEU
1	B	137	LYS
1	B	154	LEU
1	B	157	LYS
1	B	163	ARG
1	B	165	LEU
1	B	168	GLU
1	B	176	ILE
1	B	177	ARG
1	B	181	VAL
1	B	182	SER
1	B	189	GLU
1	B	191	LYS
1	B	192	LYS
1	B	194	LYS
1	B	195	ILE
1	B	197	LYS
1	B	199	GLU
1	B	208	LEU
1	B	214	THR
1	B	216	ASN
1	B	219	ARG
1	B	231	LEU
1	B	235	LYS

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Mol	Chain	Res	Type
1	B	248	LEU
1	B	255	ILE
1	B	262	GLU
1	B	264	LYS
1	B	265	ASP
1	B	269	MET
1	B	277	GLU
1	B	281	GLU
1	B	284	LEU
1	B	289	ASP
1	B	291	MET
1	B	293	SER
1	B	329	GLU
1	B	331	THR
1	B	335	ILE
1	B	339	LEU
1	B	340	LYS
1	B	342	ARG
1	B	347	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	31	ASN
1	A	34	ASN
1	A	51	ASN
1	A	178	ASN
1	A	247	ASN
1	B	10	ASN
1	B	32	ASN
1	B	34	ASN
1	B	51	ASN
1	B	124	ASN
1	B	178	ASN
1	B	216	ASN
1	B	313	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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$
2	SO4	A	2001	-	4,4,4	0.48	0	6,6,6	0.10	0
2	SO4	B	2002	-	4,4,4	0.46	0	6,6,6	0.25	0
3	NAD	A	1001	-	46,48,48	4.00	24 (52%)	64,73,73	3.50	33 (51%)
3	NAD	B	1002	-	46,48,48	4.28	24 (52%)	64,73,73	3.73	35 (54%)

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	1001	-	-	10/30/62/62	0/5/5/5
3	NAD	B	1002	-	-	7/30/62/62	0/5/5/5

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1002	NAD	PA-O3	13.87	1.74	1.59
3	A	1001	NAD	PA-O3	11.53	1.71	1.59
3	B	1002	NAD	C8A-N7A	11.18	1.53	1.31
3	A	1001	NAD	C8A-N9A	9.22	1.53	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	NAD	C8A-N7A	9.21	1.49	1.31
3	B	1002	NAD	O7N-C7N	8.38	1.39	1.24
3	B	1002	NAD	PN-O5D	8.20	1.91	1.59
3	A	1001	NAD	C3B-C4B	7.25	1.71	1.53
3	A	1001	NAD	O7N-C7N	7.10	1.37	1.24
3	B	1002	NAD	C2A-N3A	7.08	1.46	1.33
3	B	1002	NAD	C8A-N9A	6.83	1.49	1.37
3	A	1001	NAD	C2A-N1A	6.81	1.46	1.33
3	B	1002	NAD	C2N-N1N	6.73	1.42	1.35
3	A	1001	NAD	C2A-N3A	6.62	1.45	1.33
3	B	1002	NAD	O3D-C3D	6.36	1.58	1.43
3	A	1001	NAD	PN-O3	-6.06	1.53	1.59
3	A	1001	NAD	PN-O5D	5.59	1.81	1.59
3	A	1001	NAD	C5B-C4B	5.24	1.67	1.51
3	A	1001	NAD	C2N-N1N	4.98	1.40	1.35
3	B	1002	NAD	O4D-C4D	4.80	1.55	1.45
3	B	1002	NAD	O4D-C1D	4.23	1.46	1.40
3	B	1002	NAD	C6N-N1N	4.02	1.44	1.35
3	B	1002	NAD	C6N-C5N	3.95	1.46	1.38
3	A	1001	NAD	O4B-C1B	3.89	1.51	1.42
3	B	1002	NAD	PN-O3	3.69	1.63	1.59
3	B	1002	NAD	C7N-N7N	3.54	1.39	1.33
3	B	1002	NAD	C6A-N6A	3.49	1.43	1.34
3	B	1002	NAD	C2A-N1A	3.35	1.39	1.33
3	A	1001	NAD	C1B-N9A	3.28	1.55	1.46
3	B	1002	NAD	O4B-C4B	2.88	1.51	1.45
3	B	1002	NAD	C5D-C4D	2.79	1.60	1.51
3	A	1001	NAD	O4D-C4D	2.78	1.51	1.45
3	A	1001	NAD	C3D-C4D	-2.73	1.46	1.53
3	A	1001	NAD	C6N-C5N	2.71	1.44	1.38
3	B	1002	NAD	O2D-C2D	2.54	1.49	1.43
3	A	1001	NAD	C5A-N7A	-2.52	1.34	1.39
3	A	1001	NAD	C6A-N6A	2.50	1.40	1.34
3	B	1002	NAD	O4B-C1B	2.47	1.47	1.42
3	B	1002	NAD	PA-O2A	2.43	1.66	1.55
3	B	1002	NAD	C6A-N1A	2.42	1.42	1.35
3	B	1002	NAD	C5A-N7A	-2.41	1.34	1.39
3	B	1002	NAD	PN-O1N	2.31	1.58	1.50
3	A	1001	NAD	C4A-N3A	2.26	1.38	1.34
3	A	1001	NAD	O2B-C2B	2.20	1.48	1.43
3	A	1001	NAD	O4B-C4B	2.15	1.49	1.45
3	A	1001	NAD	C6N-N1N	2.11	1.40	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	NAD	PN-O1N	-2.10	1.43	1.50
3	A	1001	NAD	O3B-C3B	2.03	1.48	1.43

All (68) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	NAD	N3A-C2A-N1A	-12.15	110.19	128.58
3	B	1002	NAD	N3A-C2A-N1A	-11.83	110.67	128.58
3	A	1001	NAD	O7N-C7N-C3N	-11.46	105.58	119.60
3	B	1002	NAD	O7N-C7N-C3N	-11.39	105.67	119.60
3	A	1001	NAD	C2B-C1B-N9A	-9.26	90.31	113.30
3	B	1002	NAD	C5A-C4A-N9A	7.97	114.50	105.81
3	B	1002	NAD	N9A-C8A-N7A	-6.68	104.46	113.94
3	B	1002	NAD	C2A-N3A-C4A	6.23	127.04	111.83
3	B	1002	NAD	O7N-C7N-N7N	6.20	131.58	122.62
3	B	1002	NAD	C5A-C4A-N3A	-6.19	118.20	126.72
3	B	1002	NAD	C2B-C1B-N9A	-6.05	98.28	113.30
3	A	1001	NAD	C5A-C4A-N9A	5.90	112.24	105.81
3	B	1002	NAD	O2A-PA-O1A	5.86	139.69	112.44
3	A	1001	NAD	C3N-C7N-N7N	5.62	124.67	117.74
3	A	1001	NAD	C2A-N3A-C4A	5.26	124.67	111.83
3	A	1001	NAD	O5B-C5B-C4B	-5.25	91.12	108.99
3	A	1001	NAD	C6N-N1N-C1D	4.93	129.41	119.73
3	B	1002	NAD	C4D-O4D-C1D	-4.81	105.52	109.92
3	B	1002	NAD	O5B-C5B-C4B	-4.54	93.53	108.99
3	B	1002	NAD	C2N-C3N-C4N	4.42	123.40	118.26
3	A	1001	NAD	N9A-C8A-N7A	-4.38	107.72	113.94
3	A	1001	NAD	O7N-C7N-N7N	4.38	128.94	122.62
3	B	1002	NAD	O2N-PN-O1N	4.12	131.62	112.44
3	B	1002	NAD	C6N-N1N-C2N	-4.07	118.41	121.88
3	B	1002	NAD	O4B-C4B-C5B	-3.99	96.55	109.33
3	B	1002	NAD	C2A-N1A-C6A	3.98	125.27	118.73
3	A	1001	NAD	C5A-C4A-N3A	-3.82	121.45	126.72
3	B	1002	NAD	O4B-C1B-C2B	-3.79	98.51	106.62
3	A	1001	NAD	O2A-PA-O1A	3.67	129.53	112.44
3	B	1002	NAD	C3N-C7N-N7N	3.59	122.16	117.74
3	A	1001	NAD	O2B-C2B-C1B	-3.56	97.83	110.10
3	A	1001	NAD	C6N-N1N-C2N	-3.55	118.85	121.88
3	B	1002	NAD	O3D-C3D-C2D	-3.51	100.55	111.82
3	B	1002	NAD	O5D-C5D-C4D	-3.51	97.05	108.99
3	B	1002	NAD	O5D-PN-O1N	-3.43	95.35	108.94
3	A	1001	NAD	C2N-N1N-C1D	-3.42	111.58	119.13

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1002	NAD	C5A-N7A-C8A	3.36	108.73	103.45
3	A	1001	NAD	C5B-C4B-C3B	-3.32	103.27	115.21
3	A	1001	NAD	C2A-N1A-C6A	3.31	124.17	118.73
3	B	1002	NAD	O4B-C1B-N9A	3.26	114.35	108.09
3	B	1002	NAD	O2A-PA-O5B	-3.23	92.93	107.57
3	A	1001	NAD	N6A-C6A-N1A	-3.15	111.35	118.38
3	A	1001	NAD	C5D-C4D-C3D	-3.14	103.92	115.21
3	A	1001	NAD	C3B-C2B-C1B	-3.05	95.70	101.46
3	A	1001	NAD	C4A-N9A-C8A	-3.00	102.59	105.74
3	B	1002	NAD	C6N-N1N-C1D	2.95	125.51	119.73
3	B	1002	NAD	O2B-C2B-C3B	2.90	121.12	111.82
3	B	1002	NAD	O2B-C2B-C1B	-2.89	100.16	110.10
3	A	1001	NAD	O2N-PN-O3	2.89	115.07	107.27
3	A	1001	NAD	O4B-C4B-C3B	-2.69	99.81	105.15
3	B	1002	NAD	C4A-C5A-N7A	-2.68	107.52	110.58
3	B	1002	NAD	C6A-C5A-C4A	2.64	120.79	117.18
3	A	1001	NAD	O4B-C1B-C2B	-2.62	101.02	106.62
3	A	1001	NAD	C4B-O4B-C1B	-2.59	103.74	109.47
3	A	1001	NAD	O2N-PN-O1N	2.59	124.50	112.44
3	B	1002	NAD	O3B-C3B-C2B	-2.57	103.56	111.82
3	A	1001	NAD	PA-O5B-C5B	-2.57	106.65	121.35
3	B	1002	NAD	O3B-C3B-C4B	-2.49	103.94	111.08
3	A	1001	NAD	O2N-PN-O5D	-2.45	96.47	107.57
3	A	1001	NAD	O3D-C3D-C4D	-2.36	104.30	111.08
3	A	1001	NAD	C5N-C4N-C3N	2.24	122.57	120.36
3	B	1002	NAD	C4N-C3N-C7N	-2.20	115.06	121.06
3	A	1001	NAD	O4B-C4B-C5B	-2.17	102.37	109.33
3	B	1002	NAD	O2A-PA-O3	-2.16	101.43	107.27
3	B	1002	NAD	O3-PN-O1N	2.15	117.17	110.70
3	A	1001	NAD	O3-PA-O1A	-2.11	104.35	110.70
3	B	1002	NAD	C2B-C3B-C4B	2.07	106.61	102.61
3	A	1001	NAD	O3D-C3D-C2D	-2.00	105.41	111.82

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1001	NAD	C5D-O5D-PN-O2N
3	A	1001	NAD	O4D-C4D-C5D-O5D
3	A	1001	NAD	O4D-C1D-N1N-C6N
3	A	1001	NAD	C2D-C1D-N1N-C6N
3	B	1002	NAD	C5D-O5D-PN-O3

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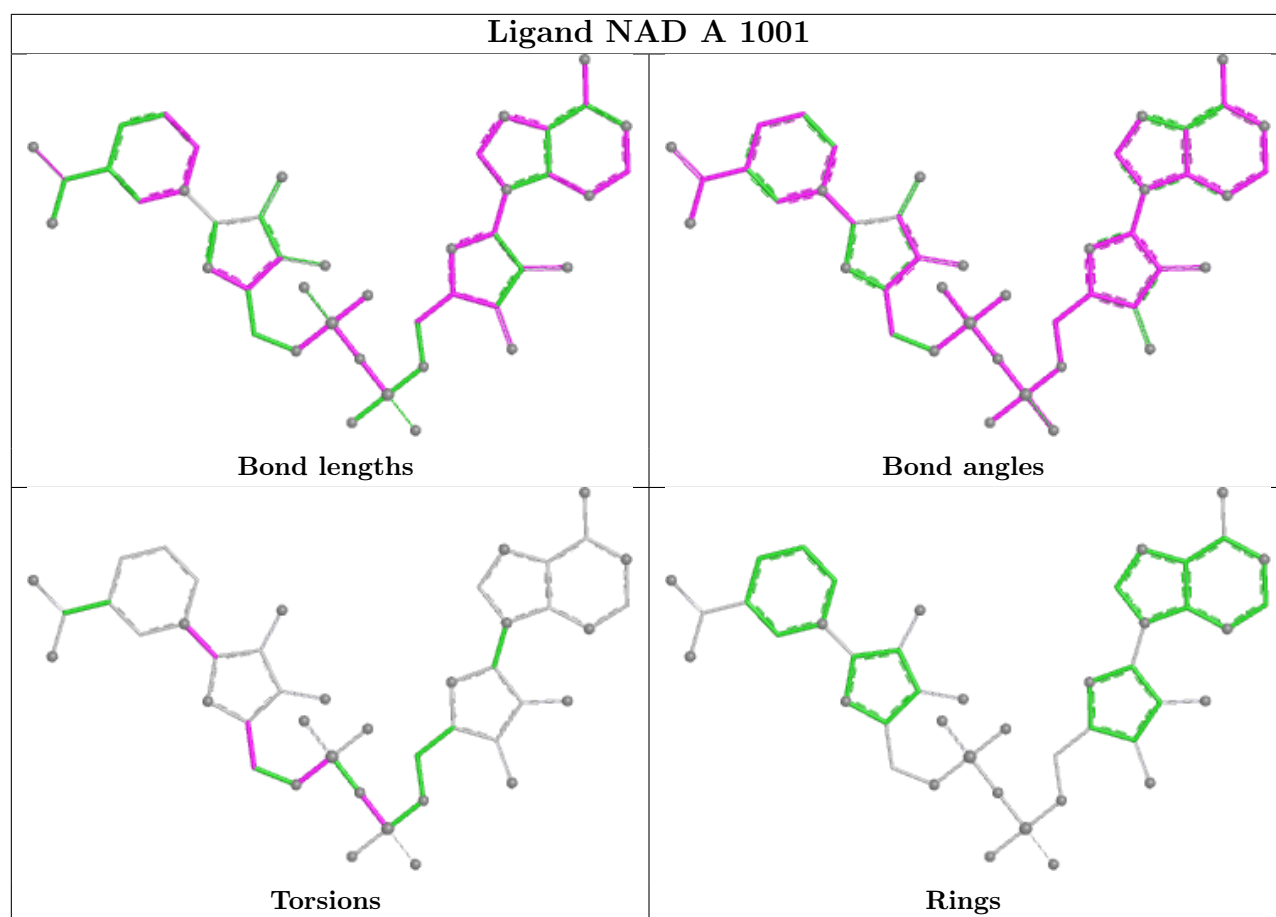
Mol	Chain	Res	Type	Atoms
3	B	1002	NAD	O4D-C4D-C5D-O5D
3	A	1001	NAD	C3D-C4D-C5D-O5D
3	B	1002	NAD	C3D-C4D-C5D-O5D
3	A	1001	NAD	C5D-O5D-PN-O3
3	A	1001	NAD	C5D-O5D-PN-O1N
3	A	1001	NAD	C2D-C1D-N1N-C2N
3	B	1002	NAD	C2D-C1D-N1N-C2N
3	A	1001	NAD	O4D-C1D-N1N-C2N
3	B	1002	NAD	O4D-C1D-N1N-C2N
3	A	1001	NAD	PN-O3-PA-O1A
3	B	1002	NAD	O4B-C4B-C5B-O5B
3	B	1002	NAD	PN-O3-PA-O2A

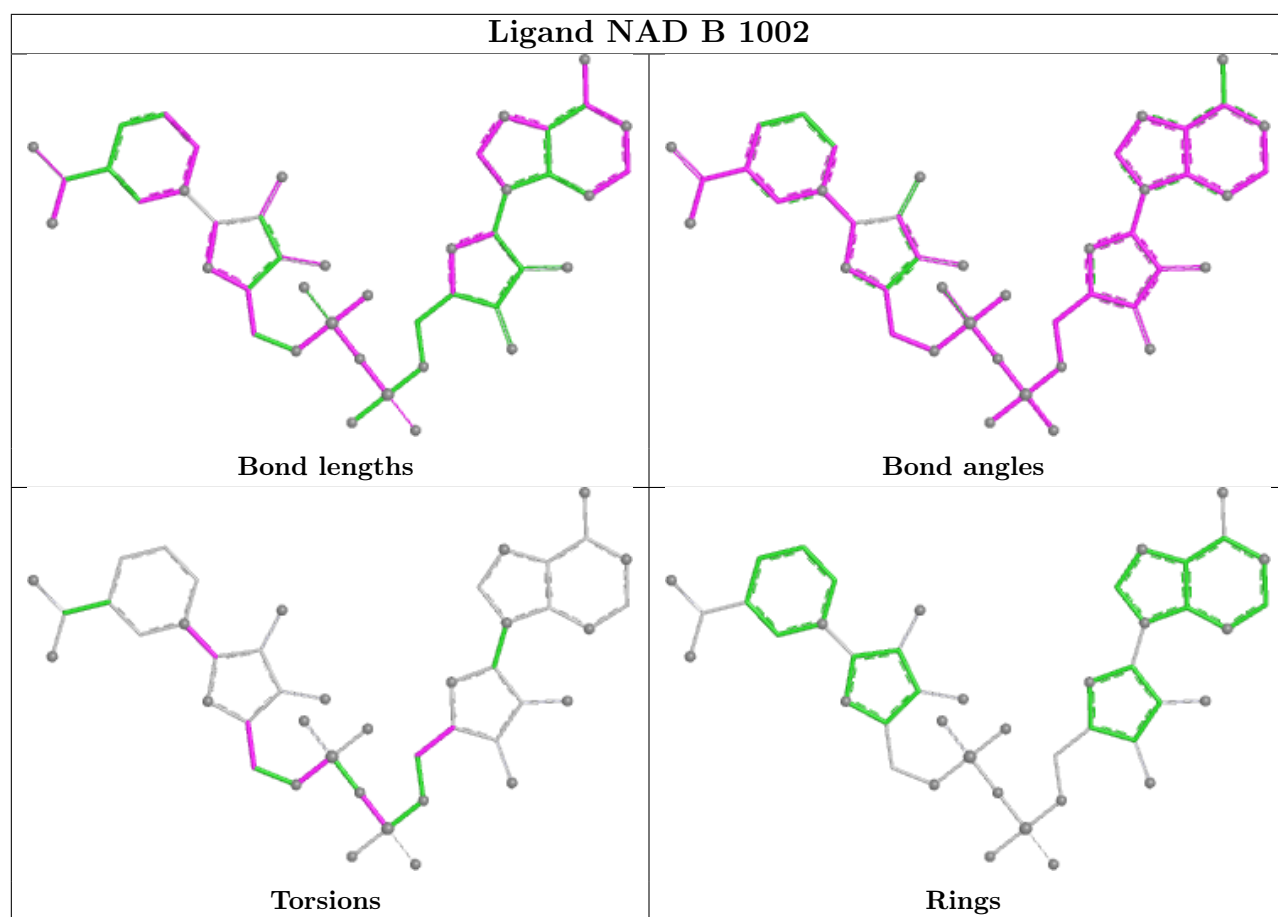
There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2001	SO4	1	0
3	A	1001	NAD	2	0
3	B	1002	NAD	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	349/365 (95%)	-0.10	2 (0%) 85 87	29, 48, 73, 93	0
1	B	345/365 (94%)	0.24	9 (2%) 57 57	33, 55, 83, 107	0
All	All	694/730 (95%)	0.07	11 (1%) 70 72	29, 51, 79, 107	0

All (11) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	162	PRO	3.6
1	A	0	HIS	2.8
1	B	250	PHE	2.7
1	B	0	HIS	2.5
1	B	157	LYS	2.4
1	A	315	CYS	2.2
1	B	195	ILE	2.2
1	B	199	GLU	2.2
1	B	278	GLY	2.1
1	B	277	GLU	2.1
1	B	57	GLU	2.1

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

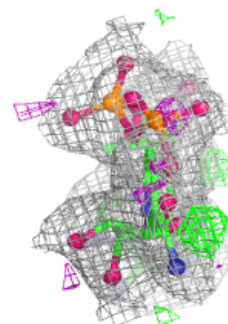
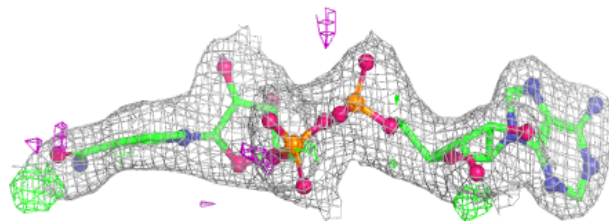
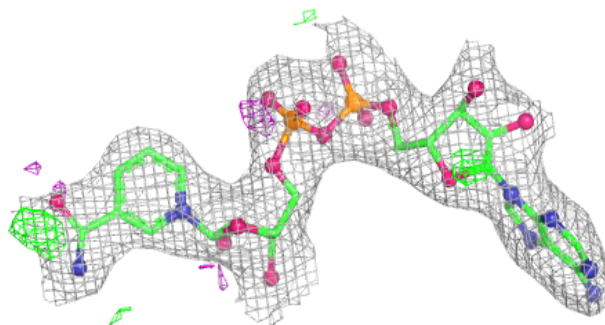
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	SO4	A	2001	5/5	0.82	0.17	53,61,70,73	0
2	SO4	B	2002	5/5	0.83	0.22	69,72,84,85	0
3	NAD	A	1001	44/44	0.93	0.09	32,47,55,65	0
3	NAD	B	1002	44/44	0.93	0.09	28,53,64,67	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.

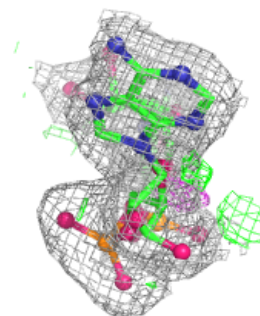
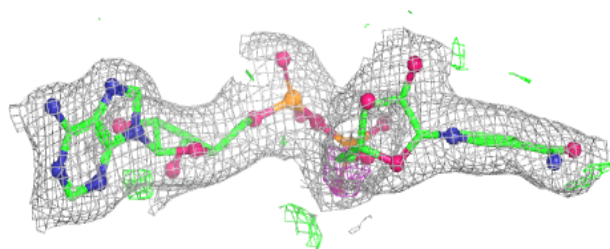
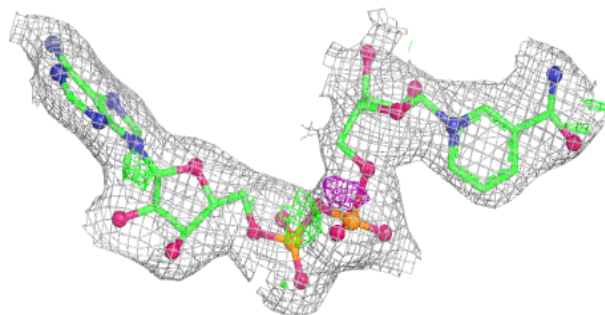
Electron density around NAD A 1001:

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 B 1002:

$2mF_o-DF_c$ (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.