



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:19 PM UTC

PDB ID : 1K0U / pdb_00001k0u
Title : Inhibition of S-adenosylhomocysteine Hydrolase by "acyclic sugar" Adenosine Analogue D-eritadenine
Authors : Takusagawa, F.; Huang, Y.; Komoto, J.; Takata, Y.; Gomi, T.; Ogawa, H.; Fujioka, M.; Powell, D.
Deposited on : 2001-09-20
Resolution : 3.00 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

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

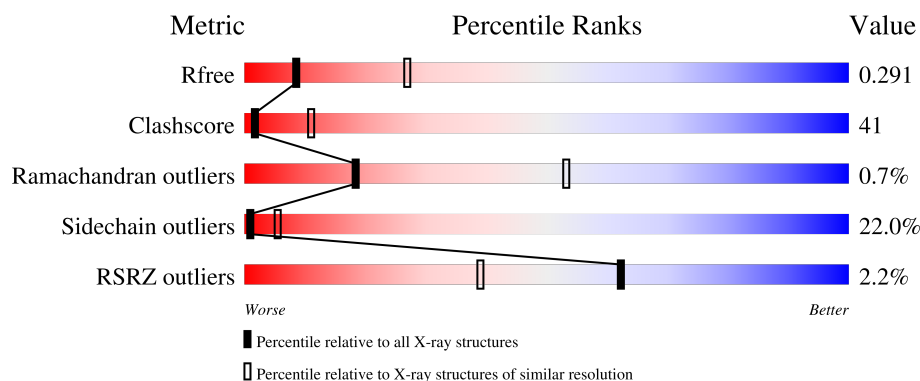
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	431	2% 45% 41% 13%
1	B	431	3% 43% 44% 13%
1	C	431	3% 46% 42% 12%
1	D	431	3% 44% 43% 13%

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Mol	Chain	Length	Quality of chain
1	E	431	% 32% 51% 16%
1	F	431	2% 35% 51% 13%
1	G	431	% 32% 51% 17%
1	H	431	3% 32% 50% 17%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 27522 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 S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE.

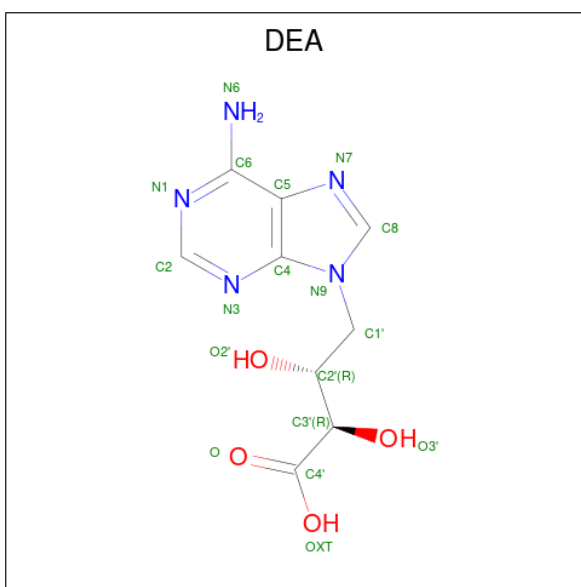
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	0	0
			3319	2108	571	615	25			
1	B	430	Total	C	N	O	S	0	0	0
			3319	2108	571	615	25			
1	C	430	Total	C	N	O	S	0	0	0
			3319	2108	571	615	25			
1	D	430	Total	C	N	O	S	0	0	0
			3319	2108	571	615	25			
1	E	430	Total	C	N	O	S	0	0	0
			3319	2108	571	615	25			
1	F	430	Total	C	N	O	S	0	0	0
			3319	2108	571	615	25			
1	G	430	Total	C	N	O	S	0	0	0
			3319	2108	571	615	25			
1	H	430	Total	C	N	O	S	0	0	0
			3319	2108	571	615	25			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	E	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	F	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	G	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
2	H	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 3 is D-ERITADENINE (CCD ID: DEA) (formula: C₉H₁₁N₅O₄).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			18	9	5	4		
3	B	1	Total	C	N	O	0	0
			18	9	5	4		
3	C	1	Total	C	N	O	0	0
			18	9	5	4		
3	D	1	Total	C	N	O	0	0
			18	9	5	4		
3	E	1	Total	C	N	O	0	0
			18	9	5	4		
3	F	1	Total	C	N	O	0	0
			18	9	5	4		
3	G	1	Total	C	N	O	0	0
			18	9	5	4		
3	H	1	Total	C	N	O	0	0
			18	9	5	4		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	69	Total	O	0	0
			69	69		
4	B	52	Total	O	0	0
			52	52		
4	C	53	Total	O	0	0
			53	53		
4	D	51	Total	O	0	0
			51	51		

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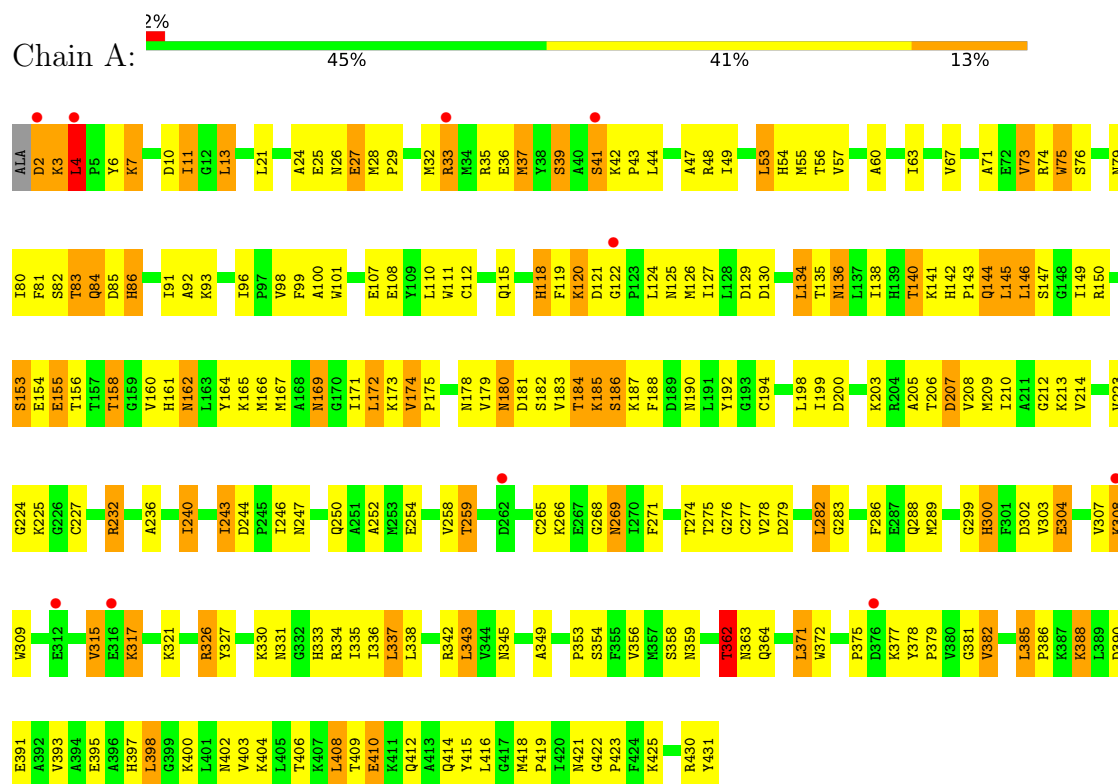
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	68	Total 68	O 68	0	0
4	F	68	Total 68	O 68	0	0
4	G	57	Total 57	O 57	0	0
4	H	56	Total 56	O 56	0	0

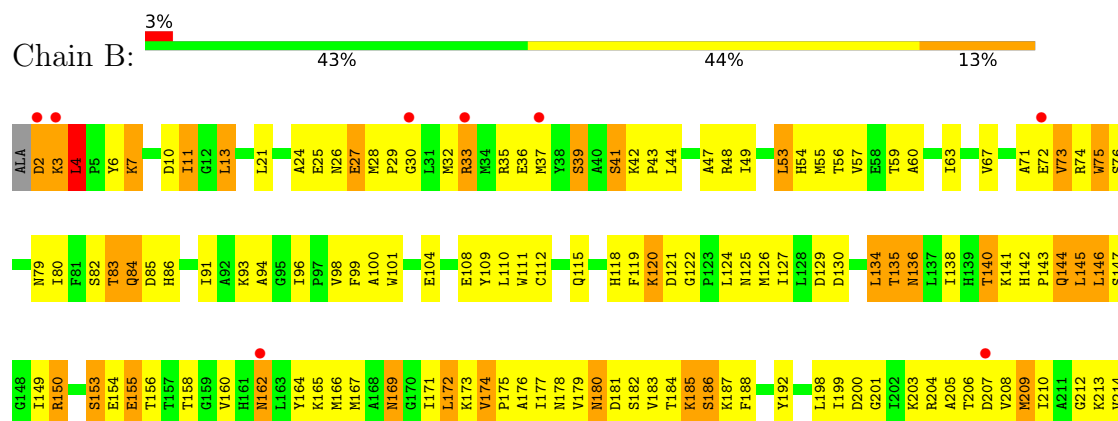
3 Residue-property plots

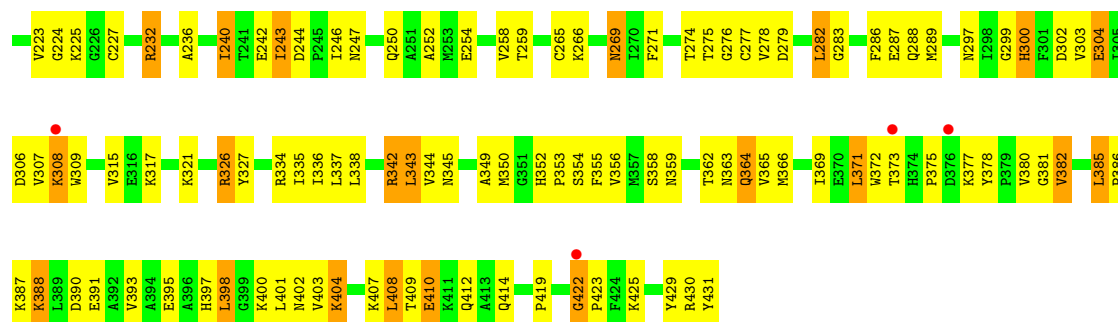
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE

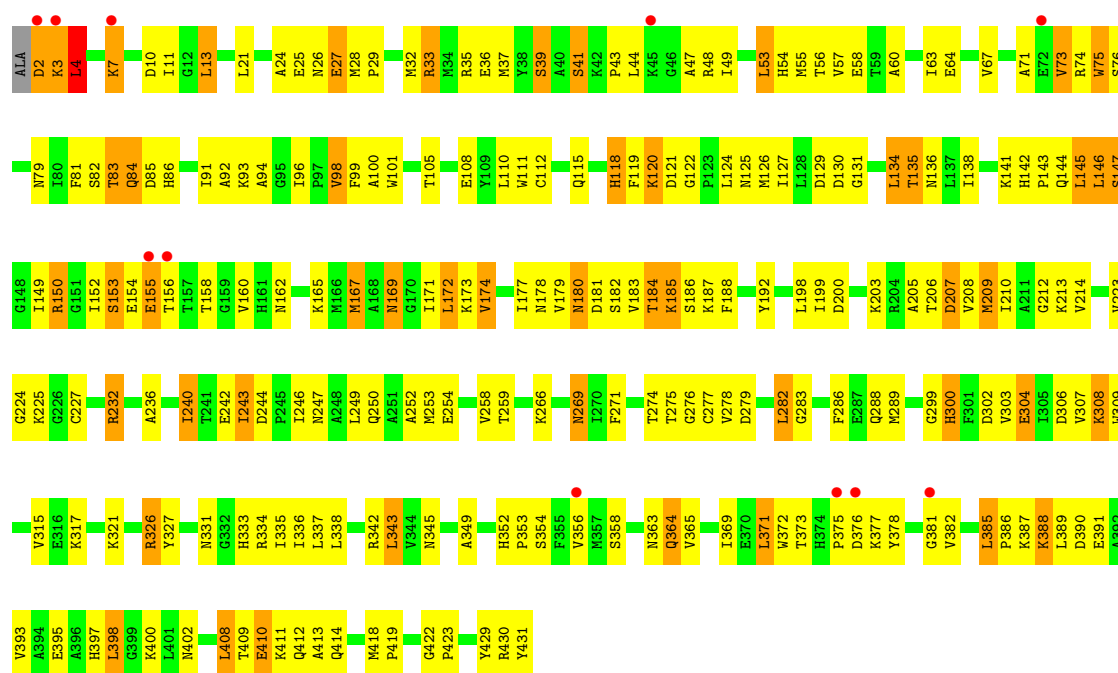


• Molecule 1: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE

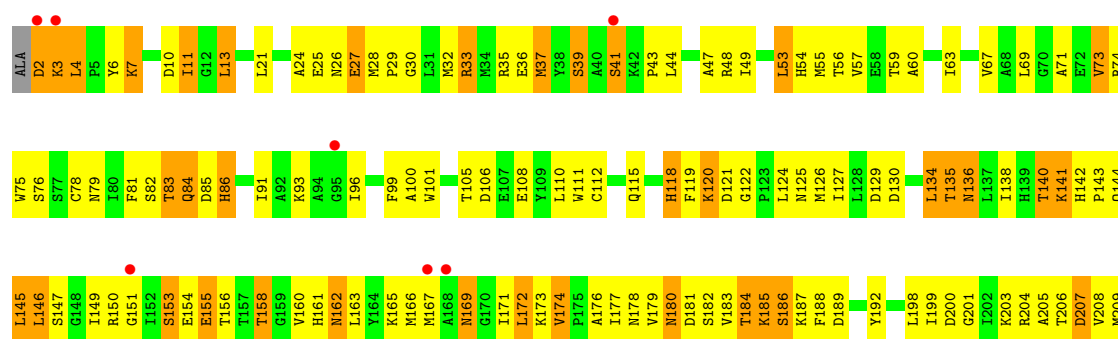
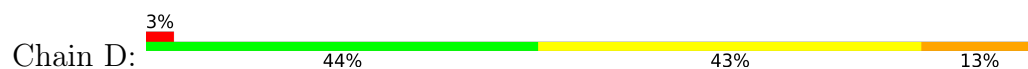


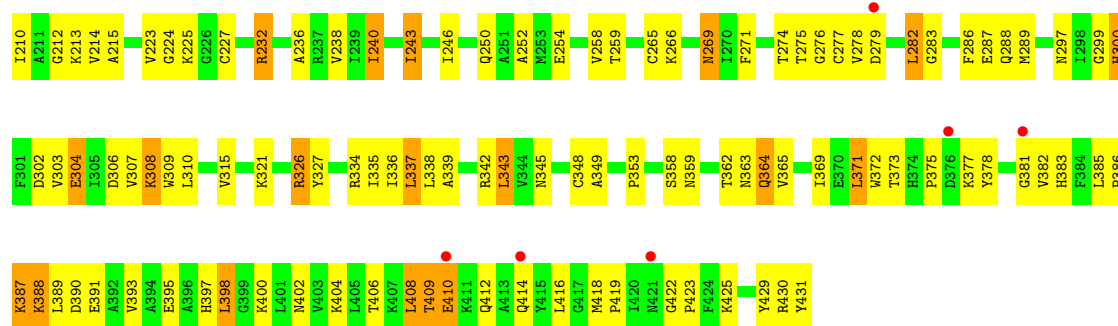


• Molecule 1: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE

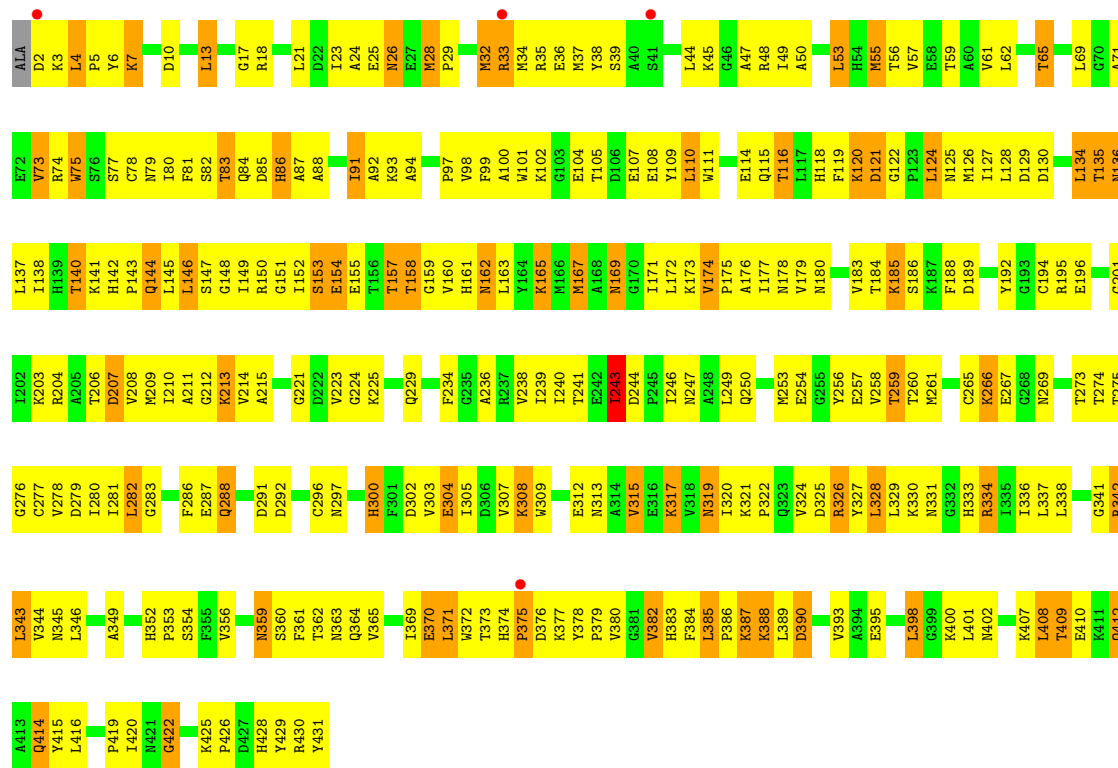


• Molecule 1: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE

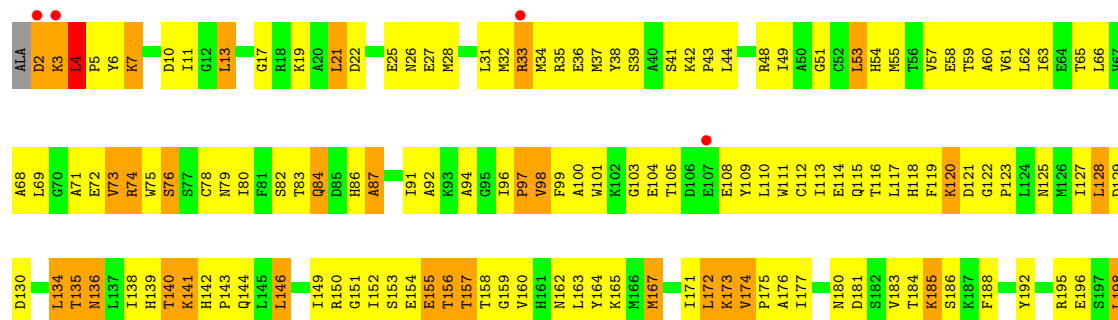


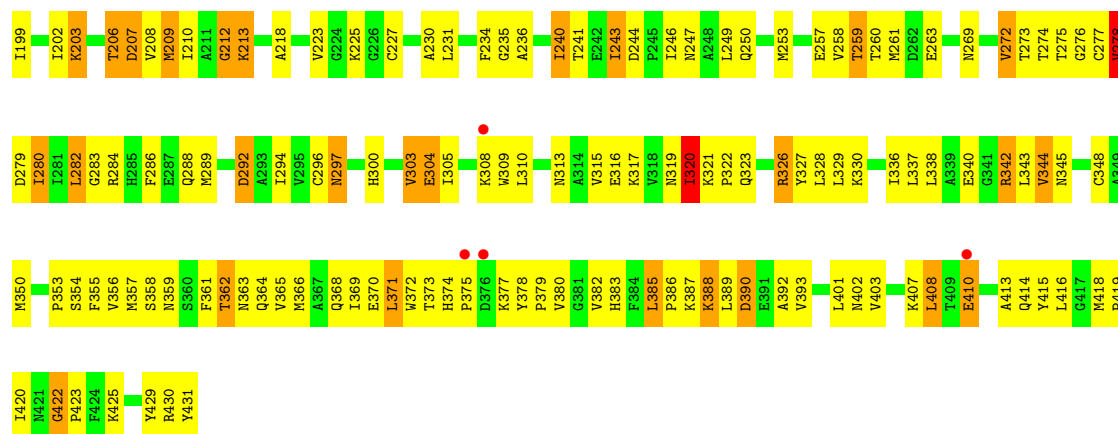


Molecule 1: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE

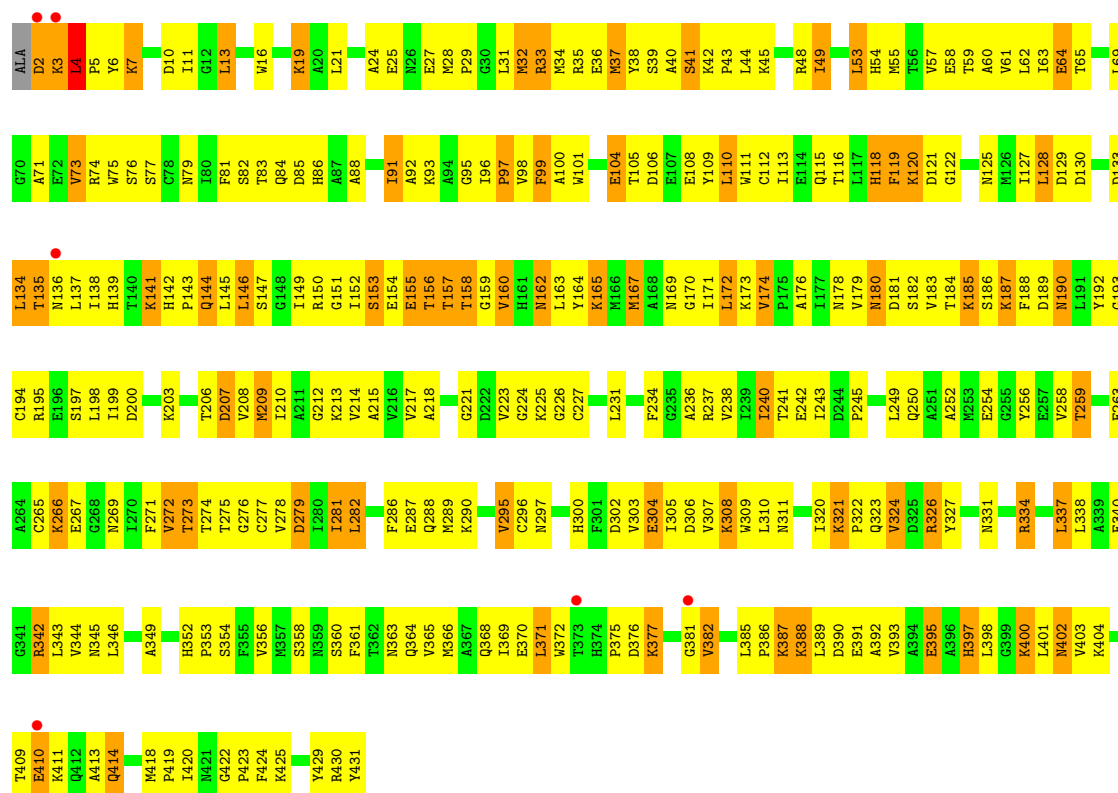


Molecule 1: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE

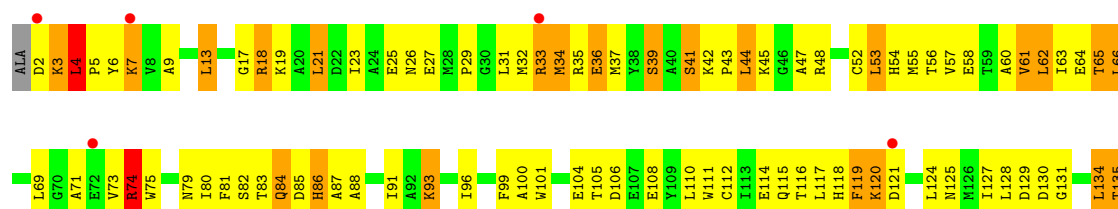




● Molecule 1: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE



● Molecule 1: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	89.87Å 177.37Å 112.16Å 90.00° 107.60° 90.00°	Depositor
Resolution (Å)	10.00 – 3.00 10.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	85.0 (10.00-3.00) 85.9 (10.00-3.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.14 (at 3.01Å)	Xtriage
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.183 , 0.265 0.215 , 0.291	Depositor DCC
R_{free} test set	5993 reflections (10.15%)	wwPDB-VP
Wilson B-factor (Å ²)	20.1	Xtriage
Anisotropy	0.541	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 70.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	27522	wwPDB-VP
Average B, all atoms (Å ²)	2.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 18.71% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: NAD, DEA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.40	0/3384	0.85	8/4579 (0.2%)
1	B	0.40	0/3384	0.86	5/4579 (0.1%)
1	C	0.41	0/3384	0.84	5/4579 (0.1%)
1	D	0.40	0/3384	0.86	6/4579 (0.1%)
1	E	0.42	0/3384	0.94	11/4579 (0.2%)
1	F	0.42	0/3384	0.94	8/4579 (0.2%)
1	G	0.43	0/3384	0.91	6/4579 (0.1%)
1	H	0.43	0/3384	0.95	8/4579 (0.2%)
All	All	0.41	0/27072	0.90	57/36632 (0.2%)

There are no bond length outliers.

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	73	VAL	N-CA-C	7.60	119.56	108.53
1	D	73	VAL	N-CA-C	7.32	119.02	108.48
1	A	73	VAL	N-CA-C	7.25	118.92	108.48
1	B	73	VAL	N-CA-C	7.12	118.73	108.48
1	G	73	VAL	N-CA-C	6.80	119.32	108.85
1	G	85	ASP	N-CA-C	6.70	119.44	111.33
1	A	85	ASP	N-CA-C	6.54	119.23	111.71
1	E	28	MET	CA-C-N	6.54	127.05	119.47
1	E	28	MET	C-N-CA	6.54	127.05	119.47
1	H	182	SER	N-CA-C	-6.48	99.74	110.17
1	C	85	ASP	N-CA-C	6.41	118.27	111.28
1	E	85	ASP	N-CA-C	6.31	118.97	111.33
1	C	73	VAL	N-CA-C	6.25	117.59	108.53
1	H	34	MET	N-CA-C	-6.18	103.85	112.45
1	F	186	SER	N-CA-C	5.97	117.45	111.07
1	F	21	LEU	N-CA-C	-5.90	104.93	111.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	65	THR	N-CA-C	-5.88	104.28	112.45
1	F	362	THR	N-CA-C	-5.87	104.96	111.36
1	G	19	LYS	N-CA-C	-5.87	104.96	111.36
1	D	85	ASP	N-CA-C	5.72	119.07	111.75
1	H	74	ARG	N-CA-C	-5.70	98.33	108.13
1	D	269	ASN	N-CA-C	-5.68	106.89	113.88
1	A	118	HIS	N-CA-C	5.63	118.14	109.07
1	F	73	VAL	N-CA-C	5.63	117.52	108.85
1	A	269	ASN	N-CA-C	-5.62	106.78	113.97
1	B	186	SER	N-CA-C	5.59	117.84	111.02
1	F	303	VAL	N-CA-C	-5.56	107.86	113.20
1	A	186	SER	N-CA-C	5.55	117.01	111.07
1	C	75	TRP	N-CA-C	5.55	118.67	110.46
1	G	118	HIS	N-CA-C	5.54	117.98	109.07
1	E	363	ASN	N-CA-C	-5.51	105.35	111.36
1	B	75	TRP	N-CA-C	5.49	118.59	110.46
1	E	243	ILE	N-CA-C	-5.49	107.00	113.42
1	D	118	HIS	N-CA-C	5.49	117.90	109.07
1	C	118	HIS	N-CA-C	5.45	118.13	109.24
1	E	83	THR	N-CA-C	5.45	118.14	110.23
1	D	186	SER	N-CA-C	5.45	116.90	111.07
1	B	269	ASN	N-CA-C	-5.43	107.20	113.88
1	E	320	ILE	N-CA-C	-5.42	105.44	110.53
1	G	133	ASP	N-CA-C	5.35	117.19	111.36
1	B	85	ASP	N-CA-C	5.35	117.86	111.71
1	F	87	ALA	N-CA-C	-5.32	105.38	111.07
1	F	320	ILE	N-CA-C	-5.31	105.54	110.53
1	A	75	TRP	N-CA-C	5.27	117.89	110.14
1	H	4	LEU	CA-C-N	5.26	125.58	119.47
1	H	4	LEU	C-N-CA	5.26	125.58	119.47
1	G	49	ILE	N-CA-C	5.23	116.28	108.54
1	H	66	LEU	N-CA-C	-5.23	105.58	111.28
1	H	257	GLU	N-CA-C	-5.21	101.97	110.20
1	E	75	TRP	N-CA-C	5.18	118.18	110.14
1	H	277	CYS	N-CA-C	5.16	118.13	110.14
1	D	151	GLY	N-CA-C	5.13	118.19	110.18
1	E	426	PRO	N-CA-C	-5.12	103.73	111.41
1	A	362	THR	N-CA-C	-5.12	105.78	111.36
1	F	278	VAL	CB-CA-C	-5.10	105.98	111.59
1	A	268	GLY	N-CA-C	5.10	117.32	111.36
1	C	269	ASN	N-CA-C	-5.04	107.68	113.88

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	3319	0	3341	252	0
1	B	3319	0	3341	260	0
1	C	3319	0	3341	247	0
1	D	3319	0	3341	252	0
1	E	3319	0	3341	320	0
1	F	3319	0	3341	297	0
1	G	3319	0	3341	360	0
1	H	3319	0	3341	341	0
2	A	44	0	26	2	0
2	B	44	0	26	3	0
2	C	44	0	26	3	0
2	D	44	0	26	2	0
2	E	44	0	26	3	0
2	F	44	0	26	2	0
2	G	44	0	26	6	0
2	H	44	0	26	5	0
3	A	18	0	10	0	0
3	B	18	0	10	0	0
3	C	18	0	10	0	0
3	D	18	0	10	0	0
3	E	18	0	10	0	0
3	F	18	0	10	1	0
3	G	18	0	10	0	0
3	H	18	0	10	0	0
4	A	69	0	0	0	0
4	B	52	0	0	1	0
4	C	53	0	0	0	0
4	D	51	0	0	0	0
4	E	68	0	0	0	0
4	F	68	0	0	0	0
4	G	57	0	0	0	0
4	H	56	0	0	0	0
All	All	27522	0	27016	2200	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 41.

All (2200) 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:H:33:ARG:HA	1:H:33:ARG:HE	0.99	1.13
1:D:33:ARG:HH21	1:D:36:GLU:HB2	1.17	1.09
1:F:150:ARG:HD3	1:F:375:PRO:HB3	1.33	1.09
1:F:33:ARG:HH11	1:F:33:ARG:HG3	0.95	1.09
1:H:33:ARG:HA	1:H:33:ARG:NE	1.64	1.07
1:E:3:LYS:HD3	1:E:115:GLN:HE22	0.96	1.07
1:F:10:ASP:HB3	1:F:13:LEU:HD22	1.38	1.05
1:H:120:LYS:H	1:H:120:LYS:HE2	1.23	1.04
1:H:33:ARG:HH22	1:H:37:MET:N	1.55	1.03
1:H:408:LEU:HD21	1:H:416:LEU:HD12	1.36	1.02
1:F:278:VAL:HG12	1:F:303:VAL:HB	1.41	1.01
1:E:395:GLU:HA	1:E:398:LEU:HD22	1.43	1.00
1:E:3:LYS:HD3	1:E:115:GLN:NE2	1.77	0.99
1:C:33:ARG:HH21	1:C:36:GLU:HB2	1.23	0.99
1:C:395:GLU:HA	1:C:398:LEU:HD22	1.44	0.99
1:B:353:PRO:HB2	1:D:209:MET:HB2	1.44	0.99
1:D:120:LYS:H	1:D:120:LYS:HE2	1.27	0.99
1:H:386:PRO:HG2	1:H:389:LEU:HD12	1.45	0.99
1:G:33:ARG:HH21	1:G:36:GLU:HB2	1.23	0.98
1:E:195:ARG:HH11	1:E:229:GLN:HE22	1.10	0.97
1:H:278:VAL:HG12	1:H:303:VAL:HB	1.47	0.97
1:A:7:LYS:HZ3	1:A:101:TRP:HE3	1.03	0.96
1:A:33:ARG:HH21	1:A:36:GLU:HB2	1.29	0.96
1:B:180:ASN:HA	1:B:185:LYS:HE3	1.48	0.96
1:F:33:ARG:HG3	1:F:33:ARG:NH1	1.76	0.95
1:E:195:ARG:NH1	1:E:229:GLN:HE22	1.64	0.95
1:G:275:THR:HG22	1:G:277:CYS:H	1.31	0.94
1:B:7:LYS:HZ3	1:B:101:TRP:HE3	1.00	0.94
1:B:33:ARG:HH21	1:B:36:GLU:HB2	1.33	0.94
1:B:275:THR:HG22	1:B:277:CYS:H	1.29	0.94
1:H:33:ARG:NH2	1:H:37:MET:H	1.64	0.94
1:C:7:LYS:HZ3	1:C:101:TRP:HE3	1.02	0.93
1:H:33:ARG:HH22	1:H:37:MET:H	0.96	0.93
1:C:275:THR:HG22	1:C:277:CYS:H	1.31	0.93
1:D:7:LYS:HZ3	1:D:101:TRP:HE3	0.93	0.92
1:F:57:VAL:H	1:F:84:GLN:NE2	1.67	0.92
1:B:120:LYS:H	1:B:120:LYS:HE2	1.36	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:277:CYS:HB2	1:F:416:LEU:HD21	1.52	0.91
1:E:275:THR:HG22	1:E:277:CYS:H	1.35	0.91
1:E:315:VAL:HG23	1:E:330:LYS:HG2	1.49	0.91
1:E:120:LYS:H	1:E:120:LYS:HE2	1.35	0.91
1:H:55:MET:HB3	1:H:83:THR:HG23	1.53	0.91
1:G:321:LYS:HD3	1:G:324:VAL:HG21	1.54	0.90
1:H:7:LYS:NZ	1:H:101:TRP:HE3	1.70	0.90
1:E:136:ASN:O	1:E:140:THR:HG23	1.71	0.90
1:E:195:ARG:HH11	1:E:229:GLN:NE2	1.68	0.90
1:F:4:LEU:HD13	1:F:99:PHE:HE1	1.34	0.90
1:A:55:MET:HB3	1:A:83:THR:HG23	1.53	0.89
1:B:395:GLU:HA	1:B:398:LEU:HD22	1.51	0.89
1:E:209:MET:HB2	1:G:353:PRO:HB2	1.55	0.89
1:D:55:MET:HB3	1:D:83:THR:HG23	1.55	0.89
1:F:275:THR:HG22	1:F:277:CYS:H	1.37	0.88
1:E:258:VAL:HB	1:F:403:VAL:HG13	1.53	0.88
1:A:395:GLU:HA	1:A:398:LEU:HD22	1.54	0.88
1:B:55:MET:HB3	1:B:83:THR:HG23	1.56	0.88
1:C:430:ARG:HD3	1:D:430:ARG:HA	1.53	0.88
1:G:7:LYS:NZ	1:G:101:TRP:HE3	1.70	0.88
1:H:419:PRO:HB2	1:H:422:GLY:H	1.38	0.87
1:E:35:ARG:HG3	1:E:65:THR:HG23	1.54	0.87
1:E:244:ASP:HB3	1:E:247:ASN:HB2	1.54	0.87
1:E:353:PRO:HB2	1:G:209:MET:HB2	1.55	0.87
1:F:198:LEU:HD22	1:F:227:CYS:HB3	1.55	0.87
1:E:150:ARG:HD3	1:E:375:PRO:HB3	1.55	0.87
1:A:53:LEU:HD12	1:A:130:ASP:HB2	1.56	0.87
1:F:7:LYS:HZ3	1:F:101:TRP:HE3	0.91	0.87
1:D:395:GLU:HA	1:D:398:LEU:HD22	1.54	0.87
1:A:120:LYS:HE2	1:A:120:LYS:H	1.37	0.86
1:C:120:LYS:HE2	1:C:120:LYS:H	1.37	0.86
1:A:37:MET:HB3	1:H:284:ARG:NH2	1.90	0.86
1:A:275:THR:HG22	1:A:277:CYS:H	1.38	0.86
1:G:395:GLU:HA	1:G:398:LEU:HD13	1.56	0.86
1:D:21:LEU:HD12	1:D:57:VAL:HG13	1.57	0.86
1:E:214:VAL:H	1:E:269:ASN:HD22	1.22	0.86
1:H:33:ARG:NE	1:H:33:ARG:CA	2.39	0.86
1:A:209:MET:HB2	1:C:353:PRO:HB2	1.58	0.85
1:F:55:MET:HB3	1:F:83:THR:HG23	1.58	0.85
1:B:33:ARG:HH11	1:B:33:ARG:HG3	1.41	0.85
1:F:33:ARG:HH11	1:F:33:ARG:CG	1.86	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:430:ARG:HA	1:D:430:ARG:HD3	1.57	0.85
1:E:3:LYS:CD	1:E:115:GLN:HE22	1.87	0.85
1:H:198:LEU:HD22	1:H:227:CYS:HB3	1.58	0.85
1:H:7:LYS:HZ3	1:H:101:TRP:HE3	0.87	0.85
1:C:150:ARG:HD3	1:C:375:PRO:HB3	1.57	0.84
1:G:33:ARG:HH11	1:G:33:ARG:HG3	1.41	0.84
1:E:7:LYS:NZ	1:E:101:TRP:HE3	1.76	0.84
1:A:326:ARG:HD2	1:A:336:ILE:HG12	1.60	0.84
1:E:33:ARG:NE	1:E:33:ARG:HA	1.93	0.83
1:G:55:MET:HB3	1:G:83:THR:HG23	1.60	0.83
1:A:180:ASN:HA	1:A:185:LYS:HE3	1.59	0.83
1:E:153:SER:HB3	1:E:364:GLN:HE22	1.43	0.83
1:F:4:LEU:N	1:F:4:LEU:HD12	1.94	0.83
1:F:54:HIS:HB3	1:F:82:SER:HB2	1.59	0.83
1:A:10:ASP:HB3	1:A:13:LEU:HD22	1.61	0.83
1:D:7:LYS:NZ	1:D:101:TRP:HE3	1.76	0.83
1:F:57:VAL:HG23	1:F:84:GLN:NE2	1.93	0.83
1:H:277:CYS:HB3	1:H:280:ILE:HD11	1.61	0.83
1:F:57:VAL:HG23	1:F:84:GLN:HE21	1.43	0.82
1:B:10:ASP:HB3	1:B:13:LEU:HD22	1.62	0.82
1:F:326:ARG:HG2	1:F:326:ARG:HH11	1.41	0.82
1:G:4:LEU:HD12	1:G:4:LEU:N	1.95	0.82
1:C:53:LEU:HD12	1:C:130:ASP:HB2	1.62	0.81
1:E:55:MET:HB3	1:E:83:THR:HG23	1.59	0.81
1:G:277:CYS:HB2	1:H:416:LEU:HD21	1.63	0.81
1:D:33:ARG:NH2	1:D:36:GLU:HB2	1.95	0.81
1:A:37:MET:HB3	1:H:284:ARG:HH21	1.44	0.81
1:D:275:THR:HG22	1:D:277:CYS:H	1.45	0.81
1:G:13:LEU:HB3	1:G:86:HIS:HA	1.63	0.81
1:H:7:LYS:HE2	1:H:112:CYS:SG	2.21	0.81
1:H:21:LEU:O	1:H:25:GLU:HG3	1.81	0.81
1:H:244:ASP:HB3	1:H:247:ASN:HD22	1.45	0.81
1:E:369:ILE:O	1:E:373:THR:HB	1.81	0.80
1:B:150:ARG:HD3	1:B:375:PRO:HB3	1.63	0.80
1:C:55:MET:HB3	1:C:83:THR:HG23	1.62	0.80
1:A:430:ARG:HD3	1:B:430:ARG:HA	1.62	0.80
1:G:295:VAL:HG13	1:G:305:ILE:HD13	1.62	0.80
1:G:7:LYS:HZ3	1:G:101:TRP:HE3	0.84	0.80
1:F:209:MET:SD	1:H:353:PRO:HG2	2.22	0.80
1:G:275:THR:HG22	1:G:276:GLY:N	1.96	0.80
1:D:7:LYS:HE2	1:D:112:CYS:SG	2.22	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:7:LYS:NZ	1:F:101:TRP:HE3	1.76	0.79
1:C:7:LYS:NZ	1:C:101:TRP:HE3	1.79	0.79
1:H:41:SER:HB2	1:H:43:PRO:HD3	1.63	0.79
1:F:7:LYS:HZ1	1:F:100:ALA:N	1.81	0.79
1:H:2:ASP:OD2	1:H:118:HIS:HB2	1.81	0.79
1:B:3:LYS:HD2	1:B:115:GLN:OE1	1.83	0.79
1:D:53:LEU:HD12	1:D:130:ASP:HB2	1.64	0.79
1:D:167:MET:HE3	1:D:381:GLY:HA2	1.65	0.79
1:B:7:LYS:HZ1	1:B:100:ALA:N	1.80	0.79
1:A:7:LYS:NZ	1:A:101:TRP:HE3	1.81	0.79
1:G:300:HIS:HA	1:G:343:LEU:HD11	1.65	0.79
1:A:353:PRO:HB2	1:C:209:MET:HB2	1.64	0.79
1:B:53:LEU:HD12	1:B:130:ASP:HB2	1.65	0.78
1:F:151:GLY:HA3	1:F:371:LEU:HG	1.66	0.78
1:G:430:ARG:HD3	1:H:430:ARG:HA	1.64	0.78
1:D:2:ASP:HB2	1:D:74:ARG:HH12	1.49	0.78
1:F:326:ARG:HD2	1:F:336:ILE:HG12	1.66	0.78
1:H:225:LYS:NZ	1:H:250:GLN:HE22	1.81	0.78
1:C:180:ASN:HA	1:C:185:LYS:HE3	1.66	0.77
1:D:180:ASN:HA	1:D:185:LYS:HE3	1.66	0.77
1:A:430:ARG:HA	1:B:430:ARG:HD3	1.66	0.77
1:B:7:LYS:NZ	1:B:101:TRP:HE3	1.81	0.77
1:E:120:LYS:H	1:E:120:LYS:CE	1.96	0.76
1:E:79:ASN:HB3	1:E:82:SER:OG	1.85	0.76
1:E:33:ARG:HG3	1:E:33:ARG:HH11	1.50	0.76
1:C:3:LYS:HD2	1:C:115:GLN:OE1	1.84	0.76
1:C:214:VAL:H	1:C:269:ASN:HD22	1.34	0.76
1:H:307:VAL:N	1:H:308:LYS:HE3	2.01	0.76
1:F:218:ALA:HA	1:F:241:THR:OG1	1.85	0.76
1:D:7:LYS:HZ1	1:D:100:ALA:N	1.83	0.76
1:F:119:PHE:HB3	1:F:120:LYS:HE2	1.67	0.76
1:E:7:LYS:HZ3	1:E:101:TRP:HE3	1.30	0.76
1:G:33:ARG:NE	1:G:33:ARG:HA	2.01	0.76
1:G:275:THR:HG22	1:G:277:CYS:N	2.02	0.75
1:H:308:LYS:CE	1:H:308:LYS:H	2.00	0.75
1:A:408:LEU:HD13	1:B:243:ILE:HG21	1.69	0.75
1:E:342:ARG:HG2	1:E:342:ARG:HH11	1.50	0.75
1:E:379:PRO:O	1:E:383:HIS:HE1	1.70	0.75
1:H:131:GLY:HA3	1:H:300:HIS:NE2	2.01	0.75
1:H:156:THR:O	1:H:160:VAL:HG23	1.86	0.75
1:C:21:LEU:HD12	1:C:57:VAL:HG13	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:120:LYS:H	1:H:120:LYS:CE	2.00	0.75
1:C:326:ARG:HD2	1:C:336:ILE:HG12	1.69	0.74
1:H:214:VAL:H	1:H:269:ASN:HD22	1.34	0.74
1:H:7:LYS:NZ	1:H:101:TRP:CE3	2.49	0.74
1:E:126:MET:HE1	1:E:371:LEU:HB3	1.69	0.74
1:A:36:GLU:HB3	1:G:409:THR:HG22	1.68	0.74
1:F:223:VAL:HG12	1:F:274:THR:HB	1.70	0.74
1:E:343:LEU:HG	2:E:5432:NAD:N7N	2.01	0.74
1:G:221:GLY:O	1:G:225:LYS:HG3	1.86	0.74
1:E:374:HIS:CG	1:E:377:LYS:HE3	2.22	0.74
1:H:194:CYS:SG	1:H:223:VAL:HG13	2.27	0.74
1:B:353:PRO:CB	1:D:209:MET:HB2	2.18	0.73
1:F:278:VAL:CG1	1:F:303:VAL:HB	2.19	0.73
1:G:214:VAL:H	1:G:269:ASN:ND2	1.85	0.73
1:H:101:TRP:HZ2	1:H:108:GLU:OE1	1.71	0.73
1:E:143:PRO:O	1:E:146:LEU:HB2	1.88	0.73
1:F:218:ALA:HB3	1:F:273:THR:HA	1.69	0.73
1:F:326:ARG:HG2	1:F:326:ARG:NH1	2.01	0.73
1:B:21:LEU:HD12	1:B:57:VAL:HG13	1.70	0.73
1:F:3:LYS:HD2	1:F:115:GLN:OE1	1.89	0.73
1:H:185:LYS:HD2	1:H:185:LYS:C	2.15	0.72
1:D:214:VAL:H	1:D:269:ASN:HD22	1.37	0.72
1:C:33:ARG:NH2	1:C:36:GLU:HB2	2.02	0.72
1:E:180:ASN:HA	1:E:185:LYS:HE3	1.71	0.72
1:A:7:LYS:HE2	1:A:112:CYS:SG	2.30	0.72
1:B:167:MET:HE3	1:B:381:GLY:HA2	1.72	0.72
1:E:412:GLN:HG2	1:F:277:CYS:SG	2.30	0.72
1:D:167:MET:HE3	1:D:381:GLY:CA	2.19	0.72
1:G:3:LYS:HD3	1:G:115:GLN:HE22	1.54	0.72
1:C:10:ASP:HB3	1:C:13:LEU:HD22	1.71	0.72
1:F:80:ILE:HD11	1:F:342:ARG:HE	1.53	0.72
1:G:7:LYS:HE3	1:G:99:PHE:HB3	1.71	0.71
1:H:105:THR:OG1	1:H:108:GLU:HG3	1.88	0.71
1:F:37:MET:HG3	1:F:38:TYR:CE2	2.24	0.71
1:G:238:VAL:HB	1:G:256:TYR:CE1	2.25	0.71
1:E:120:LYS:HE2	1:E:120:LYS:N	2.05	0.71
1:A:21:LEU:HD12	1:A:57:VAL:HG13	1.72	0.71
1:A:209:MET:HB2	1:C:353:PRO:CB	2.21	0.71
1:D:326:ARG:HD2	1:D:336:ILE:HG12	1.71	0.71
1:E:33:ARG:HH21	1:E:36:GLU:HB2	1.54	0.71
1:B:278:VAL:HG12	1:B:303:VAL:HB	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:33:ARG:HH11	1:C:33:ARG:HG3	1.56	0.71
1:C:275:THR:HG22	1:C:277:CYS:N	2.06	0.71
1:E:101:TRP:CH2	1:E:108:GLU:HB3	2.25	0.71
1:H:56:THR:HG22	1:H:84:GLN:OE1	1.90	0.71
1:H:138:ILE:HD12	1:H:149:ILE:HD11	1.72	0.71
1:A:7:LYS:HZ1	1:A:100:ALA:N	1.88	0.71
1:H:307:VAL:H	1:H:308:LYS:HE3	1.55	0.71
1:A:33:ARG:HH11	1:A:33:ARG:HG3	1.55	0.71
1:B:129:ASP:OD2	1:B:135:THR:HG23	1.91	0.71
1:H:156:THR:HG23	1:H:159:GLY:H	1.56	0.71
1:H:232:ARG:HH11	1:H:232:ARG:HG3	1.55	0.71
1:G:391:GLU:OE2	1:G:423:PRO:HA	1.90	0.71
1:F:7:LYS:HE2	1:F:112:CYS:SG	2.30	0.70
1:A:2:ASP:HB2	1:A:74:ARG:HH12	1.55	0.70
1:B:2:ASP:HB2	1:B:74:ARG:HH12	1.54	0.70
1:G:425:LYS:HE3	2:H:8432:NAD:H3B	1.72	0.70
1:A:169:ASN:HB2	1:A:171:ILE:HG12	1.73	0.70
1:B:2:ASP:HB3	1:B:3:LYS:HE3	1.72	0.70
1:D:10:ASP:HB3	1:D:13:LEU:HD22	1.73	0.70
1:E:7:LYS:HE3	1:E:99:PHE:HA	1.73	0.70
1:F:3:LYS:HB2	1:F:4:LEU:HD12	1.74	0.70
1:G:33:ARG:NH2	1:G:36:GLU:HB2	2.03	0.70
1:H:153:SER:HB3	1:H:364:GLN:HE22	1.55	0.70
1:G:214:VAL:H	1:G:269:ASN:HD22	1.38	0.70
1:G:275:THR:HG22	1:G:276:GLY:H	1.54	0.70
1:G:7:LYS:HE2	1:G:112:CYS:SG	2.32	0.70
1:F:167:MET:CE	1:F:380:VAL:HG12	2.22	0.70
1:G:138:ILE:HA	1:G:142:HIS:HB2	1.73	0.70
1:F:167:MET:HE3	1:F:380:VAL:HG12	1.72	0.70
1:E:81:PHE:CE2	1:E:342:ARG:HG3	2.27	0.69
1:F:419:PRO:HB2	1:F:422:GLY:H	1.58	0.69
1:G:10:ASP:HB3	1:G:13:LEU:HD22	1.73	0.69
1:A:198:LEU:HD22	1:A:227:CYS:SG	2.32	0.69
1:A:278:VAL:HG12	1:A:303:VAL:HB	1.73	0.69
1:D:150:ARG:HD3	1:D:375:PRO:HB3	1.75	0.69
1:F:275:THR:HG22	1:F:277:CYS:N	2.07	0.69
1:G:127:ILE:HD11	1:G:149:ILE:HD13	1.74	0.69
1:A:210:ILE:HG22	1:A:236:ALA:HB2	1.74	0.69
1:D:308:LYS:CD	1:D:308:LYS:H	2.02	0.69
1:F:37:MET:HE2	1:F:38:TYR:OH	1.93	0.69
1:F:154:GLU:HB2	1:F:163:LEU:HD11	1.75	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:143:PRO:O	1:B:146:LEU:HB2	1.93	0.69
1:C:275:THR:HG22	1:C:276:GLY:N	2.07	0.69
1:G:142:HIS:HB3	1:G:145:LEU:HG	1.74	0.69
1:B:29:PRO:O	1:B:33:ARG:HB2	1.93	0.69
1:H:171:ILE:O	1:H:173:LYS:HG2	1.93	0.69
1:B:326:ARG:HD2	1:B:336:ILE:HG12	1.74	0.68
1:G:275:THR:HG21	1:G:277:CYS:HB3	1.75	0.68
1:H:33:ARG:NH1	1:H:37:MET:SD	2.66	0.68
1:H:232:ARG:HG3	1:H:232:ARG:NH1	2.08	0.68
1:A:2:ASP:OD2	1:A:118:HIS:HB2	1.94	0.68
1:E:53:LEU:HD12	1:E:130:ASP:HB2	1.74	0.68
1:G:310:LEU:HD22	1:G:327:TYR:CG	2.28	0.68
1:H:53:LEU:HG	1:H:130:ASP:HB2	1.74	0.68
1:D:29:PRO:O	1:D:33:ARG:HB2	1.93	0.68
1:E:362:THR:HG22	1:E:393:VAL:HG22	1.75	0.68
1:F:105:THR:H	1:F:108:GLU:HB2	1.58	0.68
1:G:33:ARG:NH1	1:G:37:MET:SD	2.67	0.68
1:H:13:LEU:HB3	1:H:86:HIS:HA	1.73	0.68
1:H:185:LYS:HD3	1:H:360:SER:OG	1.93	0.68
1:A:419:PRO:HB2	1:A:422:GLY:H	1.58	0.68
1:E:13:LEU:HB3	1:E:86:HIS:HA	1.76	0.68
1:F:57:VAL:H	1:F:84:GLN:HE22	1.37	0.68
1:G:240:ILE:O	1:G:258:VAL:HA	1.92	0.68
1:E:7:LYS:HE3	1:E:99:PHE:CA	2.24	0.68
1:E:322:PRO:O	1:E:324:VAL:HG23	1.92	0.68
1:E:430:ARG:HA	1:F:430:ARG:HD3	1.74	0.68
1:C:278:VAL:HG12	1:C:303:VAL:HB	1.73	0.68
1:A:3:LYS:HD2	1:A:115:GLN:OE1	1.92	0.68
1:D:223:VAL:HG12	1:D:274:THR:HB	1.76	0.68
1:E:2:ASP:HB3	1:E:3:LYS:HD2	1.75	0.68
1:F:353:PRO:HB2	1:H:209:MET:HB2	1.76	0.68
1:C:57:VAL:HG23	1:C:84:GLN:HE21	1.58	0.68
1:E:377:LYS:HD2	1:E:378:TYR:CE1	2.29	0.68
1:D:3:LYS:HD2	1:D:115:GLN:OE1	1.94	0.68
1:G:2:ASP:OD2	1:G:118:HIS:HB2	1.94	0.68
1:H:308:LYS:HE3	1:H:308:LYS:H	1.58	0.68
1:C:101:TRP:CH2	1:C:108:GLU:HB3	2.30	0.67
1:H:275:THR:HG22	1:H:276:GLY:N	2.08	0.67
1:B:57:VAL:H	1:B:84:GLN:NE2	1.91	0.67
1:D:169:ASN:HB2	1:D:171:ILE:HG12	1.76	0.67
1:G:58:GLU:HG2	1:G:354:SER:HA	1.75	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:105:THR:H	1:G:108:GLU:HB2	1.57	0.67
1:A:33:ARG:NH2	1:A:36:GLU:HB2	2.07	0.67
1:A:150:ARG:HD3	1:A:375:PRO:HB3	1.76	0.67
1:C:246:ILE:O	1:C:250:GLN:HG3	1.94	0.67
1:E:159:GLY:O	1:E:162:ASN:ND2	2.28	0.67
1:H:48:ARG:HD2	1:H:119:PHE:CB	2.24	0.67
1:C:210:ILE:HG22	1:C:236:ALA:HB2	1.75	0.67
1:A:243:ILE:HG21	1:B:408:LEU:HD13	1.75	0.67
1:E:3:LYS:HD2	1:E:3:LYS:H	1.59	0.67
1:E:300:HIS:HA	1:E:343:LEU:HD11	1.76	0.67
1:C:57:VAL:H	1:C:84:GLN:NE2	1.91	0.67
1:C:391:GLU:OE2	1:C:423:PRO:HA	1.94	0.67
1:F:120:LYS:HE2	1:F:120:LYS:H	1.57	0.67
1:D:410:GLU:O	1:D:414:GLN:HG2	1.95	0.67
1:D:57:VAL:HG23	1:D:84:GLN:HE21	1.59	0.67
1:B:209:MET:HB2	1:D:353:PRO:HB2	1.77	0.66
1:C:7:LYS:HZ1	1:C:100:ALA:N	1.93	0.66
1:C:419:PRO:HB2	1:C:422:GLY:H	1.58	0.66
1:E:408:LEU:HD13	1:F:243:ILE:HG21	1.76	0.66
1:E:81:PHE:CD2	1:E:342:ARG:HG3	2.30	0.66
1:E:195:ARG:NH1	1:E:229:GLN:NE2	2.35	0.66
1:C:4:LEU:HD13	1:C:99:PHE:HE1	1.60	0.66
1:E:7:LYS:NZ	1:E:7:LYS:O	2.25	0.66
1:E:275:THR:HG22	1:E:277:CYS:N	2.10	0.66
1:F:429:TYR:CE2	1:F:431:TYR:HA	2.30	0.66
1:E:101:TRP:HH2	1:E:108:GLU:HB3	1.60	0.66
1:E:243:ILE:HG21	1:F:408:LEU:HD13	1.77	0.66
1:H:7:LYS:HE3	1:H:99:PHE:CA	2.25	0.66
1:H:183:VAL:O	1:H:187:LYS:HB2	1.94	0.66
1:C:240:ILE:O	1:C:258:VAL:HA	1.96	0.66
1:A:308:LYS:CD	1:A:308:LYS:H	2.08	0.66
1:D:275:THR:HG22	1:D:276:GLY:N	2.10	0.66
1:F:199:ILE:HD11	1:F:231:LEU:HD23	1.78	0.66
1:H:300:HIS:H	2:H:8432:NAD:H1D	1.59	0.66
1:D:120:LYS:H	1:D:120:LYS:CE	2.06	0.66
1:D:129:ASP:OD2	1:D:135:THR:HG23	1.94	0.66
1:H:74:ARG:HG3	1:H:119:PHE:CZ	2.31	0.66
1:H:267:GLU:HA	1:H:290:LYS:HE3	1.77	0.66
1:C:2:ASP:HB2	1:C:74:ARG:HH12	1.61	0.66
1:H:342:ARG:HH11	1:H:342:ARG:HG2	1.60	0.66
1:E:408:LEU:CD1	1:F:243:ILE:HG21	2.26	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:48:ARG:HD2	1:D:119:PHE:CB	2.26	0.65
1:F:136:ASN:O	1:F:140:THR:HG23	1.96	0.65
1:H:139:HIS:HA	1:H:146:LEU:HD11	1.78	0.65
1:B:7:LYS:HZ1	1:B:100:ALA:CA	2.08	0.65
1:D:275:THR:HG22	1:D:277:CYS:N	2.11	0.65
1:D:419:PRO:HB2	1:D:422:GLY:H	1.62	0.65
1:E:38:TYR:HB2	1:E:69:LEU:HD11	1.77	0.65
1:G:58:GLU:CG	1:G:354:SER:HA	2.26	0.65
1:A:29:PRO:O	1:A:33:ARG:HB2	1.96	0.65
1:A:232:ARG:HG3	1:A:232:ARG:HH11	1.61	0.65
1:B:169:ASN:HB2	1:B:171:ILE:HG12	1.78	0.65
1:E:224:GLY:HA2	1:E:274:THR:HG21	1.78	0.65
1:F:155:GLU:HG3	1:F:364:GLN:OE1	1.97	0.65
1:G:21:LEU:O	1:G:25:GLU:HG3	1.97	0.65
1:F:310:LEU:HD13	1:F:327:TYR:CD1	2.31	0.65
1:C:48:ARG:HD2	1:C:119:PHE:HB2	1.78	0.65
1:E:315:VAL:HB	1:E:328:LEU:O	1.96	0.65
1:F:78:CYS:HA	1:F:109:TYR:OH	1.97	0.65
1:G:129:ASP:OD2	1:G:135:THR:HG23	1.96	0.65
1:D:33:ARG:HH11	1:D:33:ARG:HG3	1.61	0.65
1:E:37:MET:HE2	1:E:38:TYR:CZ	2.32	0.65
1:D:278:VAL:HG12	1:D:303:VAL:HB	1.79	0.65
1:E:210:ILE:HG22	1:E:236:ALA:HB2	1.79	0.65
1:F:379:PRO:O	1:F:383:HIS:HE1	1.80	0.65
1:G:169:ASN:HB2	1:G:171:ILE:HG12	1.78	0.64
1:H:138:ILE:HG22	1:H:146:LEU:HD12	1.78	0.64
1:D:4:LEU:HD12	1:D:4:LEU:N	2.12	0.64
1:E:105:THR:OG1	1:E:108:GLU:HG3	1.97	0.64
1:B:419:PRO:HB2	1:B:422:GLY:H	1.60	0.64
1:B:33:ARG:HG3	1:B:33:ARG:NH1	2.04	0.64
1:C:48:ARG:HD2	1:C:119:PHE:CB	2.28	0.64
1:G:153:SER:HB2	1:G:368:GLN:NE2	2.12	0.64
1:B:2:ASP:CB	1:B:3:LYS:HE3	2.27	0.64
1:C:2:ASP:OD2	1:C:118:HIS:HB2	1.98	0.64
1:E:374:HIS:ND1	1:E:377:LYS:HE3	2.13	0.64
1:B:2:ASP:OD2	1:B:118:HIS:HB2	1.97	0.64
1:C:146:LEU:HA	1:C:149:ILE:HD12	1.80	0.64
1:C:243:ILE:HG21	1:D:408:LEU:HD13	1.79	0.64
1:F:146:LEU:HA	1:F:149:ILE:HD12	1.79	0.64
1:H:224:GLY:HA2	1:H:274:THR:HG21	1.80	0.64
1:B:4:LEU:HD13	1:B:99:PHE:HE1	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:ASN:O	1:B:400:LYS:HE2	1.96	0.64
1:E:345:ASN:O	1:E:349:ALA:HB3	1.97	0.64
1:A:53:LEU:CD1	1:A:130:ASP:HB2	2.27	0.64
1:E:121:ASP:OD1	1:E:121:ASP:N	2.28	0.64
1:E:308:LYS:O	1:E:312:GLU:HG3	1.98	0.64
1:F:297:ASN:OD1	1:F:304:GLU:HG3	1.98	0.64
1:C:7:LYS:HE2	1:C:112:CYS:SG	2.38	0.64
1:D:283:GLY:HA3	1:D:309:TRP:CE2	2.33	0.64
1:G:33:ARG:NH2	1:G:37:MET:HG2	2.13	0.64
1:G:238:VAL:HB	1:G:256:TYR:HE1	1.63	0.64
1:H:167:MET:HG2	1:H:172:LEU:HB3	1.80	0.64
1:A:416:LEU:HD21	1:B:277:CYS:HB2	1.79	0.63
1:H:188:PHE:O	1:H:192:TYR:HB2	1.97	0.63
1:E:55:MET:HE2	1:E:88:ALA:HA	1.80	0.63
1:H:418:MET:HE2	1:H:424:PHE:HA	1.79	0.63
1:H:419:PRO:HB2	1:H:422:GLY:N	2.10	0.63
1:B:48:ARG:HD2	1:B:119:PHE:CB	2.27	0.63
1:D:2:ASP:HB2	1:D:74:ARG:NH1	2.13	0.63
1:E:21:LEU:HD12	1:E:57:VAL:HG13	1.81	0.63
1:E:171:ILE:O	1:E:173:LYS:HG2	1.98	0.63
1:H:29:PRO:O	1:H:33:ARG:HB2	1.99	0.63
1:B:167:MET:HE3	1:B:381:GLY:CA	2.27	0.63
1:C:126:MET:HE2	1:C:372:TRP:HB2	1.79	0.63
1:E:209:MET:SD	1:G:356:VAL:HB	2.38	0.63
1:F:172:LEU:HD22	1:F:174:VAL:H	1.63	0.63
1:G:91:ILE:HG23	1:G:96:ILE:HB	1.80	0.63
1:A:4:LEU:HD13	1:A:99:PHE:HE1	1.64	0.63
1:A:150:ARG:HD2	1:A:372:TRP:HA	1.81	0.63
1:E:275:THR:HG21	1:E:280:ILE:HD11	1.81	0.63
1:F:4:LEU:CD2	1:F:7:LYS:HB3	2.28	0.63
1:H:7:LYS:HG2	1:H:111:TRP:CH2	2.34	0.63
1:H:120:LYS:HE2	1:H:120:LYS:N	2.05	0.63
1:F:342:ARG:HG2	1:F:342:ARG:HH11	1.62	0.63
1:A:101:TRP:CH2	1:A:108:GLU:HB3	2.34	0.63
1:B:7:LYS:NZ	1:B:100:ALA:N	2.46	0.63
1:B:210:ILE:HG22	1:B:236:ALA:HB2	1.81	0.63
1:F:198:LEU:CD2	1:F:227:CYS:HB3	2.29	0.63
1:G:105:THR:OG1	1:G:108:GLU:HG3	1.98	0.63
1:G:178:ASN:OD1	1:G:181:ASP:HB2	1.98	0.63
1:C:33:ARG:HG3	1:C:33:ARG:NH1	2.13	0.62
1:D:48:ARG:HD2	1:D:119:PHE:HB2	1.80	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:307:VAL:H	1:E:308:LYS:HE3	1.64	0.62
1:E:425:LYS:HD2	1:E:429:TYR:CD2	2.34	0.62
1:F:292:ASP:OD1	1:F:326:ARG:NE	2.29	0.62
1:F:430:ARG:HH11	1:F:430:ARG:HG3	1.64	0.62
1:H:136:ASN:O	1:H:140:THR:HG23	1.98	0.62
1:A:7:LYS:HE3	1:A:99:PHE:HB3	1.80	0.62
1:A:48:ARG:HD2	1:A:119:PHE:CB	2.29	0.62
1:H:48:ARG:HD2	1:H:119:PHE:HB2	1.80	0.62
1:H:57:VAL:O	1:H:61:VAL:HG23	2.00	0.62
1:H:162:ASN:O	1:H:166:MET:HG3	1.98	0.62
1:A:7:LYS:HE3	1:A:99:PHE:CA	2.30	0.62
1:A:391:GLU:OE2	1:A:423:PRO:HA	1.99	0.62
1:D:101:TRP:CH2	1:D:108:GLU:HB3	2.34	0.62
1:E:48:ARG:HD2	1:E:119:PHE:HB2	1.82	0.62
1:A:214:VAL:H	1:A:269:ASN:HD22	1.47	0.62
1:C:26:ASN:O	1:C:400:LYS:HE2	1.99	0.62
1:E:373:THR:HG22	1:E:374:HIS:CD2	2.34	0.62
1:F:119:PHE:HB2	1:F:122:GLY:O	1.99	0.62
1:E:212:GLY:O	1:G:401:LEU:HD22	1.98	0.62
1:G:199:ILE:HG22	1:G:203:LYS:HG3	1.82	0.62
1:G:295:VAL:HG12	1:G:337:LEU:HD23	1.82	0.62
1:H:33:ARG:NH2	1:H:37:MET:HG2	2.14	0.62
1:H:141:LYS:HB3	1:H:142:HIS:ND1	2.15	0.62
1:A:7:LYS:HZ1	1:A:100:ALA:CA	2.12	0.62
1:A:48:ARG:HD2	1:A:119:PHE:HB2	1.82	0.62
1:D:240:ILE:O	1:D:258:VAL:HA	1.98	0.62
1:F:3:LYS:HD3	1:F:115:GLN:HE22	1.64	0.62
1:F:388:LYS:HG2	1:F:423:PRO:HG3	1.81	0.62
1:H:239:ILE:HG23	1:H:257:GLU:HG2	1.82	0.62
1:A:129:ASP:OD2	1:A:135:THR:HG23	1.99	0.62
1:B:33:ARG:NH2	1:B:36:GLU:HB2	2.11	0.62
1:B:240:ILE:O	1:B:258:VAL:HA	1.99	0.62
1:B:246:ILE:O	1:B:250:GLN:HG3	2.00	0.62
1:D:4:LEU:HD13	1:D:99:PHE:HE1	1.63	0.62
1:H:4:LEU:N	1:H:4:LEU:HD12	2.14	0.62
1:E:81:PHE:O	1:E:102:LYS:HE3	2.00	0.62
1:A:33:ARG:HA	1:A:33:ARG:NE	2.14	0.62
1:C:129:ASP:OD2	1:C:135:THR:HG23	1.99	0.62
1:D:2:ASP:OD2	1:D:118:HIS:HB2	2.00	0.62
1:E:23:ILE:HD11	1:G:320:ILE:HG13	1.81	0.62
1:H:86:HIS:ND1	1:H:87:ALA:N	2.48	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:74:ARG:HB3	1:E:116:THR:HB	1.81	0.61
1:F:218:ALA:HA	1:F:241:THR:HG1	1.64	0.61
1:G:4:LEU:HD13	1:G:99:PHE:CE1	2.35	0.61
1:B:101:TRP:CH2	1:B:108:GLU:HB3	2.34	0.61
1:C:29:PRO:O	1:C:33:ARG:HB2	2.00	0.61
1:C:388:LYS:HG2	1:C:423:PRO:HD3	1.81	0.61
1:H:275:THR:CG2	1:H:277:CYS:HB2	2.30	0.61
1:A:119:PHE:HB2	1:A:122:GLY:O	2.00	0.61
1:A:167:MET:HE3	1:A:381:GLY:HA2	1.81	0.61
1:B:232:ARG:HH11	1:B:232:ARG:HG3	1.65	0.61
1:E:292:ASP:CG	1:E:326:ARG:HH21	2.08	0.61
1:F:259:THR:HG22	1:F:260:THR:H	1.66	0.61
1:F:377:LYS:O	1:F:377:LYS:HG2	2.00	0.61
1:H:240:ILE:O	1:H:258:VAL:HA	1.99	0.61
1:A:7:LYS:NZ	1:A:100:ALA:N	2.49	0.61
1:F:105:THR:HG23	1:F:108:GLU:OE1	2.01	0.61
1:A:13:LEU:HB3	1:A:86:HIS:HA	1.82	0.61
1:A:275:THR:HG22	1:A:276:GLY:N	2.15	0.61
1:D:120:LYS:HE2	1:D:120:LYS:N	2.09	0.61
1:E:247:ASN:ND2	1:F:425:LYS:HE2	2.15	0.61
1:F:143:PRO:O	1:F:146:LEU:HB2	2.01	0.61
1:G:281:ILE:HD13	1:G:289:MET:HE1	1.81	0.61
1:H:225:LYS:HZ1	1:H:250:GLN:HE22	1.48	0.61
1:A:154:GLU:HG3	1:A:160:VAL:HG23	1.81	0.61
1:F:7:LYS:NZ	1:F:7:LYS:O	2.33	0.61
1:F:249:LEU:O	1:F:253:MET:HG2	2.00	0.61
1:B:3:LYS:HE3	1:B:3:LYS:H	1.65	0.61
1:F:79:ASN:HB3	1:F:82:SER:OG	2.00	0.61
1:G:307:VAL:HG22	1:G:337:LEU:HD11	1.83	0.61
1:H:33:ARG:NH2	1:H:37:MET:N	2.33	0.61
1:H:308:LYS:H	1:H:308:LYS:CD	2.13	0.61
1:A:57:VAL:H	1:A:84:GLN:NE2	1.98	0.61
1:A:188:PHE:O	1:A:192:TYR:HB2	2.00	0.61
1:B:7:LYS:HE3	1:B:99:PHE:HB3	1.81	0.61
1:F:275:THR:HG22	1:F:276:GLY:N	2.15	0.61
1:B:308:LYS:H	1:B:308:LYS:CD	2.13	0.60
1:D:7:LYS:HZ1	1:D:100:ALA:CA	2.13	0.60
1:D:246:ILE:O	1:D:250:GLN:HG3	2.01	0.60
1:E:206:THR:HG23	1:E:338:LEU:HD21	1.82	0.60
1:E:353:PRO:CB	1:G:209:MET:HB2	2.30	0.60
1:F:297:ASN:CG	1:F:304:GLU:HG3	2.26	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:395:GLU:HA	1:H:398:LEU:HD22	1.83	0.60
1:B:33:ARG:NE	1:B:33:ARG:HA	2.16	0.60
1:D:377:LYS:HD2	1:D:378:TYR:CE1	2.35	0.60
1:A:240:ILE:O	1:A:258:VAL:HA	2.01	0.60
1:C:7:LYS:HZ1	1:C:100:ALA:CA	2.14	0.60
1:E:246:ILE:HD11	1:F:390:ASP:HB3	1.84	0.60
1:H:178:ASN:ND2	1:H:181:ASP:HB2	2.16	0.60
1:B:7:LYS:HE2	1:B:112:CYS:SG	2.41	0.60
1:C:232:ARG:HH11	1:C:232:ARG:HG3	1.66	0.60
1:C:250:GLN:O	1:C:254:GLU:HG2	2.02	0.60
1:D:7:LYS:HG2	1:D:111:TRP:CZ3	2.37	0.60
1:B:33:ARG:NH1	1:B:37:MET:SD	2.74	0.60
1:B:275:THR:HG22	1:B:277:CYS:N	2.07	0.60
1:C:4:LEU:N	1:C:4:LEU:HD12	2.15	0.60
1:G:138:ILE:HG23	1:G:142:HIS:HB2	1.84	0.60
1:H:249:LEU:O	1:H:253:MET:HG2	2.00	0.60
1:B:48:ARG:HD2	1:B:119:PHE:HB2	1.83	0.60
1:F:113:ILE:O	1:F:116:THR:HG23	2.02	0.60
1:G:162:ASN:HA	1:G:165:LYS:HB2	1.84	0.60
1:A:275:THR:HG22	1:A:277:CYS:N	2.12	0.60
1:B:119:PHE:HB2	1:B:122:GLY:O	2.01	0.60
1:B:146:LEU:HA	1:B:149:ILE:HD12	1.84	0.60
1:C:143:PRO:O	1:C:146:LEU:HB2	2.01	0.60
1:E:48:ARG:HB3	1:E:119:PHE:CD2	2.36	0.60
1:G:4:LEU:HD13	1:G:99:PHE:HE1	1.67	0.60
1:D:7:LYS:HE3	1:D:99:PHE:HB3	1.83	0.60
1:E:152:ILE:HB	1:E:176:ALA:CB	2.32	0.60
1:F:44:LEU:HB3	1:F:71:ALA:HB2	1.84	0.60
1:A:57:VAL:HG23	1:A:84:GLN:HE21	1.67	0.60
1:C:13:LEU:HB3	1:C:86:HIS:HA	1.84	0.60
1:C:167:MET:HE3	1:C:381:GLY:HA2	1.83	0.60
1:D:150:ARG:HD2	1:D:372:TRP:HA	1.84	0.60
1:B:154:GLU:HG3	1:B:160:VAL:HG23	1.84	0.59
1:E:141:LYS:C	1:E:143:PRO:HD3	2.27	0.59
1:G:127:ILE:HG23	1:G:134:LEU:HD13	1.84	0.59
1:H:79:ASN:HB3	1:H:82:SER:OG	2.01	0.59
1:A:223:VAL:HG12	1:A:274:THR:HB	1.83	0.59
1:B:179:VAL:HG13	1:B:363:ASN:HB3	1.85	0.59
1:C:223:VAL:HG12	1:C:274:THR:HB	1.83	0.59
1:D:308:LYS:H	1:D:308:LYS:HD2	1.66	0.59
1:E:419:PRO:HB2	1:E:422:GLY:HA3	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:198:LEU:HD22	1:G:227:CYS:SG	2.42	0.59
1:H:167:MET:SD	1:H:381:GLY:HA2	2.42	0.59
1:D:56:THR:HA	1:D:84:GLN:HB2	1.85	0.59
1:E:308:LYS:CE	1:E:308:LYS:H	2.13	0.59
1:G:32:MET:HE1	1:G:35:ARG:NH1	2.17	0.59
1:G:419:PRO:HB2	1:G:422:GLY:H	1.67	0.59
1:H:32:MET:HE1	1:H:35:ARG:HD2	1.84	0.59
1:A:209:MET:O	1:A:213:LYS:HD2	2.01	0.59
1:G:7:LYS:NZ	1:G:101:TRP:CE3	2.54	0.59
1:G:275:THR:CG2	1:G:276:GLY:N	2.66	0.59
1:G:307:VAL:HG21	1:G:340:GLU:O	2.03	0.59
1:H:19:LYS:O	1:H:23:ILE:HG13	2.03	0.59
1:H:225:LYS:HZ2	1:H:250:GLN:HE22	1.49	0.59
1:C:343:LEU:HG	2:C:3432:NAD:N7N	2.17	0.59
1:G:167:MET:HA	1:G:167:MET:HE2	1.84	0.59
1:H:429:TYR:CE2	1:H:431:TYR:HA	2.37	0.59
1:A:232:ARG:HG3	1:A:232:ARG:NH1	2.18	0.59
1:C:169:ASN:HB2	1:C:171:ILE:HG12	1.85	0.59
1:D:57:VAL:HG23	1:D:84:GLN:NE2	2.18	0.59
1:D:146:LEU:HA	1:D:149:ILE:HD12	1.84	0.59
1:G:151:GLY:HA2	1:G:174:VAL:HG23	1.83	0.59
1:D:53:LEU:CD1	1:D:130:ASP:HB2	2.31	0.59
1:F:183:VAL:HG21	1:F:431:TYR:CE1	2.38	0.59
1:G:35:ARG:HE	1:G:65:THR:HA	1.66	0.59
1:G:190:ASN:HB3	1:G:223:VAL:HG23	1.83	0.59
1:A:179:VAL:HG13	1:A:363:ASN:HB3	1.84	0.59
1:B:111:TRP:O	1:B:115:GLN:HG2	2.02	0.59
1:G:54:HIS:HA	1:G:77:SER:OG	2.02	0.59
1:A:300:HIS:H	2:A:1432:NAD:H1D	1.68	0.59
1:B:2:ASP:HB2	1:B:74:ARG:NH1	2.18	0.59
1:B:57:VAL:HG23	1:B:84:GLN:HE21	1.68	0.59
1:D:232:ARG:HH11	1:D:232:ARG:HG3	1.66	0.59
1:F:213:LYS:HG2	1:F:269:ASN:HB3	1.85	0.59
1:A:283:GLY:HA3	1:A:309:TRP:CE2	2.38	0.58
1:A:307:VAL:H	1:A:308:LYS:HE3	1.68	0.58
1:B:275:THR:HG22	1:B:276:GLY:N	2.16	0.58
1:D:33:ARG:HA	1:D:33:ARG:NE	2.17	0.58
1:D:119:PHE:HB2	1:D:122:GLY:O	2.03	0.58
1:D:138:ILE:HG22	1:D:146:LEU:HD13	1.85	0.58
1:D:210:ILE:HG22	1:D:236:ALA:HB2	1.84	0.58
1:E:178:ASN:HB2	1:E:382:VAL:CG2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:419:PRO:HB2	1:F:422:GLY:N	2.17	0.58
1:G:101:TRP:HZ2	1:G:108:GLU:CD	2.10	0.58
1:H:33:ARG:NH2	1:H:36:GLU:HB2	2.18	0.58
1:C:7:LYS:HE3	1:C:99:PHE:HB3	1.84	0.58
1:F:4:LEU:HD13	1:F:99:PHE:CE1	2.26	0.58
1:H:365:VAL:O	1:H:369:ILE:HG13	2.02	0.58
1:A:127:ILE:HG23	1:A:134:LEU:HD13	1.84	0.58
1:A:138:ILE:HG22	1:A:146:LEU:HD13	1.85	0.58
1:C:56:THR:HA	1:C:84:GLN:HB2	1.84	0.58
1:F:273:THR:HG22	1:F:280:ILE:HG21	1.85	0.58
1:G:387:LYS:HG2	1:G:423:PRO:HB3	1.84	0.58
1:H:278:VAL:HG12	1:H:303:VAL:CB	2.30	0.58
1:C:167:MET:HE3	1:C:381:GLY:CA	2.33	0.58
1:C:198:LEU:HD22	1:C:227:CYS:SG	2.44	0.58
1:D:2:ASP:CB	1:D:74:ARG:HH12	2.15	0.58
1:D:154:GLU:HG3	1:D:160:VAL:HG23	1.85	0.58
1:D:307:VAL:H	1:D:308:LYS:HE3	1.66	0.58
1:F:4:LEU:N	1:F:4:LEU:CD1	2.65	0.58
1:F:57:VAL:O	1:F:60:ALA:HB3	2.04	0.58
1:F:425:LYS:HD2	1:F:429:TYR:CE2	2.38	0.58
1:G:395:GLU:CA	1:G:398:LEU:HD13	2.31	0.58
1:H:7:LYS:HE3	1:H:99:PHE:C	2.27	0.58
1:A:353:PRO:CB	1:C:209:MET:HB2	2.32	0.58
1:B:120:LYS:H	1:B:120:LYS:CE	2.14	0.58
1:B:150:ARG:HD2	1:B:372:TRP:HA	1.85	0.58
1:G:7:LYS:HE3	1:G:99:PHE:CB	2.34	0.58
1:A:408:LEU:CD1	1:B:243:ILE:HG21	2.33	0.58
1:D:33:ARG:HG3	1:D:33:ARG:NH1	2.18	0.58
1:H:31:LEU:HD21	1:H:361:PHE:HB3	1.86	0.58
1:H:33:ARG:O	1:H:37:MET:HG2	2.03	0.58
1:C:33:ARG:NE	1:C:33:ARG:HA	2.19	0.58
1:F:59:THR:O	1:F:62:LEU:HB3	2.04	0.58
1:A:33:ARG:NH1	1:A:37:MET:SD	2.76	0.58
1:A:49:ILE:HD12	1:A:71:ALA:HB1	1.86	0.58
1:D:138:ILE:HG22	1:D:146:LEU:CD1	2.33	0.58
1:F:101:TRP:HZ2	1:F:108:GLU:CD	2.11	0.58
1:G:300:HIS:H	2:G:7432:NAD:H1D	1.68	0.58
1:H:275:THR:HG22	1:H:277:CYS:N	2.18	0.58
1:A:410:GLU:O	1:A:414:GLN:HG2	2.03	0.58
1:C:63:ILE:O	1:C:67:VAL:HG23	2.04	0.58
1:C:377:LYS:HD2	1:C:378:TYR:CE1	2.39	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4:LEU:HD11	1:E:111:TRP:CZ2	2.39	0.58
1:E:44:LEU:HD12	1:E:69:LEU:HB3	1.86	0.58
1:E:178:ASN:ND2	1:E:384:PHE:HE1	2.02	0.58
1:E:206:THR:CG2	1:E:338:LEU:HD21	2.34	0.58
1:B:343:LEU:HG	2:B:2432:NAD:N7N	2.19	0.58
1:C:388:LYS:HG2	1:C:423:PRO:HG3	1.85	0.58
1:E:184:THR:HA	1:E:188:PHE:CE1	2.39	0.58
1:G:7:LYS:HE3	1:G:99:PHE:CA	2.34	0.58
1:H:141:LYS:HB3	1:H:142:HIS:CE1	2.38	0.58
1:H:261:MET:HA	1:H:264:ALA:HB3	1.85	0.58
1:H:275:THR:HG21	1:H:277:CYS:HB2	1.86	0.58
1:A:33:ARG:HG3	1:A:33:ARG:NH1	2.17	0.57
1:A:143:PRO:O	1:A:146:LEU:HB2	2.04	0.57
1:C:232:ARG:HG3	1:C:232:ARG:NH1	2.19	0.57
1:G:387:LYS:O	1:G:391:GLU:HG3	2.04	0.57
1:A:388:LYS:HG2	1:A:423:PRO:HG3	1.85	0.57
1:C:41:SER:HB2	1:C:43:PRO:HD3	1.84	0.57
1:D:26:ASN:O	1:D:400:LYS:HE2	2.04	0.57
1:F:125:ASN:ND2	1:F:372:TRP:CH2	2.72	0.57
1:G:182:SER:HB2	1:G:185:LYS:HB2	1.87	0.57
1:G:277:CYS:SG	1:H:412:GLN:HB3	2.44	0.57
1:G:365:VAL:O	1:G:369:ILE:HG13	2.05	0.57
1:A:252:ALA:O	1:D:212:GLY:HA2	2.04	0.57
1:F:4:LEU:HD21	1:F:111:TRP:HH2	1.69	0.57
1:F:362:THR:CG2	1:F:393:VAL:HG22	2.33	0.57
1:G:143:PRO:O	1:G:146:LEU:HB2	2.05	0.57
1:G:171:ILE:O	1:G:173:LYS:HE3	2.05	0.57
1:G:419:PRO:HB2	1:G:422:GLY:HA3	1.85	0.57
1:B:212:GLY:HA2	1:C:252:ALA:O	2.04	0.57
1:B:410:GLU:O	1:B:414:GLN:HG2	2.05	0.57
1:F:42:LYS:NZ	1:F:68:ALA:O	2.37	0.57
1:A:146:LEU:HA	1:A:149:ILE:HD12	1.86	0.57
1:A:246:ILE:O	1:A:250:GLN:HG3	2.04	0.57
1:B:209:MET:O	1:B:213:LYS:HD2	2.04	0.57
1:D:127:ILE:HD11	1:D:138:ILE:HD12	1.87	0.57
1:D:143:PRO:O	1:D:146:LEU:HB2	2.03	0.57
1:E:143:PRO:HA	1:E:146:LEU:HD22	1.87	0.57
1:G:185:LYS:HD3	1:G:360:SER:OG	2.05	0.57
1:C:57:VAL:HG23	1:C:84:GLN:NE2	2.19	0.57
1:C:57:VAL:O	1:C:60:ALA:HB3	2.04	0.57
1:C:154:GLU:HG3	1:C:160:VAL:HG23	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:307:VAL:H	1:C:308:LYS:HE3	1.70	0.57
1:D:111:TRP:O	1:D:115:GLN:HG2	2.04	0.57
1:B:7:LYS:HG2	1:B:111:TRP:CZ3	2.40	0.57
1:B:178:ASN:ND2	1:B:181:ASP:HB2	2.20	0.57
1:H:91:ILE:HG23	1:H:96:ILE:HB	1.85	0.57
1:H:141:LYS:C	1:H:143:PRO:HD3	2.29	0.57
1:F:57:VAL:HG22	1:F:87:ALA:HB2	1.86	0.57
1:F:129:ASP:OD2	1:F:135:THR:HG23	2.05	0.57
1:F:283:GLY:HA2	1:F:286:PHE:HB2	1.86	0.57
1:G:44:LEU:HB3	1:G:71:ALA:HB2	1.86	0.57
1:G:245:PRO:HA	1:H:398:LEU:HD21	1.86	0.57
1:H:127:ILE:HD11	1:H:149:ILE:HD13	1.87	0.57
1:B:377:LYS:HD2	1:B:378:TYR:CE1	2.39	0.57
1:C:101:TRP:HH2	1:C:108:GLU:HB3	1.68	0.57
1:C:127:ILE:HG23	1:C:134:LEU:HD13	1.86	0.57
1:E:29:PRO:O	1:E:33:ARG:HB2	2.05	0.57
1:E:201:GLY:HA2	1:E:349:ALA:HB2	1.86	0.57
1:F:344:VAL:O	1:F:348:CYS:HB2	2.04	0.57
1:G:310:LEU:HD13	1:G:327:TYR:CE1	2.40	0.57
1:G:397:HIS:ND1	1:G:397:HIS:N	2.53	0.57
1:B:358:SER:HB3	1:B:397:HIS:NE2	2.19	0.57
1:E:209:MET:HB2	1:G:353:PRO:CB	2.31	0.57
1:E:259:THR:HG22	1:E:260:THR:H	1.70	0.57
1:G:75:TRP:HH2	1:G:128:LEU:HD13	1.70	0.57
1:H:246:ILE:O	1:H:250:GLN:HG3	2.05	0.57
1:E:56:THR:HG22	1:E:84:GLN:OE1	2.05	0.56
1:E:142:HIS:N	1:E:143:PRO:HD3	2.19	0.56
1:E:243:ILE:HG21	1:F:408:LEU:CD1	2.34	0.56
1:G:194:CYS:SG	1:G:223:VAL:HG22	2.45	0.56
1:E:261:MET:O	1:E:265:CYS:HB3	2.05	0.56
1:H:387:LYS:HZ3	1:H:431:TYR:HE1	1.53	0.56
1:A:406:THR:HB	1:B:242:GLU:O	2.05	0.56
1:B:13:LEU:HB3	1:B:86:HIS:HA	1.87	0.56
1:C:53:LEU:CD1	1:C:130:ASP:HB2	2.34	0.56
1:C:300:HIS:H	2:C:3432:NAD:H1D	1.70	0.56
1:C:410:GLU:O	1:C:414:GLN:HG2	2.05	0.56
1:F:199:ILE:HG22	1:F:203:LYS:HG3	1.87	0.56
1:F:246:ILE:O	1:F:250:GLN:HG3	2.05	0.56
1:G:91:ILE:HD12	1:G:96:ILE:HD12	1.88	0.56
1:G:263:GLU:HA	1:G:266:LYS:HE2	1.87	0.56
1:G:286:PHE:C	1:G:288:GLN:H	2.13	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:188:PHE:HA	1:H:192:TYR:CD2	2.40	0.56
1:A:250:GLN:O	1:A:254:GLU:HG2	2.05	0.56
1:B:153:SER:HB3	1:B:364:GLN:HE22	1.70	0.56
1:D:41:SER:HB2	1:D:43:PRO:HD3	1.86	0.56
1:G:7:LYS:NZ	1:G:7:LYS:O	2.30	0.56
1:A:2:ASP:HB2	1:A:74:ARG:NH1	2.20	0.56
1:A:171:ILE:O	1:A:173:LYS:HG2	2.06	0.56
1:E:75:TRP:HH2	1:E:128:LEU:HD13	1.70	0.56
1:E:279:ASP:HA	1:E:282:LEU:HD11	1.87	0.56
1:A:4:LEU:N	1:A:4:LEU:HD12	2.20	0.56
1:A:33:ARG:O	1:A:37:MET:HG2	2.05	0.56
1:C:358:SER:HB3	1:C:397:HIS:NE2	2.21	0.56
1:D:63:ILE:O	1:D:67:VAL:HG23	2.06	0.56
1:D:300:HIS:H	2:D:4432:NAD:H1D	1.70	0.56
1:F:35:ARG:HE	1:F:65:THR:HA	1.70	0.56
1:G:142:HIS:N	1:G:143:PRO:HD3	2.20	0.56
1:H:55:MET:HE1	1:H:91:ILE:HG13	1.87	0.56
1:H:343:LEU:HG	2:H:8432:NAD:N7N	2.21	0.56
1:A:225:LYS:NZ	1:A:250:GLN:HE22	2.03	0.56
1:B:44:LEU:HB3	1:B:71:ALA:HB2	1.87	0.56
1:B:225:LYS:NZ	1:B:250:GLN:HE22	2.04	0.56
1:C:7:LYS:HG2	1:C:111:TRP:CZ3	2.40	0.56
1:C:150:ARG:HD2	1:C:372:TRP:HA	1.88	0.56
1:D:209:MET:O	1:D:213:LYS:HD2	2.05	0.56
1:E:6:TYR:HA	1:E:99:PHE:CE1	2.41	0.56
1:H:44:LEU:HD13	1:H:71:ALA:HB2	1.88	0.56
1:B:334:ARG:O	1:B:335:ILE:HD13	2.06	0.56
1:E:17:GLY:O	1:E:21:LEU:HD13	2.05	0.56
1:E:297:ASN:OD1	1:E:304:GLU:HG3	2.05	0.56
1:F:3:LYS:C	1:F:4:LEU:HD12	2.30	0.56
1:G:31:LEU:HD21	1:G:361:PHE:HB3	1.88	0.56
1:H:74:ARG:HG3	1:H:119:PHE:CE2	2.41	0.56
1:B:391:GLU:OE2	1:B:423:PRO:HA	2.06	0.56
1:C:75:TRP:CD1	1:C:76:SER:H	2.24	0.56
1:E:209:MET:O	1:E:213:LYS:HD2	2.05	0.56
1:E:419:PRO:HB2	1:E:422:GLY:H	1.71	0.56
1:F:425:LYS:HD2	1:F:429:TYR:CD2	2.41	0.56
1:G:33:ARG:HG3	1:G:33:ARG:NH1	2.16	0.56
1:H:334:ARG:O	1:H:335:ILE:HD13	2.06	0.56
1:A:326:ARG:HD2	1:A:336:ILE:CG1	2.35	0.56
1:D:48:ARG:HD2	1:D:119:PHE:CG	2.41	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:362:THR:CG2	1:E:393:VAL:HG22	2.35	0.56
1:B:56:THR:HA	1:B:84:GLN:HB2	1.87	0.55
1:E:297:ASN:O	1:E:344:VAL:HB	2.06	0.55
1:E:300:HIS:H	2:E:5432:NAD:H1D	1.71	0.55
1:F:101:TRP:HZ2	1:F:108:GLU:OE2	1.90	0.55
1:G:185:LYS:O	1:G:189:ASP:HB3	2.05	0.55
1:H:225:LYS:NZ	1:H:250:GLN:NE2	2.54	0.55
1:A:278:VAL:HA	1:A:303:VAL:O	2.05	0.55
1:A:430:ARG:HH11	1:A:430:ARG:HG3	1.71	0.55
1:C:283:GLY:HA3	1:C:309:TRP:CE2	2.41	0.55
1:E:409:THR:H	1:E:412:GLN:HE21	1.54	0.55
1:G:259:THR:HA	1:H:404:LYS:HB2	1.87	0.55
1:H:18:ARG:HH22	1:H:64:GLU:CD	2.14	0.55
1:C:7:LYS:NZ	1:C:100:ALA:N	2.53	0.55
1:C:142:HIS:N	1:C:143:PRO:HD3	2.22	0.55
1:D:7:LYS:NZ	1:D:100:ALA:N	2.54	0.55
1:D:232:ARG:HG3	1:D:232:ARG:NH1	2.19	0.55
1:E:175:PRO:HD3	1:E:380:VAL:HG22	1.87	0.55
1:G:167:MET:HG2	1:G:172:LEU:HD12	1.87	0.55
1:G:250:GLN:HG2	1:H:188:PHE:CZ	2.40	0.55
1:G:278:VAL:HG12	1:G:303:VAL:HB	1.87	0.55
1:H:33:ARG:O	1:H:33:ARG:CZ	2.54	0.55
1:H:244:ASP:CB	1:H:247:ASN:HD22	2.15	0.55
1:B:47:ALA:HA	1:B:125:ASN:HD21	1.71	0.55
1:C:153:SER:HB3	1:C:364:GLN:HE22	1.70	0.55
1:C:185:LYS:HD2	1:C:185:LYS:C	2.31	0.55
1:F:206:THR:HG22	1:F:338:LEU:HD21	1.89	0.55
1:B:136:ASN:O	1:B:140:THR:HG23	2.06	0.55
1:B:171:ILE:O	1:B:173:LYS:HG2	2.06	0.55
1:B:232:ARG:HG3	1:B:232:ARG:NH1	2.19	0.55
1:C:167:MET:HG2	1:C:172:LEU:HD12	1.89	0.55
1:F:199:ILE:CD1	1:F:231:LEU:HD23	2.36	0.55
1:G:3:LYS:HB2	1:G:4:LEU:HD12	1.88	0.55
1:H:407:LYS:NZ	1:H:420:ILE:HD13	2.21	0.55
1:A:419:PRO:HB2	1:A:422:GLY:N	2.22	0.55
1:D:7:LYS:HE3	1:D:99:PHE:CA	2.36	0.55
1:D:136:ASN:O	1:D:140:THR:HG23	2.06	0.55
1:F:196:GLU:OE1	1:H:209:MET:HG3	2.06	0.55
1:C:308:LYS:H	1:C:308:LYS:CD	2.18	0.55
1:D:430:ARG:HH11	1:D:430:ARG:HG3	1.72	0.55
1:E:75:TRP:CH2	1:E:128:LEU:HD13	2.41	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:49:ILE:HD12	1:G:71:ALA:HB1	1.88	0.55
1:A:2:ASP:CB	1:A:3:LYS:HE3	2.37	0.55
1:B:75:TRP:CD1	1:B:76:SER:H	2.25	0.55
1:E:178:ASN:HB2	1:E:382:VAL:HG23	1.89	0.55
1:E:321:LYS:HB2	1:E:322:PRO:HD2	1.87	0.55
1:G:33:ARG:HH22	1:G:37:MET:CG	2.20	0.55
1:H:362:THR:HG22	1:H:393:VAL:HG22	1.89	0.55
1:B:223:VAL:HG12	1:B:274:THR:HB	1.89	0.55
1:B:356:VAL:HB	1:D:209:MET:SD	2.46	0.55
1:D:343:LEU:HG	2:D:4432:NAD:N7N	2.21	0.55
1:D:391:GLU:OE2	1:D:423:PRO:HA	2.07	0.55
1:E:13:LEU:CB	1:E:86:HIS:HA	2.36	0.55
1:E:278:VAL:HG13	1:F:415:TYR:CZ	2.42	0.55
1:G:150:ARG:HG3	1:G:150:ARG:O	2.06	0.55
1:G:308:LYS:CD	1:G:308:LYS:H	2.20	0.55
1:A:21:LEU:O	1:A:25:GLU:HG3	2.06	0.55
1:A:44:LEU:HB3	1:A:71:ALA:HB2	1.88	0.55
1:C:155:GLU:O	1:C:180:ASN:HB2	2.07	0.55
1:D:13:LEU:HB3	1:D:86:HIS:HA	1.89	0.55
1:E:33:ARG:NE	1:E:33:ARG:CA	2.69	0.55
1:E:124:LEU:HD21	1:E:149:ILE:HD11	1.89	0.55
1:E:329:LEU:C	1:E:331:ASN:H	2.15	0.55
1:G:3:LYS:CD	1:G:115:GLN:HE22	2.19	0.55
1:G:180:ASN:HA	1:G:185:LYS:HE3	1.88	0.55
1:H:180:ASN:HA	1:H:185:LYS:HE3	1.89	0.55
1:B:214:VAL:H	1:B:269:ASN:HD22	1.53	0.54
1:C:124:LEU:HD11	1:C:138:ILE:HD11	1.89	0.54
1:D:101:TRP:HH2	1:D:108:GLU:HB3	1.70	0.54
1:G:99:PHE:CD2	1:G:99:PHE:N	2.75	0.54
1:G:413:ALA:HB2	1:G:420:ILE:HG12	1.89	0.54
1:B:387:LYS:HE2	1:B:431:TYR:OH	2.07	0.54
1:D:142:HIS:N	1:D:143:PRO:HD3	2.22	0.54
1:E:7:LYS:NZ	1:E:101:TRP:CE3	2.67	0.54
1:E:211:ALA:HB2	1:E:234:PHE:O	2.07	0.54
1:F:210:ILE:HG22	1:F:236:ALA:HB2	1.90	0.54
1:F:353:PRO:CB	1:H:209:MET:HB2	2.36	0.54
1:G:101:TRP:CZ2	1:G:104:GLU:HB3	2.42	0.54
1:G:311:ASN:OD1	1:G:327:TYR:HE2	1.90	0.54
1:H:167:MET:HG2	1:H:172:LEU:CB	2.38	0.54
1:A:126:MET:HE1	1:A:371:LEU:HB3	1.89	0.54
1:B:53:LEU:CD1	1:B:130:ASP:HB2	2.35	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:105:THR:HG23	1:E:108:GLU:OE1	2.07	0.54
1:E:208:VAL:HG22	1:E:209:MET:N	2.22	0.54
1:E:343:LEU:HG	2:E:5432:NAD:H72N	1.72	0.54
1:F:7:LYS:HG2	1:F:111:TRP:CH2	2.42	0.54
1:A:205:ALA:HB1	1:A:338:LEU:HD22	1.88	0.54
1:B:188:PHE:O	1:B:192:TYR:HB2	2.08	0.54
1:B:225:LYS:HZ3	1:B:250:GLN:HE22	1.55	0.54
1:C:111:TRP:O	1:C:115:GLN:HG2	2.07	0.54
1:E:77:SER:O	1:E:109:TYR:HE1	1.91	0.54
1:E:196:GLU:HG2	1:G:234:PHE:CD1	2.42	0.54
1:E:407:LYS:HE2	1:E:420:ILE:HG21	1.90	0.54
1:F:57:VAL:N	1:F:84:GLN:NE2	2.46	0.54
1:G:7:LYS:HZ1	1:G:100:ALA:N	2.06	0.54
1:H:33:ARG:NH2	1:H:36:GLU:CB	2.71	0.54
1:H:271:PHE:HB2	1:H:295:VAL:HG13	1.90	0.54
1:H:407:LYS:HZ3	1:H:420:ILE:HD13	1.72	0.54
1:A:212:GLY:HA2	1:D:252:ALA:O	2.08	0.54
1:A:358:SER:HB3	1:A:397:HIS:NE2	2.22	0.54
1:C:57:VAL:H	1:C:84:GLN:HE22	1.55	0.54
1:D:126:MET:HE2	1:D:372:TRP:HB2	1.88	0.54
1:F:317:LYS:HD2	1:F:327:TYR:CE2	2.42	0.54
1:H:142:HIS:ND1	1:H:142:HIS:N	2.56	0.54
1:B:172:LEU:HD22	1:B:174:VAL:H	1.71	0.54
1:C:7:LYS:NZ	1:C:101:TRP:CE3	2.67	0.54
1:C:172:LEU:HD22	1:C:174:VAL:H	1.73	0.54
1:D:21:LEU:O	1:D:25:GLU:HG3	2.07	0.54
1:E:152:ILE:HD11	1:E:174:VAL:HG13	1.90	0.54
1:H:225:LYS:HZ2	1:H:250:GLN:NE2	2.05	0.54
1:A:279:ASP:HA	1:A:282:LEU:HD11	1.89	0.54
1:B:155:GLU:O	1:B:180:ASN:HB2	2.08	0.54
1:C:225:LYS:HZ3	1:C:250:GLN:HE22	1.56	0.54
1:C:430:ARG:HG3	1:C:430:ARG:HH11	1.73	0.54
1:E:3:LYS:HD2	1:E:3:LYS:N	2.21	0.54
1:E:379:PRO:O	1:E:383:HIS:CE1	2.57	0.54
1:H:129:ASP:OD2	1:H:135:THR:HG23	2.07	0.54
1:B:419:PRO:HB2	1:B:422:GLY:N	2.23	0.54
1:E:161:HIS:CD2	1:E:165:LYS:HD3	2.43	0.54
1:G:345:ASN:O	1:G:349:ALA:HB3	2.07	0.54
1:H:185:LYS:O	1:H:189:ASP:HB3	2.08	0.54
1:B:24:ALA:O	1:B:28:MET:HG3	2.08	0.54
1:C:419:PRO:HB2	1:C:422:GLY:N	2.22	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:49:ILE:HD12	1:D:71:ALA:HB1	1.88	0.54
1:F:275:THR:CG2	1:F:276:GLY:N	2.71	0.54
1:F:416:LEU:HB3	1:F:418:MET:HE3	1.90	0.54
1:H:29:PRO:HD2	1:H:397:HIS:CD2	2.43	0.54
1:B:49:ILE:HD12	1:B:71:ALA:HB1	1.90	0.54
1:C:2:ASP:HB2	1:C:74:ARG:NH1	2.23	0.54
1:F:198:LEU:HD21	1:F:231:LEU:HD21	1.89	0.54
1:F:310:LEU:HD13	1:F:327:TYR:CE1	2.43	0.54
1:F:328:LEU:HD12	1:F:329:LEU:N	2.22	0.54
1:G:95:GLY:O	1:G:97:PRO:HD3	2.08	0.54
1:G:306:ASP:OD1	1:G:308:LYS:HD2	2.08	0.54
1:H:4:LEU:HD11	1:H:111:TRP:HZ2	1.73	0.54
1:E:126:MET:HE1	1:E:371:LEU:CB	2.38	0.53
1:E:425:LYS:HD2	1:E:429:TYR:CG	2.44	0.53
1:G:158:THR:HB	2:G:7432:NAD:O3D	2.08	0.53
1:H:142:HIS:N	1:H:143:PRO:HD3	2.23	0.53
1:A:258:VAL:HB	1:B:403:VAL:HG13	1.90	0.53
1:C:47:ALA:HA	1:C:125:ASN:HD21	1.73	0.53
1:C:127:ILE:HD11	1:C:138:ILE:HD12	1.90	0.53
1:C:188:PHE:O	1:C:192:TYR:HB2	2.07	0.53
1:D:185:LYS:C	1:D:185:LYS:HD2	2.34	0.53
1:D:199:ILE:HG22	1:D:203:LYS:HG3	1.90	0.53
1:E:142:HIS:HB3	1:E:145:LEU:HD12	1.90	0.53
1:F:364:GLN:O	1:F:368:GLN:HG2	2.07	0.53
1:G:184:THR:HA	1:G:188:PHE:CD1	2.43	0.53
1:H:198:LEU:HD22	1:H:227:CYS:CB	2.36	0.53
1:D:47:ALA:HA	1:D:125:ASN:HD21	1.73	0.53
1:D:57:VAL:H	1:D:84:GLN:NE2	2.05	0.53
1:E:275:THR:HG22	1:E:276:GLY:N	2.24	0.53
1:E:319:ASN:HD21	1:E:321:LYS:C	2.16	0.53
1:E:386:PRO:HG2	1:E:389:LEU:HG	1.89	0.53
1:G:92:ALA:HB2	1:G:98:VAL:CG1	2.39	0.53
1:A:55:MET:HB3	1:A:83:THR:CG2	2.33	0.53
1:C:7:LYS:HE3	1:C:99:PHE:CA	2.38	0.53
1:D:44:LEU:HB2	1:D:69:LEU:O	2.07	0.53
1:E:183:VAL:HG11	1:E:431:TYR:CG	2.43	0.53
1:F:142:HIS:N	1:F:143:PRO:HD3	2.23	0.53
1:F:342:ARG:HG2	1:F:342:ARG:NH1	2.22	0.53
1:B:127:ILE:HD11	1:B:138:ILE:HD12	1.90	0.53
1:E:250:GLN:HG2	1:F:188:PHE:CZ	2.44	0.53
1:F:118:HIS:HA	1:F:123:PRO:HA	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:227:CYS:O	1:F:231:LEU:HG	2.08	0.53
1:G:275:THR:CG2	1:G:276:GLY:H	2.20	0.53
1:A:343:LEU:HG	2:A:1432:NAD:N7N	2.23	0.53
1:A:388:LYS:HG2	1:A:423:PRO:HD3	1.90	0.53
1:C:120:LYS:H	1:C:120:LYS:CE	2.14	0.53
1:E:44:LEU:HB3	1:E:71:ALA:HB2	1.90	0.53
1:E:101:TRP:HZ2	1:E:108:GLU:CD	2.17	0.53
1:E:177:ILE:HG13	1:E:371:LEU:HD21	1.91	0.53
1:E:184:THR:HA	1:E:188:PHE:CD1	2.44	0.53
1:A:185:LYS:HD2	1:A:185:LYS:C	2.34	0.53
1:B:198:LEU:HD22	1:B:227:CYS:SG	2.48	0.53
1:B:300:HIS:H	2:B:2432:NAD:H1D	1.74	0.53
1:C:247:ASN:HD21	1:D:425:LYS:HE2	1.72	0.53
1:E:48:ARG:HD2	1:E:119:PHE:CB	2.39	0.53
1:E:129:ASP:OD2	1:E:135:THR:HG22	2.07	0.53
1:H:178:ASN:CG	1:H:181:ASP:HB2	2.34	0.53
1:A:194:CYS:SG	1:A:223:VAL:HG22	2.49	0.53
1:C:247:ASN:ND2	1:D:425:LYS:HE2	2.24	0.53
1:F:320:ILE:HG13	1:H:23:ILE:HD11	1.91	0.53
1:H:27:GLU:O	1:H:355:PHE:HA	2.08	0.53
1:D:142:HIS:N	1:D:143:PRO:CD	2.72	0.53
1:E:33:ARG:HG3	1:E:33:ARG:NH1	2.22	0.53
1:E:401:LEU:HD22	1:G:212:GLY:O	2.08	0.53
1:F:120:LYS:H	1:F:120:LYS:CE	2.21	0.53
1:G:150:ARG:HD3	1:G:375:PRO:HB3	1.91	0.53
1:G:252:ALA:HB2	1:H:403:VAL:HG21	1.91	0.53
1:H:200:ASP:CG	1:H:204:ARG:HH21	2.17	0.53
1:B:283:GLY:HA3	1:B:309:TRP:CE2	2.44	0.52
1:E:28:MET:HG2	1:E:354:SER:O	2.08	0.52
1:E:119:PHE:HB2	1:E:122:GLY:O	2.08	0.52
1:F:300:HIS:HA	1:F:343:LEU:HD11	1.91	0.52
1:G:53:LEU:O	1:G:54:HIS:C	2.52	0.52
1:H:156:THR:CG2	1:H:159:GLY:H	2.21	0.52
1:H:179:VAL:HG11	1:H:364:GLN:HG2	1.91	0.52
1:A:126:MET:HE2	1:A:372:TRP:HB2	1.91	0.52
1:A:167:MET:HE3	1:A:381:GLY:CA	2.39	0.52
1:B:4:LEU:HD12	1:B:4:LEU:N	2.24	0.52
1:B:252:ALA:O	1:C:212:GLY:HA2	2.09	0.52
1:D:388:LYS:HG2	1:D:423:PRO:HG3	1.90	0.52
1:E:315:VAL:HG23	1:E:330:LYS:CG	2.31	0.52
1:G:183:VAL:HG22	1:H:430:ARG:CZ	2.40	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:THR:HA	1:B:404:LYS:HB2	1.91	0.52
1:D:275:THR:HG22	1:D:276:GLY:H	1.74	0.52
1:E:343:LEU:HD23	1:E:346:LEU:CD1	2.39	0.52
1:F:54:HIS:HB3	1:F:82:SER:CB	2.37	0.52
1:F:257:GLU:HG3	1:G:237:ARG:NH2	2.25	0.52
1:G:59:THR:O	1:G:62:LEU:HB3	2.09	0.52
1:C:119:PHE:HB2	1:C:122:GLY:O	2.09	0.52
1:E:356:VAL:O	1:E:359:ASN:HB2	2.09	0.52
1:F:175:PRO:HB3	1:F:379:PRO:O	2.10	0.52
1:F:387:LYS:HE2	1:F:431:TYR:OH	2.09	0.52
1:G:7:LYS:HD3	1:G:111:TRP:HZ3	1.73	0.52
1:G:154:GLU:HG3	1:G:160:VAL:HG23	1.92	0.52
1:A:345:ASN:O	1:A:349:ALA:HB3	2.09	0.52
1:A:403:VAL:HG13	1:B:258:VAL:HB	1.92	0.52
1:B:138:ILE:HG22	1:B:146:LEU:HD13	1.90	0.52
1:D:179:VAL:HG13	1:D:363:ASN:HB3	1.91	0.52
1:E:21:LEU:O	1:E:25:GLU:HG3	2.09	0.52
1:F:2:ASP:C	1:F:3:LYS:HE3	2.34	0.52
1:F:114:GLU:HA	1:F:117:LEU:HG	1.91	0.52
1:F:316:GLU:HB3	1:F:328:LEU:HB3	1.91	0.52
1:G:29:PRO:O	1:G:33:ARG:HB2	2.09	0.52
1:H:35:ARG:O	1:H:39:SER:HB2	2.10	0.52
1:A:35:ARG:O	1:A:39:SER:HB2	2.09	0.52
1:C:275:THR:CG2	1:C:276:GLY:N	2.72	0.52
1:F:17:GLY:HA2	1:F:86:HIS:CD2	2.45	0.52
1:F:33:ARG:O	1:F:37:MET:HG2	2.10	0.52
1:A:7:LYS:HG2	1:A:111:TRP:CZ3	2.44	0.52
1:B:126:MET:HE2	1:B:372:TRP:HB2	1.90	0.52
1:B:279:ASP:HA	1:B:282:LEU:HD11	1.91	0.52
1:E:428:HIS:NE2	1:F:181:ASP:OD2	2.42	0.52
1:G:210:ILE:HG22	1:G:236:ALA:HB2	1.91	0.52
1:H:131:GLY:CA	1:H:300:HIS:NE2	2.72	0.52
1:A:155:GLU:O	1:A:180:ASN:HB2	2.10	0.52
1:A:307:VAL:N	1:A:308:LYS:HE3	2.25	0.52
1:E:153:SER:CB	1:E:364:GLN:HE22	2.18	0.52
1:G:7:LYS:HD3	1:G:111:TRP:CZ3	2.45	0.52
1:G:116:THR:O	1:G:119:PHE:HE1	1.92	0.52
1:G:134:LEU:HD22	1:G:138:ILE:HD11	1.92	0.52
1:H:2:ASP:CA	1:H:3:LYS:HE3	2.40	0.52
1:A:142:HIS:HB3	1:A:145:LEU:HG	1.92	0.52
1:E:101:TRP:HZ2	1:E:108:GLU:OE1	1.92	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:297:ASN:HB2	1:E:305:ILE:HD12	1.91	0.52
1:E:342:ARG:O	1:E:343:LEU:C	2.52	0.52
1:F:7:LYS:HE3	1:F:99:PHE:HA	1.92	0.52
1:F:127:ILE:HD11	1:F:138:ILE:CD1	2.40	0.52
1:G:35:ARG:NE	1:G:65:THR:HA	2.24	0.52
1:G:75:TRP:CH2	1:G:128:LEU:HD13	2.45	0.52
1:G:125:ASN:C	1:G:125:ASN:OD1	2.53	0.52
1:C:409:THR:H	1:C:412:GLN:HE21	1.58	0.52
1:D:127:ILE:HG23	1:D:134:LEU:HD13	1.90	0.52
1:D:188:PHE:O	1:D:192:TYR:HB2	2.10	0.52
1:D:345:ASN:O	1:D:349:ALA:HB3	2.09	0.52
1:E:266:LYS:HD3	1:E:288:GLN:HG2	1.92	0.52
1:B:41:SER:HB2	1:B:43:PRO:HD3	1.91	0.51
1:B:250:GLN:O	1:B:254:GLU:HG2	2.10	0.51
1:D:283:GLY:HA2	1:D:286:PHE:HB2	1.92	0.51
1:F:7:LYS:HE3	1:F:99:PHE:CA	2.41	0.51
1:F:33:ARG:NH1	1:F:37:MET:SD	2.77	0.51
1:F:209:MET:SD	1:H:356:VAL:HB	2.50	0.51
1:F:430:ARG:O	1:F:431:TYR:C	2.52	0.51
1:G:179:VAL:HG13	1:G:363:ASN:HB3	1.91	0.51
1:H:73:VAL:HG12	1:H:74:ARG:N	2.25	0.51
1:C:179:VAL:HG13	1:C:363:ASN:HB3	1.92	0.51
1:E:343:LEU:HD23	1:E:346:LEU:HD12	1.92	0.51
1:F:297:ASN:HB2	1:F:305:ILE:HD12	1.92	0.51
1:A:7:LYS:HE3	1:A:99:PHE:CB	2.41	0.51
1:A:48:ARG:HD2	1:A:119:PHE:CG	2.45	0.51
1:G:33:ARG:HH21	1:G:36:GLU:CB	2.09	0.51
1:G:308:LYS:H	1:G:308:LYS:HE3	1.75	0.51
1:C:138:ILE:HG22	1:C:146:LEU:HD13	1.91	0.51
1:E:2:ASP:OD2	1:E:118:HIS:HB2	2.10	0.51
1:F:19:LYS:O	1:F:22:ASP:HB2	2.09	0.51
1:F:141:LYS:HB3	1:F:142:HIS:ND1	2.26	0.51
1:F:322:PRO:O	1:F:323:GLN:HB2	2.10	0.51
1:G:203:LYS:O	1:G:207:ASP:N	2.44	0.51
1:B:409:THR:H	1:B:412:GLN:HE21	1.58	0.51
1:C:275:THR:HG22	1:C:276:GLY:H	1.75	0.51
1:F:198:LEU:HG	1:F:199:ILE:N	2.25	0.51
1:G:275:THR:CG2	1:G:277:CYS:HB3	2.40	0.51
1:G:307:VAL:O	1:G:310:LEU:HB2	2.09	0.51
1:H:360:SER:O	1:H:363:ASN:HB2	2.09	0.51
1:A:4:LEU:HD11	1:A:111:TRP:CZ2	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:300:HIS:HA	1:A:343:LEU:HD11	1.92	0.51
1:C:124:LEU:HD11	1:C:138:ILE:CD1	2.40	0.51
1:C:138:ILE:HG22	1:C:146:LEU:CD1	2.40	0.51
1:C:209:MET:O	1:C:213:LYS:HD2	2.11	0.51
1:F:389:LEU:O	1:F:392:ALA:HB3	2.11	0.51
1:G:159:GLY:O	1:G:162:ASN:ND2	2.42	0.51
1:H:326:ARG:HD2	1:H:336:ILE:HG12	1.92	0.51
1:A:41:SER:HB2	1:A:43:PRO:HD3	1.91	0.51
1:A:56:THR:HA	1:A:84:GLN:HB2	1.92	0.51
1:B:429:TYR:CE2	1:B:431:TYR:HA	2.46	0.51
1:C:171:ILE:O	1:C:173:LYS:HG2	2.11	0.51
1:E:308:LYS:H	1:E:308:LYS:CD	2.24	0.51
1:H:29:PRO:O	1:H:33:ARG:N	2.43	0.51
1:B:57:VAL:O	1:B:60:ALA:HB3	2.10	0.51
1:C:33:ARG:O	1:C:37:MET:HG2	2.10	0.51
1:E:25:GLU:HB3	1:E:32:MET:HE2	1.93	0.51
1:H:362:THR:CG2	1:H:393:VAL:HG22	2.41	0.51
1:H:369:ILE:O	1:H:373:THR:HB	2.11	0.51
1:A:167:MET:HG2	1:A:172:LEU:HD12	1.93	0.51
1:D:162:ASN:O	1:D:166:MET:HG3	2.10	0.51
1:E:152:ILE:HD12	1:E:176:ALA:HB2	1.93	0.51
1:F:138:ILE:HG22	1:F:146:LEU:HD13	1.93	0.51
1:H:155:GLU:O	1:H:180:ASN:HB2	2.10	0.51
1:H:275:THR:CG2	1:H:276:GLY:N	2.73	0.51
1:C:244:ASP:HB3	1:C:247:ASN:HB2	1.93	0.51
1:D:158:THR:O	1:D:161:HIS:HB3	2.11	0.51
1:F:386:PRO:HD2	1:F:389:LEU:HD12	1.93	0.51
1:H:7:LYS:HG2	1:H:111:TRP:CZ3	2.45	0.51
1:B:142:HIS:N	1:B:143:PRO:HD3	2.26	0.50
1:B:283:GLY:HA2	1:B:286:PHE:HB2	1.92	0.50
1:B:306:ASP:OD2	1:B:309:TRP:HB2	2.11	0.50
1:C:2:ASP:CB	1:C:3:LYS:HE3	2.41	0.50
1:D:167:MET:HG2	1:D:172:LEU:HD12	1.93	0.50
1:E:53:LEU:CD1	1:E:130:ASP:HB2	2.41	0.50
1:E:188:PHE:HA	1:E:192:TYR:CD2	2.46	0.50
1:G:152:ILE:HG13	1:G:174:VAL:CG2	2.41	0.50
1:A:172:LEU:HD22	1:A:174:VAL:H	1.76	0.50
1:A:317:LYS:HD2	1:A:327:TYR:CZ	2.46	0.50
1:G:279:ASP:OD2	1:H:411:LYS:HD3	2.10	0.50
1:H:7:LYS:HE3	1:H:99:PHE:HA	1.92	0.50
1:A:32:MET:O	1:A:36:GLU:HG3	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:HIS:N	1:A:143:PRO:HD3	2.26	0.50
1:B:33:ARG:O	1:B:37:MET:HG2	2.11	0.50
1:D:33:ARG:HE	1:D:36:GLU:CD	2.19	0.50
1:E:319:ASN:ND2	1:E:321:LYS:O	2.45	0.50
1:F:130:ASP:OD1	1:F:156:THR:HB	2.11	0.50
1:F:152:ILE:HB	1:F:176:ALA:HB2	1.93	0.50
1:H:189:ASP:C	1:H:189:ASP:OD1	2.55	0.50
1:H:275:THR:HG22	1:H:277:CYS:H	1.74	0.50
1:D:306:ASP:OD2	1:D:309:TRP:HB2	2.11	0.50
1:D:430:ARG:O	1:D:431:TYR:C	2.55	0.50
1:E:137:LEU:O	1:E:137:LEU:HD12	2.11	0.50
1:G:152:ILE:HB	1:G:176:ALA:HB2	1.93	0.50
1:G:389:LEU:O	1:G:392:ALA:HB3	2.11	0.50
1:H:7:LYS:NZ	1:H:100:ALA:N	2.59	0.50
1:H:48:ARG:HB3	1:H:119:PHE:CD2	2.46	0.50
1:H:99:PHE:O	1:H:112:CYS:SG	2.69	0.50
1:A:120:LYS:H	1:A:120:LYS:CE	2.16	0.50
1:A:138:ILE:HG22	1:A:146:LEU:CD1	2.42	0.50
1:A:178:ASN:ND2	1:A:181:ASP:HB2	2.26	0.50
1:D:279:ASP:HA	1:D:282:LEU:HD11	1.92	0.50
1:D:307:VAL:N	1:D:308:LYS:HE3	2.27	0.50
1:F:7:LYS:HG2	1:F:111:TRP:CZ3	2.46	0.50
1:F:76:SER:HB3	1:F:116:THR:HG21	1.94	0.50
1:F:413:ALA:HB2	1:F:420:ILE:HG12	1.92	0.50
1:G:41:SER:HB2	1:G:43:PRO:HD3	1.92	0.50
1:H:32:MET:O	1:H:36:GLU:HG3	2.12	0.50
1:H:44:LEU:HB3	1:H:71:ALA:HB2	1.94	0.50
1:H:185:LYS:C	1:H:185:LYS:CD	2.85	0.50
1:E:303:VAL:HG21	1:F:415:TYR:OH	2.10	0.50
1:F:286:PHE:HA	1:F:289:MET:HG3	1.94	0.50
1:G:53:LEU:HG	1:G:130:ASP:OD2	2.11	0.50
1:G:331:ASN:C	1:G:331:ASN:OD1	2.54	0.50
1:H:3:LYS:H	1:H:3:LYS:HD2	1.75	0.50
1:H:342:ARG:HG2	1:H:342:ARG:NH1	2.24	0.50
1:A:63:ILE:O	1:A:67:VAL:HG23	2.12	0.50
1:A:208:VAL:CG2	1:A:213:LYS:HE2	2.42	0.50
1:A:430:ARG:HG3	1:A:430:ARG:NH1	2.27	0.50
1:A:430:ARG:O	1:A:431:TYR:C	2.55	0.50
1:B:7:LYS:HE3	1:B:99:PHE:CA	2.42	0.50
1:B:127:ILE:HG23	1:B:134:LEU:HD13	1.93	0.50
1:C:225:LYS:NZ	1:C:250:GLN:HE22	2.09	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:142:HIS:HB3	1:G:145:LEU:CG	2.41	0.50
1:H:114:GLU:OE2	1:H:142:HIS:NE2	2.45	0.50
1:H:343:LEU:HG	2:H:8432:NAD:H72N	1.77	0.50
1:A:101:TRP:HZ2	1:A:108:GLU:OE1	1.94	0.50
1:B:120:LYS:HE2	1:B:120:LYS:N	2.17	0.50
1:B:185:LYS:HD2	1:B:185:LYS:C	2.36	0.50
1:C:127:ILE:HG21	1:C:135:THR:HG22	1.93	0.50
1:D:127:ILE:HG21	1:D:135:THR:HG22	1.94	0.50
1:D:177:ILE:HD12	1:D:371:LEU:HD22	1.94	0.50
1:E:37:MET:HG3	1:E:38:TYR:CD2	2.46	0.50
1:G:33:ARG:HH22	1:G:37:MET:HG2	1.77	0.50
1:H:386:PRO:HG2	1:H:389:LEU:CD1	2.29	0.50
1:A:377:LYS:HD2	1:A:378:TYR:CE1	2.47	0.50
1:B:101:TRP:HH2	1:B:108:GLU:HB3	1.76	0.50
1:D:153:SER:HB3	1:D:364:GLN:HE22	1.76	0.50
1:E:302:ASP:CG	1:E:302:ASP:O	2.55	0.50
1:G:404:LYS:HB2	1:H:259:THR:HA	1.94	0.50
1:H:250:GLN:O	1:H:254:GLU:HG2	2.11	0.50
1:A:317:LYS:HD2	1:A:327:TYR:CE2	2.47	0.49
1:D:430:ARG:HG3	1:D:430:ARG:NH1	2.27	0.49
1:E:419:PRO:HB2	1:E:422:GLY:CA	2.42	0.49
1:H:4:LEU:HD12	1:H:4:LEU:H	1.75	0.49
1:C:430:ARG:HG3	1:C:430:ARG:NH1	2.27	0.49
1:D:208:VAL:CG2	1:D:213:LYS:HE2	2.42	0.49
1:B:184:THR:HA	1:B:188:PHE:CD1	2.47	0.49
1:C:412:GLN:HG2	1:D:277:CYS:SG	2.52	0.49
1:E:240:ILE:O	1:E:258:VAL:HA	2.13	0.49
1:F:66:LEU:O	1:F:71:ALA:HB3	2.12	0.49
1:F:99:PHE:CD2	1:F:99:PHE:N	2.79	0.49
1:F:183:VAL:HB	1:F:390:ASP:OD2	2.12	0.49
1:G:48:ARG:HD2	1:G:119:PHE:CB	2.42	0.49
1:G:419:PRO:HB2	1:G:422:GLY:N	2.27	0.49
1:A:153:SER:HB3	1:A:364:GLN:HE22	1.77	0.49
1:B:127:ILE:HG21	1:B:135:THR:HG22	1.94	0.49
1:B:199:ILE:HG22	1:B:203:LYS:HG3	1.94	0.49
1:D:142:HIS:O	1:D:145:LEU:HG	2.13	0.49
1:E:127:ILE:HD11	1:E:138:ILE:HD12	1.93	0.49
1:E:154:GLU:O	1:E:179:VAL:HB	2.12	0.49
1:F:127:ILE:HD11	1:F:138:ILE:HD12	1.93	0.49
1:G:171:ILE:O	1:G:173:LYS:HG2	2.11	0.49
1:G:278:VAL:CG1	1:G:303:VAL:HB	2.42	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:279:ASP:HA	1:G:282:LEU:HD11	1.94	0.49
1:H:150:ARG:HD3	1:H:375:PRO:HB3	1.94	0.49
1:C:101:TRP:HZ2	1:C:108:GLU:CD	2.20	0.49
1:D:224:GLY:HA2	1:D:274:THR:HG21	1.93	0.49
1:E:34:MET:HE3	1:E:365:VAL:HG12	1.95	0.49
1:E:80:ILE:HG22	1:E:104:GLU:HB2	1.94	0.49
1:E:126:MET:HE2	1:E:372:TRP:HB2	1.94	0.49
1:F:374:HIS:CG	1:F:377:LYS:HE3	2.48	0.49
1:H:183:VAL:HG11	1:H:431:TYR:CG	2.47	0.49
1:B:2:ASP:CB	1:B:74:ARG:HH12	2.23	0.49
1:B:79:ASN:HB3	1:B:82:SER:CB	2.43	0.49
1:C:49:ILE:HD12	1:C:71:ALA:HB1	1.93	0.49
1:C:79:ASN:HB3	1:C:82:SER:CB	2.42	0.49
1:C:317:LYS:HD2	1:C:327:TYR:CZ	2.48	0.49
1:D:409:THR:H	1:D:412:GLN:HE21	1.61	0.49
1:G:198:LEU:HD22	1:G:227:CYS:CB	2.43	0.49
1:G:386:PRO:HG2	1:G:389:LEU:HD12	1.93	0.49
1:H:35:ARG:NE	1:H:65:THR:OG1	2.45	0.49
1:A:244:ASP:HB3	1:A:247:ASN:HB2	1.94	0.49
1:B:167:MET:HG2	1:B:172:LEU:HD12	1.95	0.49
1:B:430:ARG:O	1:B:431:TYR:C	2.55	0.49
1:C:48:ARG:HD2	1:C:119:PHE:CG	2.47	0.49
1:F:27:GLU:HB3	1:F:354:SER:OG	2.11	0.49
1:F:49:ILE:HD13	1:F:368:GLN:OE1	2.13	0.49
1:G:7:LYS:HG2	1:G:111:TRP:CH2	2.48	0.49
1:G:419:PRO:HB2	1:G:422:GLY:CA	2.42	0.49
1:A:24:ALA:O	1:A:28:MET:HG3	2.13	0.49
1:A:75:TRP:CD1	1:A:76:SER:H	2.30	0.49
1:A:79:ASN:HB3	1:A:82:SER:CB	2.42	0.49
1:B:28:MET:HE3	1:B:354:SER:O	2.13	0.49
1:B:224:GLY:HA2	1:B:274:THR:HG21	1.95	0.49
1:B:302:ASP:O	1:B:302:ASP:CG	2.55	0.49
1:D:6:TYR:OH	1:D:11:ILE:HD13	2.12	0.49
1:D:206:THR:HG23	1:D:338:LEU:HD21	1.95	0.49
1:E:250:GLN:O	1:E:254:GLU:HG2	2.12	0.49
1:G:142:HIS:HB3	1:G:145:LEU:CD1	2.42	0.49
1:G:430:ARG:HG3	1:G:430:ARG:NH1	2.26	0.49
1:C:430:ARG:CA	1:D:430:ARG:HD3	2.38	0.49
1:D:225:LYS:NZ	1:D:250:GLN:HE22	2.11	0.49
1:E:5:PRO:O	1:E:97:PRO:HB3	2.13	0.49
1:F:156:THR:HG22	1:F:159:GLY:H	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:369:ILE:O	1:F:373:THR:HB	2.13	0.49
1:G:150:ARG:HD2	1:G:372:TRP:CE3	2.47	0.49
1:G:321:LYS:O	1:G:322:PRO:C	2.56	0.49
1:H:127:ILE:HG23	1:H:134:LEU:HD12	1.94	0.49
1:H:409:THR:OG1	1:H:412:GLN:HG3	2.12	0.49
1:B:79:ASN:HB3	1:B:82:SER:OG	2.12	0.49
1:B:126:MET:HE1	1:B:371:LEU:HB3	1.94	0.49
1:B:205:ALA:HB1	1:B:338:LEU:HD22	1.94	0.49
1:D:126:MET:HE1	1:D:371:LEU:HB3	1.94	0.49
1:F:28:MET:CB	1:F:358:SER:HB2	2.43	0.49
1:F:223:VAL:HG12	1:F:274:THR:CB	2.42	0.49
1:G:287:GLU:HG3	1:G:309:TRP:CZ2	2.48	0.49
1:H:206:THR:O	1:H:207:ASP:HB2	2.12	0.49
1:H:358:SER:HB3	1:H:397:HIS:NE2	2.27	0.49
1:B:345:ASN:O	1:B:349:ALA:HB3	2.13	0.48
1:D:300:HIS:HA	1:D:343:LEU:HD11	1.95	0.48
1:E:246:ILE:O	1:E:250:GLN:HG3	2.13	0.48
1:E:329:LEU:C	1:E:331:ASN:N	2.71	0.48
1:F:379:PRO:O	1:F:383:HIS:CE1	2.64	0.48
1:G:73:VAL:HG12	1:G:74:ARG:N	2.27	0.48
1:G:386:PRO:O	1:G:389:LEU:N	2.42	0.48
1:A:101:TRP:HH2	1:A:108:GLU:HB3	1.76	0.48
1:D:79:ASN:HB3	1:D:82:SER:CB	2.43	0.48
1:D:419:PRO:HB2	1:D:422:GLY:N	2.25	0.48
1:F:120:LYS:H	1:F:120:LYS:CD	2.25	0.48
1:F:430:ARG:HG3	1:F:430:ARG:NH1	2.28	0.48
1:B:21:LEU:O	1:B:25:GLU:HG3	2.12	0.48
1:B:142:HIS:HB3	1:B:145:LEU:HG	1.94	0.48
1:D:172:LEU:HD22	1:D:174:VAL:H	1.78	0.48
1:E:7:LYS:HZ1	1:E:100:ALA:C	2.21	0.48
1:E:328:LEU:C	1:E:328:LEU:HD12	2.38	0.48
1:F:142:HIS:N	1:F:143:PRO:CD	2.76	0.48
1:F:320:ILE:N	1:F:320:ILE:HD13	2.27	0.48
1:G:33:ARG:HE	1:G:36:GLU:CD	2.20	0.48
1:H:128:LEU:HG	1:H:364:GLN:NE2	2.29	0.48
1:B:72:GLU:OE2	1:B:120:LYS:HE3	2.13	0.48
1:C:79:ASN:HB3	1:C:82:SER:HB3	1.95	0.48
1:C:183:VAL:HG11	1:D:246:ILE:HG21	1.95	0.48
1:C:430:ARG:HD3	1:D:430:ARG:CA	2.33	0.48
1:D:24:ALA:O	1:D:28:MET:HG3	2.14	0.48
1:A:101:TRP:HZ2	1:A:108:GLU:CD	2.22	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:7:LYS:NZ	1:B:101:TRP:CE3	2.69	0.48
1:B:63:ILE:O	1:B:67:VAL:HG23	2.13	0.48
1:C:206:THR:CG2	1:C:338:LEU:HD21	2.44	0.48
1:E:185:LYS:HD2	1:E:185:LYS:C	2.38	0.48
1:G:110:LEU:O	1:G:110:LEU:HD22	2.13	0.48
1:H:75:TRP:HH2	1:H:128:LEU:HD13	1.78	0.48
1:H:138:ILE:HG21	1:H:149:ILE:CD1	2.43	0.48
1:H:198:LEU:CD2	1:H:227:CYS:HB3	2.38	0.48
1:H:409:THR:H	1:H:412:GLN:HE21	1.62	0.48
1:A:33:ARG:HE	1:A:36:GLU:CD	2.22	0.48
1:C:208:VAL:CG2	1:C:213:LYS:HE2	2.44	0.48
1:E:13:LEU:HB3	1:E:86:HIS:CA	2.43	0.48
1:F:3:LYS:CB	1:F:4:LEU:HD12	2.43	0.48
1:G:119:PHE:CD1	1:G:119:PHE:N	2.81	0.48
1:A:142:HIS:N	1:A:143:PRO:CD	2.77	0.48
1:B:142:HIS:N	1:B:143:PRO:CD	2.77	0.48
1:D:7:LYS:HG2	1:D:111:TRP:CH2	2.48	0.48
1:D:223:VAL:CG1	1:D:274:THR:HB	2.43	0.48
1:E:342:ARG:HG2	1:E:342:ARG:NH1	2.24	0.48
1:E:429:TYR:CE2	1:E:431:TYR:HA	2.48	0.48
1:F:28:MET:HB3	1:F:358:SER:HB2	1.94	0.48
1:F:300:HIS:H	2:F:6432:NAD:H1D	1.78	0.48
1:G:48:ARG:HD2	1:G:119:PHE:HB2	1.96	0.48
1:G:155:GLU:O	1:G:185:LYS:HE3	2.14	0.48
1:A:304:GLU:H	1:A:304:GLU:HG2	1.46	0.48
1:A:308:LYS:H	1:A:308:LYS:HD2	1.78	0.48
1:B:35:ARG:O	1:B:39:SER:HB2	2.14	0.48
1:C:224:GLY:HA2	1:C:274:THR:HG21	1.96	0.48
1:D:7:LYS:NZ	1:D:101:TRP:CE3	2.64	0.48
1:E:86:HIS:ND1	1:E:87:ALA:N	2.61	0.48
1:E:277:CYS:SG	1:E:278:VAL:N	2.86	0.48
1:G:60:ALA:O	1:G:64:GLU:HG3	2.13	0.48
1:G:65:THR:O	1:G:69:LEU:HD13	2.14	0.48
1:G:249:LEU:HB3	1:H:188:PHE:CE2	2.49	0.48
1:H:183:VAL:HG21	1:H:431:TYR:CE1	2.48	0.48
1:H:223:VAL:HG23	2:H:8432:NAD:O2N	2.14	0.48
1:A:7:LYS:HE3	1:A:99:PHE:C	2.39	0.48
1:C:199:ILE:HG22	1:C:203:LYS:HG3	1.95	0.48
1:E:161:HIS:CD2	1:E:161:HIS:C	2.91	0.48
1:E:425:LYS:HG3	1:E:431:TYR:CZ	2.48	0.48
1:F:283:GLY:HA3	1:F:309:TRP:CE2	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:55:MET:HG2	1:G:88:ALA:HB2	1.95	0.48
1:G:99:PHE:N	1:G:99:PHE:HD2	2.11	0.48
1:G:155:GLU:HB2	1:G:364:GLN:OE1	2.14	0.48
1:G:389:LEU:O	1:G:393:VAL:HG23	2.13	0.48
1:H:58:GLU:C	1:H:361:PHE:HE2	2.22	0.48
1:C:180:ASN:C	1:C:180:ASN:ND2	2.71	0.48
1:D:4:LEU:HD11	1:D:111:TRP:CZ2	2.49	0.48
1:E:152:ILE:HB	1:E:176:ALA:HB2	1.94	0.48
1:E:408:LEU:HD21	1:E:416:LEU:HD12	1.96	0.48
1:F:72:GLU:OE2	1:F:120:LYS:HE3	2.14	0.48
1:F:74:ARG:HG3	1:F:119:PHE:CE2	2.49	0.48
1:F:385:LEU:HD12	1:F:386:PRO:HD2	1.96	0.48
1:G:24:ALA:O	1:G:28:MET:HG3	2.13	0.48
1:H:63:ILE:O	1:H:66:LEU:HB2	2.14	0.48
1:H:127:ILE:HG23	1:H:134:LEU:CD1	2.43	0.48
1:H:373:THR:HG22	1:H:374:HIS:CD2	2.48	0.48
1:A:7:LYS:NZ	1:A:101:TRP:CE3	2.69	0.47
1:A:225:LYS:HZ3	1:A:250:GLN:HE22	1.62	0.47
1:B:206:THR:CG2	1:B:338:LEU:HD21	2.44	0.47
1:C:141:LYS:HB3	1:C:142:HIS:ND1	2.29	0.47
1:C:249:LEU:O	1:C:253:MET:HG2	2.13	0.47
1:E:161:HIS:CD2	1:E:165:LYS:HZ2	2.28	0.47
1:E:215:ALA:O	1:E:238:VAL:HA	2.14	0.47
1:G:169:ASN:CB	1:G:171:ILE:HG12	2.44	0.47
1:G:375:PRO:C	1:G:377:LYS:H	2.21	0.47
1:H:3:LYS:HD3	1:H:115:GLN:NE2	2.29	0.47
1:H:138:ILE:HG22	1:H:146:LEU:CD1	2.44	0.47
1:H:210:ILE:HG22	1:H:236:ALA:HB2	1.96	0.47
1:A:2:ASP:HB3	1:A:3:LYS:HE3	1.96	0.47
1:A:271:PHE:CE1	1:A:289:MET:HG2	2.49	0.47
1:B:7:LYS:HG2	1:B:111:TRP:CH2	2.49	0.47
1:B:142:HIS:O	1:B:145:LEU:HG	2.14	0.47
1:C:142:HIS:N	1:C:143:PRO:CD	2.77	0.47
1:C:306:ASP:OD2	1:C:309:TRP:HB2	2.15	0.47
1:D:3:LYS:N	1:D:3:LYS:HE3	2.29	0.47
1:E:101:TRP:CD2	1:E:104:GLU:HG2	2.50	0.47
1:G:83:THR:HG21	1:G:100:ALA:C	2.39	0.47
1:G:152:ILE:HG22	1:G:153:SER:N	2.28	0.47
1:G:344:VAL:HG13	1:G:345:ASN:N	2.29	0.47
1:C:430:ARG:O	1:C:431:TYR:C	2.57	0.47
1:D:275:THR:CG2	1:D:276:GLY:N	2.76	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:319:ASN:HA	1:E:325:ASP:OD2	2.15	0.47
1:F:4:LEU:CD1	1:F:99:PHE:HE1	2.15	0.47
1:F:101:TRP:CZ2	1:F:108:GLU:OE2	2.67	0.47
1:G:79:ASN:HB3	1:G:82:SER:HB3	1.95	0.47
1:G:221:GLY:HA3	2:G:7432:NAD:O5B	2.14	0.47
1:G:279:ASP:N	1:G:279:ASP:OD1	2.47	0.47
1:H:153:SER:CB	1:H:364:GLN:HE22	2.26	0.47
1:A:6:TYR:HB2	1:A:98:VAL:O	2.14	0.47
1:C:429:TYR:CE2	1:C:431:TYR:HA	2.49	0.47
1:D:205:ALA:HB1	1:D:338:LEU:HD22	1.96	0.47
1:E:214:VAL:HG11	1:E:267:GLU:HG2	1.96	0.47
1:G:31:LEU:O	1:G:35:ARG:HG3	2.13	0.47
1:G:178:ASN:CG	1:G:181:ASP:HB2	2.39	0.47
1:G:296:CYS:HB3	1:G:338:LEU:HB2	1.97	0.47
1:C:91:ILE:HG23	1:C:96:ILE:HB	1.95	0.47
1:D:365:VAL:O	1:D:369:ILE:HG13	2.14	0.47
1:F:386:PRO:HG2	1:F:389:LEU:CD1	2.43	0.47
1:A:111:TRP:O	1:A:115:GLN:HG2	2.15	0.47
1:B:342:ARG:O	1:B:343:LEU:C	2.57	0.47
1:C:4:LEU:HD11	1:C:111:TRP:CZ2	2.49	0.47
1:D:44:LEU:HB3	1:D:71:ALA:HB2	1.95	0.47
1:D:304:GLU:H	1:D:304:GLU:HG2	1.43	0.47
1:E:2:ASP:HB3	1:E:3:LYS:H	1.43	0.47
1:G:101:TRP:O	1:G:104:GLU:HG2	2.13	0.47
1:G:125:ASN:HA	1:G:149:ILE:HA	1.97	0.47
1:G:419:PRO:HG2	1:G:422:GLY:HA3	1.97	0.47
1:H:7:LYS:HZ1	1:H:100:ALA:CA	2.28	0.47
1:H:198:LEU:HG	1:H:199:ILE:N	2.28	0.47
1:A:74:ARG:NH1	1:A:115:GLN:O	2.48	0.47
1:A:385:LEU:O	1:A:386:PRO:C	2.58	0.47
1:B:3:LYS:H	1:B:3:LYS:CE	2.27	0.47
1:B:430:ARG:HH11	1:B:430:ARG:HG3	1.80	0.47
1:C:126:MET:HE1	1:C:371:LEU:HB3	1.96	0.47
1:C:388:LYS:HG2	1:C:423:PRO:CG	2.45	0.47
1:D:278:VAL:HA	1:D:303:VAL:O	2.13	0.47
1:E:234:PHE:HE1	1:G:195:ARG:O	1.97	0.47
1:E:388:LYS:HD3	1:E:388:LYS:HA	1.70	0.47
1:E:430:ARG:CZ	1:F:183:VAL:HG22	2.44	0.47
1:G:152:ILE:HB	1:G:176:ALA:CB	2.44	0.47
1:G:152:ILE:CD1	1:G:174:VAL:HG22	2.45	0.47
1:G:218:ALA:HB3	1:G:273:THR:HA	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:308:LYS:O	1:G:311:ASN:N	2.48	0.47
1:H:33:ARG:NH2	1:H:33:ARG:O	2.47	0.47
1:H:55:MET:CB	1:H:83:THR:HG23	2.37	0.47
1:H:85:ASP:OD2	1:H:101:TRP:HA	2.15	0.47
1:H:379:PRO:HD2	1:H:383:HIS:CE1	2.50	0.47
1:B:4:LEU:HD11	1:B:111:TRP:CZ2	2.49	0.47
1:C:279:ASP:HA	1:C:282:LEU:HD11	1.96	0.47
1:D:334:ARG:O	1:D:335:ILE:HD13	2.14	0.47
1:E:57:VAL:H	1:E:84:GLN:NE2	2.13	0.47
1:E:307:VAL:N	1:E:308:LYS:HE3	2.27	0.47
1:G:53:LEU:HG	1:G:130:ASP:HB2	1.97	0.47
1:G:296:CYS:HB3	1:G:338:LEU:HD12	1.97	0.47
1:H:117:LEU:HD13	1:H:142:HIS:CD2	2.50	0.47
1:H:177:ILE:HD13	1:H:385:LEU:CD1	2.45	0.47
1:H:302:ASP:HB3	1:H:342:ARG:HA	1.96	0.47
1:A:39:SER:O	1:A:42:LYS:HG2	2.14	0.47
1:A:362:THR:HG22	1:A:393:VAL:HG22	1.97	0.47
1:D:7:LYS:HG2	1:D:111:TRP:HZ3	1.79	0.47
1:D:75:TRP:CD1	1:D:76:SER:H	2.32	0.47
1:F:141:LYS:HB3	1:F:142:HIS:CE1	2.50	0.47
1:F:326:ARG:HH11	1:F:326:ARG:CG	2.16	0.47
1:H:42:LYS:O	1:H:45:LYS:HB3	2.15	0.47
1:H:331:ASN:OD1	1:H:333:HIS:HB2	2.15	0.47
1:H:344:VAL:HG13	1:H:345:ASN:N	2.30	0.47
1:A:91:ILE:HG23	1:A:96:ILE:HB	1.97	0.47
1:A:180:ASN:C	1:A:180:ASN:ND2	2.72	0.47
1:B:124:LEU:HD11	1:B:138:ILE:CD1	2.45	0.47
1:B:208:VAL:CG2	1:B:213:LYS:HE2	2.45	0.47
1:C:203:LYS:O	1:C:207:ASP:N	2.48	0.47
1:C:278:VAL:CG1	1:C:303:VAL:HB	2.44	0.47
1:C:388:LYS:HG2	1:C:423:PRO:CD	2.45	0.47
1:D:271:PHE:CE1	1:D:289:MET:HG2	2.50	0.47
1:E:7:LYS:HZ1	1:E:100:ALA:N	2.11	0.47
1:E:57:VAL:O	1:E:61:VAL:HG23	2.15	0.47
1:F:38:TYR:HB3	1:F:43:PRO:CD	2.45	0.47
1:F:206:THR:HG21	1:F:294:ILE:HD13	1.97	0.47
1:G:215:ALA:CB	1:G:231:LEU:HD22	2.44	0.47
1:H:142:HIS:HB3	1:H:145:LEU:HG	1.97	0.47
1:A:79:ASN:HB3	1:A:82:SER:OG	2.14	0.46
1:C:243:ILE:HG21	1:D:408:LEU:CD1	2.44	0.46
1:D:203:LYS:O	1:D:207:ASP:N	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:208:VAL:HG22	1:D:213:LYS:HE2	1.97	0.46
1:F:344:VAL:CG1	1:F:345:ASN:N	2.77	0.46
1:G:243:ILE:HA	1:H:406:THR:O	2.14	0.46
1:H:80:ILE:HG13	1:H:81:PHE:CD1	2.50	0.46
1:A:47:ALA:HA	1:A:125:ASN:HD21	1.81	0.46
1:B:138:ILE:HG22	1:B:146:LEU:CD1	2.45	0.46
1:C:33:ARG:NH1	1:C:37:MET:SD	2.87	0.46
1:C:283:GLY:HA2	1:C:286:PHE:HB2	1.97	0.46
1:C:408:LEU:HD13	1:D:243:ILE:HG21	1.97	0.46
1:D:74:ARG:NH1	1:D:115:GLN:O	2.48	0.46
1:D:141:LYS:HB3	1:D:142:HIS:ND1	2.30	0.46
1:D:302:ASP:CG	1:D:302:ASP:O	2.56	0.46
1:D:429:TYR:CE2	1:D:431:TYR:HA	2.51	0.46
1:E:7:LYS:HG2	1:E:111:TRP:CH2	2.51	0.46
1:E:33:ARG:O	1:E:37:MET:HG2	2.15	0.46
1:E:37:MET:HE2	1:E:38:TYR:OH	2.14	0.46
1:G:105:THR:O	1:G:109:TYR:N	2.46	0.46
1:A:141:LYS:HB3	1:A:142:HIS:ND1	2.29	0.46
1:A:425:LYS:HE2	1:B:247:ASN:ND2	2.29	0.46
1:B:48:ARG:HD2	1:B:119:PHE:CG	2.50	0.46
1:C:7:LYS:HG2	1:C:111:TRP:CH2	2.51	0.46
1:D:79:ASN:HB3	1:D:82:SER:HB3	1.97	0.46
1:D:155:GLU:O	1:D:180:ASN:HB2	2.16	0.46
1:D:326:ARG:NH1	1:D:326:ARG:HG2	2.30	0.46
1:D:419:PRO:HB2	1:D:422:GLY:HA3	1.97	0.46
1:E:210:ILE:CG2	1:E:236:ALA:HB2	2.44	0.46
1:F:160:VAL:HG12	1:F:164:TYR:CE2	2.49	0.46
1:G:33:ARG:NE	1:G:36:GLU:OE1	2.48	0.46
1:G:167:MET:HG3	1:G:381:GLY:HA2	1.97	0.46
1:G:267:GLU:HA	1:G:290:LYS:HE3	1.97	0.46
1:B:373:THR:O	1:B:375:PRO:HD3	2.14	0.46
1:D:206:THR:CG2	1:D:338:LEU:HD21	2.45	0.46
1:E:26:ASN:O	1:E:400:LYS:HE2	2.15	0.46
1:E:138:ILE:HG22	1:E:146:LEU:HD13	1.96	0.46
1:E:419:PRO:HB2	1:E:422:GLY:N	2.29	0.46
1:F:21:LEU:HD12	1:F:57:VAL:HG13	1.97	0.46
1:F:34:MET:HE2	1:F:366:MET:HG3	1.97	0.46
1:G:154:GLU:HA	1:G:154:GLU:OE2	2.15	0.46
1:G:162:ASN:ND2	1:G:163:LEU:N	2.63	0.46
1:G:178:ASN:OD1	1:G:178:ASN:C	2.59	0.46
1:G:286:PHE:C	1:G:288:GLN:N	2.72	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:342:ARG:O	1:G:343:LEU:C	2.59	0.46
1:G:366:MET:O	1:G:370:GLU:HG2	2.15	0.46
1:G:404:LYS:HB2	1:H:259:THR:HG22	1.98	0.46
1:G:430:ARG:CZ	1:H:183:VAL:HG22	2.44	0.46
1:H:183:VAL:HG21	1:H:431:TYR:CD1	2.50	0.46
1:B:27:GLU:C	1:B:29:PRO:HD3	2.40	0.46
1:C:3:LYS:HE3	1:C:3:LYS:H	1.80	0.46
1:E:110:LEU:HD22	1:E:114:GLU:HG3	1.97	0.46
1:E:375:PRO:C	1:E:377:LYS:H	2.23	0.46
1:F:25:GLU:HB3	1:F:32:MET:HE2	1.97	0.46
1:G:25:GLU:O	1:G:32:MET:HG2	2.16	0.46
1:G:223:VAL:O	1:G:226:GLY:N	2.48	0.46
1:H:93:LYS:HA	1:H:93:LYS:HD3	1.74	0.46
1:H:105:THR:HG23	1:H:108:GLU:OE1	2.16	0.46
1:A:7:LYS:HG2	1:A:111:TRP:CH2	2.51	0.46
1:A:127:ILE:HG21	1:A:135:THR:HG22	1.98	0.46
1:A:206:THR:CG2	1:A:338:LEU:HD21	2.46	0.46
1:A:356:VAL:HB	1:C:209:MET:SD	2.55	0.46
1:C:2:ASP:HB3	1:C:3:LYS:HE3	1.97	0.46
1:C:74:ARG:NH1	1:C:115:GLN:O	2.49	0.46
1:C:307:VAL:N	1:C:308:LYS:HE3	2.29	0.46
1:D:358:SER:HB3	1:D:397:HIS:NE2	2.31	0.46
1:E:2:ASP:HB2	1:E:74:ARG:HH12	1.81	0.46
1:G:157:THR:O	1:G:160:VAL:N	2.49	0.46
1:H:178:ASN:ND2	1:H:384:PHE:CE1	2.83	0.46
1:H:379:PRO:O	1:H:383:HIS:HE1	1.98	0.46
1:A:37:MET:CB	1:H:284:ARG:NH2	2.73	0.46
1:A:57:VAL:O	1:A:60:ALA:HB3	2.16	0.46
1:B:91:ILE:HG23	1:B:96:ILE:HB	1.97	0.46
1:B:278:VAL:CG1	1:B:303:VAL:HB	2.41	0.46
1:G:242:GLU:OE1	1:G:243:ILE:N	2.45	0.46
1:H:52:CYS:HB3	1:H:129:ASP:OD1	2.14	0.46
1:H:65:THR:O	1:H:69:LEU:HD13	2.16	0.46
1:A:2:ASP:CB	1:A:74:ARG:HH12	2.26	0.46
1:A:101:TRP:CZ2	1:A:108:GLU:CD	2.94	0.46
1:A:136:ASN:O	1:A:140:THR:HG23	2.16	0.46
1:A:283:GLY:HA2	1:A:286:PHE:HB2	1.97	0.46
1:A:419:PRO:HB2	1:A:422:GLY:HA3	1.98	0.46
1:B:419:PRO:HB2	1:B:422:GLY:HA3	1.98	0.46
1:E:203:LYS:O	1:E:207:ASP:N	2.48	0.46
1:E:373:THR:O	1:E:375:PRO:HD3	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:362:THR:CG2	1:F:366:MET:HE3	2.45	0.46
1:G:48:ARG:HH21	1:G:122:GLY:C	2.24	0.46
1:G:190:ASN:OD1	1:G:190:ASN:N	2.49	0.46
1:G:224:GLY:HA2	1:G:274:THR:HG21	1.98	0.46
1:H:7:LYS:HG2	1:H:111:TRP:HH2	1.77	0.46
1:B:101:TRP:HZ2	1:B:108:GLU:CD	2.23	0.46
1:B:362:THR:O	1:B:366:MET:HG3	2.16	0.46
1:C:184:THR:HA	1:C:188:PHE:CD1	2.51	0.46
1:E:105:THR:H	1:E:108:GLU:HB2	1.80	0.46
1:F:92:ALA:HB2	1:F:98:VAL:CG1	2.46	0.46
1:G:3:LYS:HB2	1:G:4:LEU:CD1	2.46	0.46
1:G:34:MET:O	1:G:38:TYR:HD2	1.99	0.46
1:H:144:GLN:CD	1:H:144:GLN:H	2.23	0.46
1:H:154:GLU:O	1:H:179:VAL:HB	2.16	0.46
1:H:416:LEU:HD13	1:H:418:MET:SD	2.56	0.46
1:B:141:LYS:HB3	1:B:142:HIS:ND1	2.31	0.46
1:C:7:LYS:NZ	1:C:7:LYS:O	2.37	0.46
1:E:120:LYS:HG2	1:E:121:ASP:OD1	2.15	0.46
1:E:283:GLY:O	1:E:287:GLU:HG3	2.16	0.46
1:E:342:ARG:NH1	1:E:342:ARG:CG	2.79	0.46
1:E:387:LYS:HA	1:E:390:ASP:HB2	1.97	0.46
1:F:4:LEU:HD22	1:F:6:TYR:O	2.15	0.46
1:F:315:VAL:N	1:F:328:LEU:O	2.49	0.46
1:F:350:MET:HB2	1:H:207:ASP:OD1	2.16	0.46
1:G:74:ARG:HB3	1:G:116:THR:HG22	1.96	0.46
1:G:225:LYS:NZ	1:G:250:GLN:HE22	2.13	0.46
1:H:55:MET:HE2	1:H:88:ALA:HA	1.98	0.46
1:H:101:TRP:CZ2	1:H:108:GLU:OE1	2.61	0.46
1:A:190:ASN:HB3	1:A:223:VAL:HG23	1.98	0.45
1:A:430:ARG:CA	1:B:430:ARG:HD3	2.44	0.45
1:B:99:PHE:CD2	1:B:99:PHE:N	2.84	0.45
1:B:275:THR:CG2	1:B:276:GLY:N	2.78	0.45
1:B:304:GLU:H	1:B:304:GLU:HG2	1.43	0.45
1:C:35:ARG:O	1:C:39:SER:HB2	2.16	0.45
1:D:124:LEU:HD11	1:D:138:ILE:HD11	1.98	0.45
1:E:152:ILE:HG13	1:E:174:VAL:HG22	1.97	0.45
1:F:195:ARG:O	1:F:230:ALA:HB2	2.16	0.45
1:G:119:PHE:N	1:G:119:PHE:HD1	2.15	0.45
1:G:258:VAL:HB	1:H:403:VAL:HG13	1.98	0.45
1:H:262:ASP:O	1:H:266:LYS:HE2	2.16	0.45
1:B:91:ILE:O	1:B:94:ALA:HB3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:LYS:HD2	1:B:327:TYR:CE2	2.51	0.45
1:C:334:ARG:O	1:C:335:ILE:HD13	2.17	0.45
1:D:215:ALA:O	1:D:238:VAL:HA	2.17	0.45
1:E:48:ARG:HB3	1:E:119:PHE:CG	2.51	0.45
1:E:92:ALA:HB2	1:E:98:VAL:CG1	2.45	0.45
1:E:370:GLU:HG3	1:E:378:TYR:OH	2.16	0.45
1:F:57:VAL:HA	1:F:87:ALA:HB1	1.98	0.45
1:H:188:PHE:N	1:H:188:PHE:CD1	2.84	0.45
1:A:203:LYS:O	1:A:207:ASP:N	2.49	0.45
1:A:308:LYS:H	1:A:308:LYS:CE	2.28	0.45
1:A:421:ASN:ND2	1:H:312:GLU:OE2	2.49	0.45
1:B:180:ASN:ND2	1:B:180:ASN:C	2.75	0.45
1:C:101:TRP:CZ2	1:C:108:GLU:CD	2.94	0.45
1:C:430:ARG:CD	1:D:430:ARG:HA	2.35	0.45
1:D:308:LYS:H	1:D:308:LYS:CE	2.30	0.45
1:G:83:THR:HG21	1:G:101:TRP:N	2.32	0.45
1:G:271:PHE:CE2	1:G:289:MET:HE2	2.51	0.45
1:G:363:ASN:ND2	1:G:393:VAL:HG11	2.31	0.45
1:H:5:PRO:HB2	1:H:6:TYR:HD2	1.82	0.45
1:H:321:LYS:HD3	1:H:324:VAL:HG21	1.98	0.45
1:B:74:ARG:NH1	1:B:115:GLN:O	2.49	0.45
1:D:3:LYS:O	1:D:4:LEU:C	2.59	0.45
1:D:33:ARG:NH1	1:D:37:MET:SD	2.89	0.45
1:E:10:ASP:HB3	1:E:13:LEU:HD22	1.98	0.45
1:E:292:ASP:N	1:E:334:ARG:O	2.49	0.45
1:F:6:TYR:HB2	1:F:98:VAL:O	2.16	0.45
1:F:370:GLU:HB3	1:F:378:TYR:CE1	2.52	0.45
1:G:278:VAL:HA	1:G:303:VAL:O	2.17	0.45
1:B:178:ASN:HD21	1:B:181:ASP:HB2	1.81	0.45
1:C:369:ILE:O	1:C:373:THR:HB	2.17	0.45
1:D:7:LYS:HE3	1:D:99:PHE:CB	2.46	0.45
1:E:37:MET:HG3	1:E:38:TYR:CE2	2.52	0.45
1:E:188:PHE:O	1:E:192:TYR:HB2	2.16	0.45
1:F:66:LEU:HD11	1:F:128:LEU:CD1	2.46	0.45
1:F:208:VAL:HG11	1:F:294:ILE:HD12	1.98	0.45
1:F:261:MET:C	1:F:263:GLU:N	2.74	0.45
1:F:356:VAL:HB	1:H:209:MET:SD	2.57	0.45
1:G:153:SER:CB	1:G:368:GLN:NE2	2.79	0.45
1:G:167:MET:HG2	1:G:172:LEU:CD1	2.46	0.45
1:G:250:GLN:O	1:G:254:GLU:HG2	2.16	0.45
1:H:9:ALA:HB2	1:H:101:TRP:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:17:GLY:O	1:H:21:LEU:HB2	2.17	0.45
1:H:143:PRO:HA	1:H:146:LEU:HD13	1.98	0.45
1:A:53:LEU:O	1:A:54:HIS:C	2.60	0.45
1:A:175:PRO:HB3	1:A:379:PRO:O	2.16	0.45
1:B:7:LYS:HE3	1:B:99:PHE:CB	2.46	0.45
1:B:308:LYS:H	1:B:308:LYS:HD2	1.80	0.45
1:C:178:ASN:C	1:C:178:ASN:OD1	2.58	0.45
1:D:2:ASP:HB3	1:D:3:LYS:H	1.57	0.45
1:D:27:GLU:C	1:D:29:PRO:HD3	2.42	0.45
1:D:171:ILE:O	1:D:173:LYS:HG2	2.15	0.45
1:E:177:ILE:HD13	1:E:385:LEU:CD1	2.47	0.45
1:F:74:ARG:NH1	1:F:115:GLN:O	2.49	0.45
1:F:410:GLU:O	1:F:414:GLN:HG2	2.16	0.45
1:G:74:ARG:HD2	1:G:119:PHE:CD1	2.51	0.45
1:G:155:GLU:O	1:G:180:ASN:HB2	2.16	0.45
1:H:60:ALA:O	1:H:64:GLU:HG3	2.16	0.45
1:A:3:LYS:O	1:A:4:LEU:C	2.60	0.45
1:A:162:ASN:O	1:A:166:MET:HG3	2.16	0.45
1:A:342:ARG:O	1:A:343:LEU:C	2.59	0.45
1:B:363:ASN:ND2	1:B:393:VAL:HG21	2.32	0.45
1:C:7:LYS:HG2	1:C:111:TRP:HZ3	1.82	0.45
1:D:287:GLU:HG3	1:D:309:TRP:CZ2	2.52	0.45
1:E:291:ASP:HA	1:E:333:HIS:HB3	1.98	0.45
1:G:91:ILE:CG2	1:G:96:ILE:HB	2.45	0.45
1:H:32:MET:CE	1:H:35:ARG:HD2	2.46	0.45
1:H:172:LEU:HD22	1:H:174:VAL:H	1.81	0.45
1:A:430:ARG:HD3	1:B:430:ARG:CA	2.40	0.45
1:B:209:MET:HB2	1:D:353:PRO:CB	2.45	0.45
1:B:271:PHE:CE1	1:B:289:MET:HG2	2.51	0.45
1:C:413:ALA:HB1	1:C:418:MET:O	2.16	0.45
1:D:7:LYS:HE3	1:D:99:PHE:C	2.41	0.45
1:E:13:LEU:HB3	1:E:86:HIS:CB	2.46	0.45
1:E:18:ARG:NH1	1:E:21:LEU:HD22	2.32	0.45
1:E:125:ASN:C	1:E:125:ASN:OD1	2.60	0.45
1:F:198:LEU:HD22	1:F:227:CYS:CB	2.36	0.45
1:G:143:PRO:HA	1:G:146:LEU:HD22	1.99	0.45
1:G:302:ASP:OD1	1:G:342:ARG:NH1	2.50	0.45
1:H:47:ALA:HA	1:H:125:ASN:HD21	1.82	0.45
1:H:124:LEU:HD11	1:H:138:ILE:HD11	1.98	0.45
1:H:419:PRO:HG2	1:H:422:GLY:HA3	1.99	0.45
1:B:104:GLU:OE1	1:B:109:TYR:HA	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:LYS:NZ	1:B:250:GLN:NE2	2.65	0.45
1:B:307:VAL:H	1:B:308:LYS:HE3	1.81	0.45
1:D:91:ILE:HG23	1:D:96:ILE:HB	1.98	0.45
1:F:119:PHE:CB	1:F:120:LYS:HE2	2.41	0.45
1:G:155:GLU:OE2	1:G:360:SER:HB3	2.17	0.45
1:G:265:CYS:SG	1:G:288:GLN:HG2	2.56	0.45
1:H:141:LYS:C	1:H:142:HIS:ND1	2.75	0.45
1:A:224:GLY:HA2	1:A:274:THR:HG21	1.99	0.45
1:A:275:THR:CG2	1:A:276:GLY:N	2.80	0.45
1:A:326:ARG:NH1	1:A:326:ARG:HG2	2.31	0.45
1:A:416:LEU:HB3	1:A:418:MET:HE3	1.99	0.45
1:C:430:ARG:CZ	1:D:183:VAL:HG22	2.47	0.45
1:E:7:LYS:CE	1:E:101:TRP:CE3	3.00	0.45
1:E:24:ALA:O	1:E:28:MET:HG3	2.17	0.45
1:E:55:MET:CE	1:E:88:ALA:HA	2.47	0.45
1:E:283:GLY:HA2	1:E:286:PHE:HD2	1.82	0.45
1:E:415:TYR:OH	1:F:303:VAL:HG21	2.17	0.45
1:F:31:LEU:CD1	1:F:61:VAL:HG12	2.47	0.45
1:F:240:ILE:O	1:F:258:VAL:HA	2.16	0.45
1:G:183:VAL:HG21	1:G:431:TYR:CE1	2.52	0.45
1:H:316:GLU:HB3	1:H:328:LEU:HB3	1.98	0.45
1:H:321:LYS:HG2	1:H:324:VAL:HG23	1.99	0.45
1:B:208:VAL:HG22	1:B:213:LYS:HE2	1.98	0.44
1:B:419:PRO:HG2	1:B:422:GLY:HA3	1.99	0.44
1:F:3:LYS:HB2	1:F:4:LEU:CD1	2.45	0.44
1:F:5:PRO:O	1:F:97:PRO:HA	2.17	0.44
1:F:6:TYR:CD1	1:F:6:TYR:C	2.95	0.44
1:G:7:LYS:CD	1:G:111:TRP:HZ3	2.30	0.44
1:G:183:VAL:HG11	1:H:246:ILE:HG21	1.98	0.44
1:H:119:PHE:N	1:H:119:PHE:CD1	2.85	0.44
1:A:57:VAL:H	1:A:84:GLN:HE22	1.65	0.44
1:A:81:PHE:CE2	1:A:342:ARG:HG3	2.52	0.44
1:B:350:MET:HB2	1:D:207:ASP:OD1	2.16	0.44
1:C:214:VAL:H	1:C:269:ASN:ND2	2.10	0.44
1:E:7:LYS:NZ	1:E:100:ALA:N	2.64	0.44
1:E:101:TRP:CE2	1:E:104:GLU:HG2	2.52	0.44
1:E:189:ASP:OD1	1:E:352:HIS:CE1	2.70	0.44
1:F:154:GLU:HB2	1:F:163:LEU:CD1	2.46	0.44
1:F:353:PRO:O	1:F:357:MET:HG2	2.16	0.44
1:F:419:PRO:HG2	1:F:422:GLY:HA3	1.99	0.44
1:G:144:GLN:HE21	1:G:144:GLN:HB2	1.57	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:ASN:C	1:A:178:ASN:OD1	2.59	0.44
1:A:208:VAL:HG22	1:A:213:LYS:HE2	1.99	0.44
1:C:24:ALA:O	1:C:28:MET:HG3	2.17	0.44
1:C:317:LYS:HD2	1:C:327:TYR:CE2	2.52	0.44
1:D:53:LEU:O	1:D:54:HIS:C	2.61	0.44
1:D:119:PHE:HB3	1:D:120:LYS:HE2	2.00	0.44
1:F:171:ILE:O	1:F:173:LYS:HG2	2.17	0.44
1:G:141:LYS:C	1:G:143:PRO:HD3	2.43	0.44
1:G:183:VAL:HG11	1:G:431:TYR:CG	2.52	0.44
1:G:411:LYS:NZ	1:H:279:ASP:OD2	2.48	0.44
1:H:7:LYS:HD3	1:H:111:TRP:CZ3	2.52	0.44
1:A:182:SER:HB2	1:A:185:LYS:HB2	1.99	0.44
1:B:430:ARG:HG3	1:B:430:ARG:NH1	2.32	0.44
1:C:178:ASN:ND2	1:C:181:ASP:HB2	2.33	0.44
1:F:51:GLY:HA3	1:F:75:TRP:CZ3	2.53	0.44
1:F:227:CYS:SG	1:F:274:THR:HG21	2.58	0.44
1:G:98:VAL:C	1:G:99:PHE:CD2	2.96	0.44
1:G:185:LYS:HD2	1:G:185:LYS:C	2.42	0.44
1:H:238:VAL:HG12	1:H:240:ILE:HD12	2.00	0.44
1:B:57:VAL:H	1:B:84:GLN:HE22	1.61	0.44
1:C:7:LYS:HE3	1:C:99:PHE:C	2.42	0.44
1:C:205:ALA:HB1	1:C:338:LEU:HD22	1.99	0.44
1:C:208:VAL:HG22	1:C:213:LYS:HE2	1.98	0.44
1:E:3:LYS:O	1:E:4:LEU:C	2.59	0.44
1:F:58:GLU:OE2	3:F:6433:DEA:N6	2.47	0.44
1:G:33:ARG:NH1	1:G:33:ARG:CG	2.78	0.44
1:G:430:ARG:NE	1:H:183:VAL:HG22	2.32	0.44
1:H:105:THR:O	1:H:106:ASP:C	2.60	0.44
1:H:275:THR:HG22	1:H:277:CYS:HB2	1.98	0.44
1:H:336:ILE:HG22	1:H:338:LEU:CD2	2.48	0.44
1:A:183:VAL:HG11	1:B:246:ILE:HG21	1.99	0.44
1:C:81:PHE:CE2	1:C:342:ARG:HG3	2.52	0.44
1:E:49:ILE:HB	1:E:73:VAL:HG22	2.00	0.44
1:E:74:ARG:NH1	1:E:115:GLN:O	2.48	0.44
1:F:48:ARG:HA	1:F:72:GLU:HB3	2.00	0.44
1:F:203:LYS:O	1:F:207:ASP:N	2.49	0.44
1:G:82:SER:HB2	1:G:346:LEU:HD22	1.99	0.44
1:G:172:LEU:HD22	1:G:174:VAL:H	1.83	0.44
1:H:160:VAL:HG21	1:H:180:ASN:HB3	2.00	0.44
1:C:33:ARG:HE	1:C:36:GLU:CD	2.25	0.44
1:C:308:LYS:H	1:C:308:LYS:CE	2.29	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:33:ARG:NH1	1:F:33:ARG:CG	2.56	0.44
1:G:3:LYS:HD2	1:G:115:GLN:OE1	2.18	0.44
1:G:57:VAL:HG23	1:G:84:GLN:NE2	2.32	0.44
1:G:62:LEU:HD22	1:G:361:PHE:CD1	2.52	0.44
1:G:400:LYS:C	1:G:402:ASN:H	2.26	0.44
1:H:17:GLY:O	1:H:21:LEU:HD13	2.18	0.44
1:A:164:TYR:CZ	1:A:382:VAL:HG21	2.53	0.44
1:A:246:ILE:HG21	1:B:183:VAL:HG11	1.99	0.44
1:B:278:VAL:HA	1:B:303:VAL:O	2.17	0.44
1:C:363:ASN:ND2	1:C:393:VAL:HG21	2.32	0.44
1:D:3:LYS:HE3	1:D:3:LYS:H	1.82	0.44
1:G:11:ILE:HD12	1:G:11:ILE:HA	1.89	0.44
1:G:58:GLU:HB3	1:G:361:PHE:HE2	1.82	0.44
1:H:91:ILE:CG2	1:H:96:ILE:HB	2.48	0.44
1:H:214:VAL:HG13	1:H:237:ARG:O	2.17	0.44
1:A:3:LYS:HE3	1:A:3:LYS:N	2.32	0.44
1:A:315:VAL:HG23	1:A:330:LYS:HG2	1.99	0.44
1:B:53:LEU:O	1:B:54:HIS:C	2.61	0.44
1:B:160:VAL:HG21	1:B:178:ASN:OD1	2.17	0.44
1:C:358:SER:CB	1:C:397:HIS:NE2	2.80	0.44
1:C:412:GLN:HG2	1:D:277:CYS:HG	1.83	0.44
1:D:419:PRO:HG2	1:D:422:GLY:HA3	2.00	0.44
1:G:63:ILE:HG21	1:G:96:ILE:HG21	2.00	0.44
1:H:176:ALA:O	1:H:382:VAL:HA	2.17	0.44
1:H:200:ASP:O	1:H:204:ARG:HB2	2.18	0.44
1:A:7:LYS:NZ	1:A:7:LYS:O	2.36	0.43
1:A:199:ILE:HG22	1:A:203:LYS:HG3	2.00	0.43
1:B:30:GLY:HA3	1:B:362:THR:OG1	2.18	0.43
1:C:304:GLU:H	1:C:304:GLU:HG2	1.40	0.43
1:C:387:LYS:HE2	1:C:431:TYR:OH	2.17	0.43
1:D:35:ARG:O	1:D:39:SER:HB2	2.18	0.43
1:D:265:CYS:HA	1:D:271:PHE:CE2	2.54	0.43
1:D:277:CYS:SG	1:D:278:VAL:N	2.91	0.43
1:D:287:GLU:HG3	1:D:309:TRP:CH2	2.52	0.43
1:F:34:MET:CE	1:F:366:MET:HG3	2.48	0.43
1:F:209:MET:HB2	1:H:353:PRO:HB2	1.99	0.43
1:F:419:PRO:HB2	1:F:422:GLY:CA	2.48	0.43
1:G:193:GLY:C	1:G:352:HIS:CD2	2.95	0.43
1:H:47:ALA:HB2	1:H:372:TRP:CE2	2.52	0.43
1:B:388:LYS:HG2	1:B:423:PRO:HD3	1.99	0.43
1:C:32:MET:O	1:C:36:GLU:HG3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:120:LYS:HE2	1:C:120:LYS:N	2.18	0.43
1:C:152:ILE:HG13	1:C:174:VAL:HG22	2.00	0.43
1:E:194:CYS:SG	1:E:223:VAL:HG13	2.58	0.43
1:F:388:LYS:HG2	1:F:423:PRO:CG	2.47	0.43
1:G:6:TYR:HB2	1:G:98:VAL:O	2.18	0.43
1:G:35:ARG:HE	1:G:65:THR:CA	2.30	0.43
1:G:142:HIS:N	1:G:143:PRO:CD	2.81	0.43
1:H:7:LYS:CE	1:H:99:PHE:C	2.91	0.43
1:H:386:PRO:CG	1:H:389:LEU:HD12	2.32	0.43
1:A:425:LYS:HE2	1:B:247:ASN:HD21	1.83	0.43
1:C:271:PHE:CE1	1:C:289:MET:HG2	2.53	0.43
1:C:331:ASN:OD1	1:C:333:HIS:HB2	2.19	0.43
1:D:363:ASN:ND2	1:D:393:VAL:HG21	2.34	0.43
1:D:388:LYS:HG2	1:D:423:PRO:HD3	1.98	0.43
1:E:47:ALA:HB2	1:E:372:TRP:CE2	2.53	0.43
1:E:50:ALA:HB3	1:E:124:LEU:HD12	2.01	0.43
1:E:144:GLN:HE21	1:E:144:GLN:HB2	1.58	0.43
1:E:151:GLY:HA3	1:E:371:LEU:HG	2.01	0.43
1:G:79:ASN:HB3	1:G:82:SER:CB	2.48	0.43
1:G:198:LEU:HD22	1:G:227:CYS:HB3	1.99	0.43
1:G:278:VAL:HB	1:G:279:ASP:OD1	2.19	0.43
1:H:33:ARG:O	1:H:37:MET:CG	2.66	0.43
1:A:6:TYR:OH	1:A:11:ILE:HD13	2.18	0.43
1:A:144:GLN:HE21	1:A:144:GLN:HB2	1.70	0.43
1:B:3:LYS:HE3	1:B:3:LYS:N	2.31	0.43
1:C:4:LEU:HD13	1:C:99:PHE:CE1	2.48	0.43
1:C:365:VAL:O	1:C:369:ILE:HG13	2.19	0.43
1:E:180:ASN:O	1:E:180:ASN:ND2	2.52	0.43
1:G:75:TRP:CD1	1:G:76:SER:H	2.35	0.43
1:G:180:ASN:HA	1:G:185:LYS:HG3	1.99	0.43
1:G:308:LYS:H	1:G:308:LYS:CE	2.31	0.43
1:H:155:GLU:C	1:H:180:ASN:HB2	2.43	0.43
1:A:119:PHE:N	1:A:119:PHE:CD1	2.86	0.43
1:A:409:THR:H	1:A:412:GLN:HE21	1.66	0.43
1:B:162:ASN:O	1:B:166:MET:HG3	2.18	0.43
1:B:180:ASN:HA	1:B:185:LYS:CE	2.33	0.43
1:B:183:VAL:HG21	1:B:431:TYR:CE1	2.53	0.43
1:B:244:ASP:HB3	1:B:247:ASN:HB2	2.00	0.43
1:C:188:PHE:HA	1:C:192:TYR:CD2	2.53	0.43
1:D:32:MET:O	1:D:35:ARG:HB2	2.18	0.43
1:D:54:HIS:CE1	1:D:78:CYS:SG	3.12	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:4:LEU:HD11	1:E:111:TRP:HZ2	1.82	0.43
1:G:152:ILE:HG13	1:G:174:VAL:HG21	2.01	0.43
1:G:210:ILE:HB	1:G:234:PHE:HB3	2.00	0.43
1:H:2:ASP:HA	1:H:3:LYS:HE3	2.00	0.43
1:H:3:LYS:HB2	1:H:4:LEU:HD12	2.01	0.43
1:H:143:PRO:O	1:H:146:LEU:HB2	2.19	0.43
1:H:336:ILE:HG22	1:H:338:LEU:HD23	2.01	0.43
1:A:26:ASN:O	1:A:400:LYS:HE2	2.18	0.43
1:A:27:GLU:C	1:A:29:PRO:HD3	2.44	0.43
1:B:39:SER:O	1:B:42:LYS:HG2	2.18	0.43
1:C:2:ASP:HB3	1:C:3:LYS:H	1.55	0.43
1:C:3:LYS:HE3	1:C:3:LYS:N	2.32	0.43
1:C:183:VAL:HG21	1:C:431:TYR:CE1	2.54	0.43
1:D:310:LEU:HB3	1:D:327:TYR:CE2	2.53	0.43
1:F:209:MET:O	1:F:213:LYS:HD2	2.18	0.43
1:G:275:THR:O	1:G:304:GLU:OE2	2.36	0.43
1:G:387:LYS:HE2	1:G:431:TYR:OH	2.18	0.43
1:A:275:THR:HG22	1:A:276:GLY:H	1.82	0.43
1:A:415:TYR:OH	1:B:303:VAL:HG21	2.18	0.43
1:C:142:HIS:HB3	1:C:145:LEU:HG	2.00	0.43
1:C:419:PRO:HB2	1:C:422:GLY:HA3	2.01	0.43
1:D:101:TRP:HZ2	1:D:108:GLU:OE1	2.02	0.43
1:E:169:ASN:HB2	1:E:171:ILE:HG12	2.00	0.43
1:E:247:ASN:HD21	1:F:425:LYS:HE2	1.83	0.43
1:G:130:ASP:OD1	1:G:156:THR:HB	2.18	0.43
1:H:232:ARG:HH11	1:H:232:ARG:CG	2.25	0.43
1:H:342:ARG:O	1:H:343:LEU:C	2.62	0.43
1:A:334:ARG:O	1:A:335:ILE:HD13	2.19	0.43
1:B:101:TRP:HZ2	1:B:108:GLU:OE1	2.01	0.43
1:B:201:GLY:HA2	1:B:349:ALA:HB2	2.00	0.43
1:B:385:LEU:O	1:B:386:PRO:C	2.61	0.43
1:C:35:ARG:NH2	1:C:64:GLU:HB2	2.33	0.43
1:C:58:GLU:CD	1:C:58:GLU:H	2.27	0.43
1:C:345:ASN:O	1:C:349:ALA:HB3	2.18	0.43
1:C:430:ARG:HA	1:D:430:ARG:CD	2.40	0.43
1:D:124:LEU:HD11	1:D:138:ILE:CD1	2.48	0.43
1:D:208:VAL:HG22	1:D:209:MET:N	2.33	0.43
1:E:273:THR:OG1	1:E:297:ASN:OD1	2.33	0.43
1:F:257:GLU:HG3	1:G:237:ARG:CZ	2.48	0.43
1:G:91:ILE:HD13	1:G:91:ILE:HA	1.76	0.43
1:B:2:ASP:HB3	1:B:3:LYS:H	1.62	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:33:ARG:HE	1:B:36:GLU:CD	2.27	0.43
1:B:176:ALA:O	1:B:382:VAL:HA	2.19	0.43
1:B:182:SER:HB2	1:B:185:LYS:HB2	2.01	0.43
1:D:99:PHE:CD2	1:D:99:PHE:N	2.86	0.43
1:F:419:PRO:HB2	1:F:422:GLY:HA3	1.99	0.43
1:H:7:LYS:CD	1:H:101:TRP:HZ3	2.32	0.43
1:H:62:LEU:O	1:H:66:LEU:HG	2.19	0.43
1:H:391:GLU:OE2	1:H:423:PRO:HA	2.18	0.43
1:A:180:ASN:HA	1:A:185:LYS:CE	2.42	0.43
1:A:232:ARG:HH11	1:A:232:ARG:CG	2.31	0.43
1:A:388:LYS:HG2	1:A:423:PRO:CG	2.48	0.43
1:B:4:LEU:HD11	1:B:111:TRP:CH2	2.53	0.43
1:C:7:LYS:HE3	1:C:99:PHE:CB	2.47	0.43
1:C:105:THR:HG23	1:C:108:GLU:OE1	2.19	0.43
1:E:91:ILE:O	1:E:94:ALA:HB3	2.19	0.43
1:F:183:VAL:HG11	1:F:431:TYR:CG	2.54	0.43
1:G:105:THR:N	1:G:108:GLU:HB2	2.29	0.43
1:G:209:MET:O	1:G:213:LYS:HD2	2.19	0.43
1:G:287:GLU:HG3	1:G:309:TRP:CH2	2.54	0.43
1:B:297:ASN:OD1	1:B:304:GLU:HG3	2.18	0.42
1:C:182:SER:HB2	1:C:185:LYS:HB2	2.01	0.42
1:D:119:PHE:N	1:D:119:PHE:CD1	2.87	0.42
1:D:163:LEU:HD11	1:D:176:ALA:HB1	2.01	0.42
1:G:74:ARG:HD2	1:G:119:PHE:CE1	2.54	0.42
1:H:32:MET:HE1	1:H:35:ARG:HH11	1.84	0.42
1:A:57:VAL:HG23	1:A:84:GLN:NE2	2.34	0.42
1:C:44:LEU:HB3	1:C:71:ALA:HB2	2.01	0.42
1:C:105:THR:H	1:C:108:GLU:HB2	1.84	0.42
1:C:142:HIS:O	1:C:145:LEU:HG	2.19	0.42
1:D:142:HIS:HB3	1:D:145:LEU:HG	2.01	0.42
1:D:422:GLY:O	1:D:423:PRO:C	2.62	0.42
1:F:225:LYS:NZ	1:F:250:GLN:HE22	2.17	0.42
1:G:3:LYS:C	1:G:4:LEU:HD12	2.44	0.42
1:G:266:LYS:HG2	1:G:288:GLN:HG2	2.00	0.42
1:H:53:LEU:O	1:H:54:HIS:C	2.62	0.42
1:H:209:MET:O	1:H:213:LYS:HD2	2.19	0.42
1:H:315:VAL:HG23	1:H:330:LYS:HG2	2.01	0.42
1:A:208:VAL:HG22	1:A:209:MET:N	2.34	0.42
1:B:3:LYS:O	1:B:4:LEU:C	2.62	0.42
1:C:386:PRO:HG2	1:C:389:LEU:HG	2.01	0.42
1:D:375:PRO:C	1:D:377:LYS:N	2.77	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:342:ARG:HH11	1:E:342:ARG:CG	2.21	0.42
1:F:196:GLU:HA	1:H:234:PHE:CE1	2.52	0.42
1:F:321:LYS:HB2	1:F:322:PRO:HD2	2.01	0.42
1:G:54:HIS:HB3	1:G:82:SER:OG	2.19	0.42
1:H:163:LEU:HD11	1:H:176:ALA:HB1	2.01	0.42
1:A:79:ASN:HB3	1:A:82:SER:HB3	2.00	0.42
1:A:412:GLN:HG2	1:B:277:CYS:SG	2.60	0.42
1:B:3:LYS:CE	1:B:3:LYS:N	2.82	0.42
1:C:154:GLU:HG2	1:C:160:VAL:N	2.33	0.42
1:E:415:TYR:CE1	1:F:278:VAL:HG13	2.53	0.42
1:F:127:ILE:HG23	1:F:134:LEU:CD1	2.50	0.42
1:F:244:ASP:CG	1:F:247:ASN:HD22	2.27	0.42
1:H:208:VAL:HG11	1:H:294:ILE:CD1	2.49	0.42
1:B:355:PHE:CZ	1:B:401:LEU:HD21	2.55	0.42
1:C:53:LEU:O	1:C:54:HIS:C	2.63	0.42
1:E:7:LYS:HZ1	1:E:100:ALA:CA	2.32	0.42
1:E:21:LEU:O	1:E:25:GLU:N	2.53	0.42
1:E:240:ILE:HD12	1:E:256:TYR:HB3	2.01	0.42
1:F:37:MET:HG2	1:F:37:MET:H	1.66	0.42
1:F:141:LYS:C	1:F:143:PRO:HD3	2.45	0.42
1:G:153:SER:HB2	1:G:368:GLN:HE22	1.82	0.42
1:H:152:ILE:HG22	1:H:153:SER:N	2.34	0.42
1:H:321:LYS:HG2	1:H:324:VAL:CG2	2.50	0.42
1:B:101:TRP:CZ2	1:B:108:GLU:CD	2.98	0.42
1:C:28:MET:HE3	1:C:354:SER:O	2.18	0.42
1:C:198:LEU:HD22	1:C:227:CYS:CB	2.49	0.42
1:C:275:THR:CG2	1:C:276:GLY:H	2.32	0.42
1:D:146:LEU:HA	1:D:146:LEU:HD12	1.89	0.42
1:D:183:VAL:HG21	1:D:431:TYR:CE1	2.55	0.42
1:D:416:LEU:HB3	1:D:418:MET:HE3	2.01	0.42
1:E:6:TYR:CD1	1:E:6:TYR:C	2.98	0.42
1:E:221:GLY:O	1:E:225:LYS:HB2	2.19	0.42
1:E:326:ARG:HG3	1:E:336:ILE:HG12	2.00	0.42
1:F:7:LYS:NZ	1:F:101:TRP:CE3	2.65	0.42
1:F:152:ILE:CG2	1:F:153:SER:N	2.82	0.42
1:F:319:ASN:ND2	1:F:321:LYS:O	2.49	0.42
1:F:319:ASN:HD21	1:F:321:LYS:C	2.27	0.42
1:G:170:GLY:C	1:G:171:ILE:HD13	2.45	0.42
1:G:187:LYS:HD2	1:G:187:LYS:HA	1.87	0.42
1:G:188:PHE:HA	1:G:192:TYR:CD2	2.55	0.42
1:H:3:LYS:CD	1:H:3:LYS:N	2.82	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:365:VAL:O	1:B:369:ILE:HG13	2.20	0.42
1:F:2:ASP:OD2	1:F:118:HIS:HB2	2.20	0.42
1:F:101:TRP:CZ2	1:F:108:GLU:CD	2.94	0.42
1:F:180:ASN:HA	1:F:185:LYS:HE3	2.02	0.42
1:F:319:ASN:O	1:H:19:LYS:HE2	2.20	0.42
1:G:425:LYS:HE2	1:G:429:TYR:CE2	2.54	0.42
1:G:430:ARG:HH11	1:G:430:ARG:CG	2.33	0.42
1:H:221:GLY:O	1:H:222:ASP:C	2.63	0.42
1:H:278:VAL:HA	1:H:303:VAL:O	2.18	0.42
1:A:28:MET:HE3	1:A:354:SER:O	2.19	0.42
1:A:247:ASN:ND2	1:B:425:LYS:HE2	2.35	0.42
1:B:32:MET:O	1:B:36:GLU:HG3	2.20	0.42
1:C:152:ILE:HG22	1:C:153:SER:N	2.35	0.42
1:C:242:GLU:O	1:D:406:THR:HB	2.20	0.42
1:D:198:LEU:HD22	1:D:227:CYS:SG	2.59	0.42
1:E:38:TYR:HB2	1:E:69:LEU:CD1	2.48	0.42
1:E:302:ASP:HB2	1:E:341:GLY:O	2.19	0.42
1:F:4:LEU:HD23	1:F:7:LYS:HB3	2.00	0.42
1:F:157:THR:O	1:F:158:THR:C	2.61	0.42
1:F:342:ARG:O	1:F:343:LEU:C	2.62	0.42
1:G:101:TRP:CH2	1:G:108:GLU:HB3	2.55	0.42
1:G:116:THR:O	1:G:119:PHE:CE1	2.72	0.42
1:G:171:ILE:O	1:G:172:LEU:C	2.62	0.42
1:G:300:HIS:HB2	2:G:7432:NAD:O2D	2.20	0.42
1:G:300:HIS:N	2:G:7432:NAD:H1D	2.34	0.42
1:G:311:ASN:OD1	1:G:327:TYR:CE2	2.72	0.42
1:G:400:LYS:C	1:G:402:ASN:N	2.77	0.42
1:H:177:ILE:HD12	1:H:371:LEU:HD13	2.02	0.42
1:H:216:VAL:HG21	1:H:271:PHE:CE2	2.54	0.42
1:H:326:ARG:HD2	1:H:336:ILE:CG1	2.50	0.42
1:H:419:PRO:C	1:H:421:ASN:N	2.74	0.42
1:A:158:THR:O	1:A:161:HIS:HB3	2.19	0.42
1:A:184:THR:HA	1:A:188:PHE:CD1	2.55	0.42
1:A:265:CYS:HA	1:A:271:PHE:CE2	2.55	0.42
1:A:331:ASN:OD1	1:A:333:HIS:HB2	2.20	0.42
1:B:4:LEU:HD13	1:B:99:PHE:CE1	2.48	0.42
1:B:7:LYS:HG2	1:B:111:TRP:HZ3	1.84	0.42
1:B:419:PRO:HB2	1:B:422:GLY:CA	2.50	0.42
1:C:79:ASN:HB3	1:C:82:SER:OG	2.20	0.42
1:D:10:ASP:O	1:D:13:LEU:HB2	2.20	0.42
1:E:127:ILE:HG23	1:E:134:LEU:HD13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:257:GLU:HB2	1:H:237:ARG:NE	2.34	0.42
1:F:272:VAL:HA	1:F:296:CYS:O	2.20	0.42
1:G:370:GLU:O	1:G:371:LEU:C	2.63	0.42
1:H:155:GLU:OE2	1:H:360:SER:HB3	2.20	0.42
1:H:291:ASP:OD2	1:H:334:ARG:NH2	2.52	0.42
1:H:410:GLU:O	1:H:414:GLN:CG	2.68	0.42
1:H:425:LYS:HD2	1:H:429:TYR:CE1	2.55	0.42
1:H:430:ARG:O	1:H:431:TYR:C	2.63	0.42
1:A:80:ILE:HD11	1:A:342:ARG:HE	1.85	0.42
1:A:150:ARG:HE	1:A:150:ARG:HB2	1.67	0.42
1:C:302:ASP:CG	1:C:302:ASP:O	2.63	0.42
1:D:185:LYS:O	1:D:189:ASP:HB3	2.20	0.42
1:F:53:LEU:HB2	1:F:75:TRP:HZ2	1.83	0.42
1:F:316:GLU:O	1:F:328:LEU:N	2.49	0.42
1:F:373:THR:HG22	1:F:374:HIS:CE1	2.55	0.42
1:H:180:ASN:HA	1:H:185:LYS:HG3	2.02	0.42
1:H:339:ALA:HB2	1:H:348:CYS:SG	2.59	0.42
1:A:92:ALA:HB2	1:A:98:VAL:CG1	2.50	0.41
1:A:107:GLU:H	1:A:107:GLU:CD	2.28	0.41
1:A:120:LYS:HE2	1:A:120:LYS:N	2.19	0.41
1:B:7:LYS:CE	1:B:101:TRP:CE3	3.03	0.41
1:B:37:MET:HG2	1:B:37:MET:H	1.61	0.41
1:B:79:ASN:HB3	1:B:82:SER:HB3	2.02	0.41
1:B:208:VAL:HG22	1:B:209:MET:N	2.35	0.41
1:B:287:GLU:HG3	1:B:309:TRP:CZ2	2.55	0.41
1:C:21:LEU:O	1:C:25:GLU:HG3	2.19	0.41
1:C:99:PHE:CD2	1:C:99:PHE:N	2.87	0.41
1:C:223:VAL:CG1	1:C:274:THR:HB	2.50	0.41
1:C:375:PRO:C	1:C:377:LYS:N	2.78	0.41
1:D:105:THR:OG1	1:D:108:GLU:HG3	2.20	0.41
1:E:213:LYS:HG2	1:E:269:ASN:HB3	2.02	0.41
1:E:249:LEU:O	1:E:253:MET:HG2	2.19	0.41
1:E:278:VAL:HA	1:E:303:VAL:O	2.20	0.41
1:E:309:TRP:O	1:E:313:ASN:N	2.52	0.41
1:F:7:LYS:HZ1	1:F:100:ALA:CA	2.33	0.41
1:F:28:MET:HG2	1:F:354:SER:O	2.19	0.41
1:G:53:LEU:O	1:G:77:SER:HA	2.20	0.41
1:G:210:ILE:O	1:G:213:LYS:HB2	2.20	0.41
1:G:249:LEU:HD13	1:H:398:LEU:CD1	2.50	0.41
1:H:169:ASN:HB2	1:H:171:ILE:HG12	2.02	0.41
1:H:286:PHE:C	1:H:288:GLN:H	2.28	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:167:MET:HE3	1:B:380:VAL:C	2.45	0.41
1:C:105:THR:OG1	1:C:108:GLU:HG3	2.20	0.41
1:D:178:ASN:OD1	1:D:178:ASN:C	2.61	0.41
1:E:167:MET:HE3	1:E:380:VAL:O	2.20	0.41
1:F:80:ILE:O	1:F:103:GLY:N	2.47	0.41
1:F:111:TRP:O	1:F:115:GLN:HG2	2.20	0.41
1:F:180:ASN:OD1	1:F:185:LYS:NZ	2.45	0.41
1:G:203:LYS:HE2	1:G:210:ILE:HG12	2.02	0.41
1:G:223:VAL:O	1:G:224:GLY:C	2.63	0.41
1:G:388:LYS:HG2	1:G:423:PRO:HD3	2.02	0.41
1:H:142:HIS:N	1:H:143:PRO:CD	2.83	0.41
1:H:302:ASP:CG	1:H:302:ASP:O	2.63	0.41
1:H:389:LEU:O	1:H:392:ALA:HB3	2.20	0.41
1:A:209:MET:SD	1:C:356:VAL:HB	2.60	0.41
1:A:299:GLY:O	1:A:300:HIS:C	2.63	0.41
1:B:300:HIS:HA	1:B:343:LEU:HD11	2.03	0.41
1:B:388:LYS:HG2	1:B:423:PRO:HG3	2.02	0.41
1:C:131:GLY:HA3	1:C:300:HIS:NE2	2.35	0.41
1:E:157:THR:O	1:E:158:THR:C	2.62	0.41
1:E:188:PHE:O	1:E:356:VAL:HG21	2.19	0.41
1:E:414:GLN:O	1:E:415:TYR:C	2.63	0.41
1:F:27:GLU:O	1:F:355:PHE:HA	2.19	0.41
1:F:139:HIS:ND1	1:F:146:LEU:HD11	2.36	0.41
1:F:188:PHE:O	1:F:192:TYR:HB2	2.19	0.41
1:F:296:CYS:HB2	1:F:344:VAL:HG21	2.02	0.41
1:G:183:VAL:CG1	1:H:246:ILE:HG21	2.50	0.41
1:G:308:LYS:O	1:G:309:TRP:C	2.63	0.41
1:G:326:ARG:HH12	1:G:334:ARG:HD2	1.85	0.41
1:G:411:LYS:O	1:G:414:GLN:HB2	2.20	0.41
1:H:31:LEU:HD21	1:H:361:PHE:CB	2.50	0.41
1:H:35:ARG:CG	1:H:65:THR:OG1	2.68	0.41
1:H:138:ILE:CG2	1:H:146:LEU:HD12	2.50	0.41
1:H:154:GLU:HG3	1:H:160:VAL:CG2	2.50	0.41
1:A:419:PRO:HB2	1:A:422:GLY:CA	2.49	0.41
1:B:352:HIS:CE1	2:B:2432:NAD:H4N	2.56	0.41
1:C:91:ILE:O	1:C:94:ALA:HB3	2.21	0.41
1:D:33:ARG:O	1:D:37:MET:HG2	2.21	0.41
1:D:299:GLY:O	1:D:300:HIS:C	2.63	0.41
1:D:342:ARG:O	1:D:343:LEU:C	2.63	0.41
1:E:2:ASP:HB2	1:E:74:ARG:NH1	2.35	0.41
1:E:214:VAL:CG1	1:E:239:ILE:HD12	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:387:LYS:O	1:E:388:LYS:C	2.62	0.41
1:G:101:TRP:HZ2	1:G:108:GLU:OE1	2.02	0.41
1:G:217:VAL:HA	1:G:272:VAL:O	2.19	0.41
1:G:275:THR:HG23	2:G:7432:NAD:C8A	2.51	0.41
1:G:410:GLU:OE2	1:G:414:GLN:HG2	2.19	0.41
1:H:4:LEU:HD11	1:H:111:TRP:CZ2	2.55	0.41
1:H:101:TRP:HZ2	1:H:108:GLU:CD	2.27	0.41
1:H:158:THR:HG21	1:H:301:PHE:CD2	2.55	0.41
1:H:179:VAL:O	1:H:185:LYS:HG3	2.20	0.41
1:B:408:LEU:HD12	1:B:408:LEU:HA	1.91	0.41
1:D:81:PHE:CE2	1:D:342:ARG:HG3	2.55	0.41
1:E:100:ALA:HA	1:E:104:GLU:OE2	2.20	0.41
1:F:154:GLU:HG3	1:F:160:VAL:HG23	2.03	0.41
1:F:212:GLY:N	1:F:235:GLY:O	2.53	0.41
1:G:215:ALA:HB2	1:G:231:LEU:HD22	2.02	0.41
1:G:424:PHE:C	1:G:425:LYS:HG2	2.44	0.41
1:G:429:TYR:CE2	1:G:431:TYR:HA	2.55	0.41
1:H:42:LYS:N	1:H:43:PRO:CD	2.84	0.41
1:H:154:GLU:HG3	1:H:160:VAL:N	2.35	0.41
1:H:308:LYS:CE	1:H:308:LYS:N	2.76	0.41
1:H:321:LYS:O	1:H:322:PRO:C	2.61	0.41
1:A:362:THR:CG2	1:A:393:VAL:HG22	2.50	0.41
1:B:7:LYS:HE2	1:B:101:TRP:CZ3	2.54	0.41
1:C:2:ASP:CB	1:C:74:ARG:HH12	2.31	0.41
1:D:7:LYS:CE	1:D:101:TRP:CE3	3.04	0.41
1:D:57:VAL:O	1:D:60:ALA:HB3	2.20	0.41
1:D:178:ASN:ND2	1:D:181:ASP:HB2	2.35	0.41
1:D:250:GLN:O	1:D:254:GLU:HG2	2.20	0.41
1:E:142:HIS:HB3	1:E:145:LEU:CD1	2.51	0.41
1:E:213:LYS:HG2	1:E:269:ASN:CB	2.51	0.41
1:F:313:ASN:HD22	1:F:313:ASN:N	2.19	0.41
1:G:104:GLU:OE1	1:G:109:TYR:HA	2.20	0.41
1:H:128:LEU:HG	1:H:364:GLN:HE22	1.86	0.41
1:A:2:ASP:CA	1:A:3:LYS:HE3	2.51	0.41
1:A:127:ILE:HD11	1:A:138:ILE:HD12	2.02	0.41
1:B:27:GLU:O	1:B:355:PHE:HA	2.20	0.41
1:B:80:ILE:HD11	1:B:342:ARG:HE	1.86	0.41
1:B:175:PRO:HA	1:B:381:GLY:H	1.85	0.41
1:B:206:THR:HG23	1:B:338:LEU:HD21	2.02	0.41
1:B:265:CYS:HA	1:B:271:PHE:CE2	2.55	0.41
1:C:150:ARG:HE	1:C:150:ARG:HB2	1.65	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:375:PRO:C	1:C:377:LYS:H	2.28	0.41
1:D:105:THR:O	1:D:106:ASP:C	2.63	0.41
1:D:167:MET:HE3	1:D:381:GLY:N	2.35	0.41
1:D:297:ASN:OD1	1:D:304:GLU:HG3	2.21	0.41
1:E:80:ILE:HB	1:E:104:GLU:O	2.21	0.41
1:E:125:ASN:ND2	1:E:372:TRP:CH2	2.89	0.41
1:E:313:ASN:O	1:E:330:LYS:HE3	2.21	0.41
1:E:375:PRO:C	1:E:377:LYS:N	2.78	0.41
1:F:11:ILE:O	1:F:11:ILE:HG13	2.20	0.41
1:G:81:PHE:CD2	1:G:342:ARG:HG3	2.55	0.41
1:H:297:ASN:OD1	1:H:298:ILE:N	2.54	0.41
1:B:59:THR:O	1:B:63:ILE:HG13	2.21	0.41
1:B:299:GLY:O	1:B:300:HIS:C	2.64	0.41
1:B:344:VAL:HG13	1:B:345:ASN:N	2.36	0.41
1:C:13:LEU:HD12	1:C:13:LEU:HA	1.94	0.41
1:D:30:GLY:HA3	1:D:362:THR:OG1	2.21	0.41
1:D:32:MET:O	1:D:36:GLU:HG3	2.20	0.41
1:D:59:THR:O	1:D:63:ILE:HG13	2.21	0.41
1:D:79:ASN:HB3	1:D:82:SER:OG	2.20	0.41
1:D:91:ILE:CG2	1:D:96:ILE:HB	2.50	0.41
1:D:378:TYR:HD2	1:D:383:HIS:ND1	2.18	0.41
1:E:4:LEU:HD11	1:E:111:TRP:CH2	2.56	0.41
1:E:53:LEU:HA	1:E:78:CYS:SG	2.60	0.41
1:E:386:PRO:O	1:E:389:LEU:HB2	2.20	0.41
1:F:63:ILE:HD11	1:F:75:TRP:CG	2.55	0.41
1:F:75:TRP:CD1	1:F:76:SER:H	2.39	0.41
1:F:362:THR:HG22	1:F:393:VAL:HG22	2.03	0.41
1:F:386:PRO:HG2	1:F:389:LEU:HG	2.03	0.41
1:G:28:MET:HB3	1:G:358:SER:CB	2.51	0.41
1:G:42:LYS:C	1:G:44:LEU:H	2.28	0.41
1:G:58:GLU:HG3	1:G:354:SER:HA	2.01	0.41
1:G:152:ILE:HD12	1:G:174:VAL:HG22	2.03	0.41
1:G:278:VAL:HG22	1:H:415:TYR:CG	2.56	0.41
1:H:29:PRO:HD2	1:H:397:HIS:HD2	1.84	0.41
1:A:275:THR:HG21	1:A:277:CYS:HB3	2.03	0.41
1:A:302:ASP:O	1:A:302:ASP:CG	2.64	0.41
1:A:337:LEU:HD22	1:A:338:LEU:N	2.35	0.41
1:B:430:ARG:NH2	4:B:9213:HOH:O	2.54	0.41
1:C:27:GLU:C	1:C:29:PRO:HD3	2.46	0.41
1:C:35:ARG:HH22	1:C:64:GLU:HB2	1.84	0.41
1:C:299:GLY:O	1:C:300:HIS:C	2.64	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:385:LEU:O	1:C:386:PRO:C	2.63	0.41
1:D:326:ARG:HG2	1:D:326:ARG:HH11	1.86	0.41
1:D:337:LEU:HD22	1:D:338:LEU:N	2.36	0.41
1:D:339:ALA:HB2	1:D:348:CYS:SG	2.61	0.41
1:E:124:LEU:O	1:E:124:LEU:HD23	2.21	0.41
1:E:178:ASN:ND2	1:E:384:PHE:CE1	2.85	0.41
1:E:184:THR:HB	1:E:359:ASN:ND2	2.36	0.41
1:E:296:CYS:O	1:E:305:ILE:HD11	2.20	0.41
1:F:195:ARG:O	1:H:234:PHE:HE1	2.04	0.41
1:F:202:ILE:O	1:F:206:THR:HG23	2.20	0.41
1:F:361:PHE:O	1:F:365:VAL:HG23	2.21	0.41
1:G:40:ALA:O	1:G:42:LYS:HG2	2.21	0.41
1:G:105:THR:O	1:G:106:ASP:C	2.63	0.41
1:G:129:ASP:OD2	1:G:135:THR:CG2	2.67	0.41
1:G:138:ILE:O	1:G:142:HIS:C	2.64	0.41
1:G:164:TYR:CZ	1:G:382:VAL:HG21	2.55	0.41
1:G:206:THR:OG1	1:G:208:VAL:HG12	2.20	0.41
1:G:430:ARG:HD3	1:H:430:ARG:CA	2.44	0.41
1:H:137:LEU:O	1:H:141:LYS:HB2	2.21	0.41
1:A:124:LEU:HD11	1:A:138:ILE:CD1	2.51	0.41
1:A:430:ARG:CD	1:B:430:ARG:HA	2.42	0.41
1:B:7:LYS:HE3	1:B:99:PHE:C	2.45	0.41
1:B:11:ILE:C	1:B:13:LEU:H	2.28	0.41
1:C:206:THR:HG23	1:C:338:LEU:HD21	2.03	0.41
1:D:6:TYR:CD1	1:D:6:TYR:C	2.98	0.41
1:D:7:LYS:HE2	1:D:101:TRP:CZ3	2.56	0.41
1:D:13:LEU:HD12	1:D:13:LEU:HA	1.87	0.41
1:D:386:PRO:O	1:D:389:LEU:HB2	2.21	0.41
1:D:419:PRO:HB2	1:D:422:GLY:CA	2.51	0.41
1:E:33:ARG:O	1:E:33:ARG:NH2	2.54	0.41
1:E:107:GLU:CD	1:E:107:GLU:H	2.29	0.41
1:E:107:GLU:CD	1:E:107:GLU:N	2.79	0.41
1:E:160:VAL:HG11	1:E:178:ASN:ND2	2.35	0.41
1:E:300:HIS:HA	1:E:343:LEU:CD1	2.50	0.41
1:F:91:ILE:O	1:F:94:ALA:HB3	2.21	0.41
1:G:7:LYS:CE	1:G:101:TRP:CZ3	3.03	0.41
1:G:113:ILE:HG22	1:G:137:LEU:HD23	2.02	0.41
1:G:138:ILE:O	1:G:142:HIS:N	2.54	0.41
1:G:322:PRO:O	1:G:323:GLN:HB2	2.21	0.41
1:H:199:ILE:H	1:H:199:ILE:HG12	1.62	0.41
1:H:279:ASP:OD1	1:H:279:ASP:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:399:GLY:O	1:H:402:ASN:N	2.49	0.41
1:B:119:PHE:N	1:B:119:PHE:CD1	2.89	0.40
1:B:308:LYS:H	1:B:308:LYS:CE	2.34	0.40
1:E:44:LEU:HD12	1:E:69:LEU:CB	2.50	0.40
1:E:188:PHE:HA	1:E:192:TYR:HD2	1.85	0.40
1:E:196:GLU:HA	1:G:234:PHE:CE1	2.56	0.40
1:E:408:LEU:HG	1:E:412:GLN:HB3	2.04	0.40
1:F:51:GLY:HA3	1:F:75:TRP:CE3	2.56	0.40
1:F:101:TRP:O	1:F:104:GLU:HG3	2.21	0.40
1:F:343:LEU:HG	2:F:6432:NAD:N7N	2.36	0.40
1:G:386:PRO:O	1:G:387:LYS:C	2.64	0.40
1:H:44:LEU:CD1	1:H:71:ALA:HB2	2.49	0.40
1:A:2:ASP:HB3	1:A:3:LYS:H	1.58	0.40
1:A:37:MET:HB3	1:H:284:ARG:CZ	2.50	0.40
1:A:142:HIS:O	1:A:145:LEU:HG	2.21	0.40
1:A:247:ASN:HD21	1:B:425:LYS:HE2	1.86	0.40
1:A:430:ARG:CZ	1:B:183:VAL:HG22	2.51	0.40
1:C:3:LYS:O	1:C:4:LEU:C	2.64	0.40
1:C:4:LEU:HD11	1:C:111:TRP:CH2	2.56	0.40
1:C:11:ILE:C	1:C:13:LEU:H	2.29	0.40
1:C:125:ASN:ND2	1:C:372:TRP:CH2	2.90	0.40
1:C:278:VAL:HA	1:C:303:VAL:O	2.22	0.40
1:C:352:HIS:CE1	2:C:3432:NAD:H4N	2.57	0.40
1:D:32:MET:HA	1:D:35:ARG:HD2	2.03	0.40
1:D:369:ILE:O	1:D:373:THR:CB	2.69	0.40
1:E:59:THR:HA	1:E:361:PHE:CE2	2.57	0.40
1:E:125:ASN:HA	1:E:148:GLY:O	2.22	0.40
1:E:317:LYS:HD2	1:E:327:TYR:CE2	2.57	0.40
1:F:19:LYS:HE2	1:H:319:ASN:O	2.22	0.40
1:F:359:ASN:O	1:F:363:ASN:ND2	2.48	0.40
1:F:416:LEU:CB	1:F:418:MET:HG2	2.52	0.40
1:G:5:PRO:O	1:G:6:TYR:HB3	2.22	0.40
1:G:16:TRP:O	1:G:19:LYS:HB2	2.21	0.40
1:G:243:ILE:HG22	1:H:406:THR:O	2.20	0.40
1:B:164:TYR:CZ	1:B:382:VAL:HG21	2.56	0.40
1:D:387:LYS:HE2	1:D:431:TYR:OH	2.21	0.40
1:E:142:HIS:N	1:E:143:PRO:CD	2.83	0.40
1:F:31:LEU:HD13	1:F:61:VAL:HG12	2.03	0.40
1:F:32:MET:O	1:F:36:GLU:HG3	2.21	0.40
1:G:35:ARG:HG2	1:G:65:THR:HG23	2.03	0.40
1:G:249:LEU:HB3	1:H:188:PHE:HE2	1.85	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:275:THR:CG2	1:G:277:CYS:H	2.17	0.40
1:A:154:GLU:CG	1:A:160:VAL:HG23	2.51	0.40
1:A:160:VAL:HG21	1:A:178:ASN:OD1	2.22	0.40
1:A:358:SER:CB	1:A:397:HIS:NE2	2.84	0.40
1:B:6:TYR:CD1	1:B:6:TYR:C	2.99	0.40
1:B:124:LEU:HD11	1:B:138:ILE:HD11	2.03	0.40
1:B:144:GLN:HE21	1:B:144:GLN:HB2	1.55	0.40
1:B:178:ASN:CG	1:B:181:ASP:HB2	2.47	0.40
1:C:92:ALA:HB2	1:C:98:VAL:CG1	2.52	0.40
1:C:225:LYS:NZ	1:C:250:GLN:NE2	2.70	0.40
1:D:198:LEU:HD22	1:D:227:CYS:CB	2.52	0.40
1:D:232:ARG:HH11	1:D:232:ARG:CG	2.33	0.40
1:D:369:ILE:O	1:D:373:THR:HB	2.21	0.40
1:E:129:ASP:OD1	1:E:130:ASP:N	2.53	0.40
1:F:13:LEU:HB3	1:F:86:HIS:HA	2.03	0.40
1:F:37:MET:HE2	1:F:38:TYR:CZ	2.56	0.40
1:F:146:LEU:HA	1:F:146:LEU:HD12	1.91	0.40
1:G:4:LEU:CD1	1:G:99:PHE:HE1	2.33	0.40
1:G:57:VAL:O	1:G:61:VAL:HG23	2.21	0.40
1:B:254:GLU:OE1	1:B:254:GLU:HA	2.21	0.40
1:B:369:ILE:O	1:B:373:THR:HB	2.21	0.40
1:D:2:ASP:CB	1:D:3:LYS:HE3	2.52	0.40
1:D:184:THR:HA	1:D:188:PHE:CD1	2.56	0.40
1:D:201:GLY:HA2	1:D:349:ALA:HB2	2.02	0.40
1:E:160:VAL:HG11	1:E:178:ASN:CG	2.46	0.40
1:F:57:VAL:CG2	1:F:87:ALA:HB2	2.51	0.40
1:F:152:ILE:HB	1:F:176:ALA:CB	2.50	0.40
1:F:279:ASP:HA	1:F:282:LEU:HD11	2.02	0.40
1:G:81:PHE:HE2	1:G:342:ARG:HE	1.69	0.40
1:G:120:LYS:CD	1:G:120:LYS:H	2.35	0.40
1:G:342:ARG:H	1:G:342:ARG:HG2	1.45	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	428/431 (99%)	399 (93%)	27 (6%)	2 (0%)	24	60
1	B	428/431 (99%)	395 (92%)	30 (7%)	3 (1%)	18	53
1	C	428/431 (99%)	401 (94%)	23 (5%)	4 (1%)	14	48
1	D	428/431 (99%)	402 (94%)	25 (6%)	1 (0%)	43	76
1	E	428/431 (99%)	395 (92%)	28 (6%)	5 (1%)	10	40
1	F	428/431 (99%)	395 (92%)	29 (7%)	4 (1%)	14	48
1	G	428/431 (99%)	394 (92%)	30 (7%)	4 (1%)	14	48
1	H	428/431 (99%)	400 (94%)	27 (6%)	1 (0%)	43	76
All	All	3424/3448 (99%)	3181 (93%)	219 (6%)	24 (1%)	18	53

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	4	LEU
1	F	212	GLY
1	B	300	HIS
1	C	300	HIS
1	D	300	HIS
1	E	147	SER
1	G	4	LEU
1	G	376	ASP
1	A	300	HIS
1	C	376	ASP
1	E	300	HIS
1	E	376	ASP
1	E	375	PRO
1	F	422	GLY
1	G	157	THR
1	C	4	LEU
1	C	147	SER
1	G	97	PRO
1	A	4	LEU
1	B	4	LEU
1	E	422	GLY
1	F	97	PRO
1	B	422	GLY
1	H	422	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	353/353 (100%)	283 (80%)	70 (20%)	1	8
1	B	353/353 (100%)	279 (79%)	74 (21%)	1	6
1	C	353/353 (100%)	283 (80%)	70 (20%)	1	8
1	D	353/353 (100%)	278 (79%)	75 (21%)	1	6
1	E	353/353 (100%)	277 (78%)	76 (22%)	1	6
1	F	353/353 (100%)	276 (78%)	77 (22%)	1	6
1	G	353/353 (100%)	269 (76%)	84 (24%)	1	4
1	H	353/353 (100%)	259 (73%)	94 (27%)	0	3
All	All	2824/2824 (100%)	2204 (78%)	620 (22%)	1	5

All (620) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASP
1	A	3	LYS
1	A	4	LEU
1	A	7	LYS
1	A	11	ILE
1	A	13	LEU
1	A	27	GLU
1	A	33	ARG
1	A	37	MET
1	A	39	SER
1	A	41	SER
1	A	53	LEU
1	A	73	VAL
1	A	83	THR
1	A	84	GLN
1	A	86	HIS
1	A	93	LYS
1	A	110	LEU
1	A	120	LYS

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Mol	Chain	Res	Type
1	A	121	ASP
1	A	134	LEU
1	A	136	ASN
1	A	140	THR
1	A	144	GLN
1	A	145	LEU
1	A	146	LEU
1	A	147	SER
1	A	153	SER
1	A	155	GLU
1	A	156	THR
1	A	158	THR
1	A	162	ASN
1	A	165	LYS
1	A	169	ASN
1	A	172	LEU
1	A	174	VAL
1	A	180	ASN
1	A	184	THR
1	A	185	LYS
1	A	186	SER
1	A	187	LYS
1	A	200	ASP
1	A	207	ASP
1	A	232	ARG
1	A	240	ILE
1	A	243	ILE
1	A	259	THR
1	A	266	LYS
1	A	282	LEU
1	A	288	GLN
1	A	304	GLU
1	A	308	LYS
1	A	315	VAL
1	A	317	LYS
1	A	321	LYS
1	A	326	ARG
1	A	337	LEU
1	A	343	LEU
1	A	359	ASN
1	A	362	THR
1	A	371	LEU

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Mol	Chain	Res	Type
1	A	382	VAL
1	A	385	LEU
1	A	388	LYS
1	A	390	ASP
1	A	398	LEU
1	A	402	ASN
1	A	404	LYS
1	A	408	LEU
1	A	410	GLU
1	B	2	ASP
1	B	3	LYS
1	B	4	LEU
1	B	7	LYS
1	B	11	ILE
1	B	13	LEU
1	B	27	GLU
1	B	33	ARG
1	B	39	SER
1	B	41	SER
1	B	53	LEU
1	B	73	VAL
1	B	83	THR
1	B	84	GLN
1	B	93	LYS
1	B	98	VAL
1	B	110	LEU
1	B	120	LYS
1	B	121	ASP
1	B	134	LEU
1	B	135	THR
1	B	136	ASN
1	B	140	THR
1	B	144	GLN
1	B	145	LEU
1	B	146	LEU
1	B	147	SER
1	B	150	ARG
1	B	153	SER
1	B	155	GLU
1	B	156	THR
1	B	158	THR
1	B	162	ASN

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Mol	Chain	Res	Type
1	B	165	LYS
1	B	169	ASN
1	B	172	LEU
1	B	174	VAL
1	B	177	ILE
1	B	180	ASN
1	B	185	LYS
1	B	186	SER
1	B	187	LYS
1	B	200	ASP
1	B	204	ARG
1	B	207	ASP
1	B	209	MET
1	B	232	ARG
1	B	240	ILE
1	B	243	ILE
1	B	259	THR
1	B	266	LYS
1	B	282	LEU
1	B	288	GLN
1	B	304	GLU
1	B	308	LYS
1	B	315	VAL
1	B	321	LYS
1	B	326	ARG
1	B	337	LEU
1	B	342	ARG
1	B	343	LEU
1	B	359	ASN
1	B	364	GLN
1	B	371	LEU
1	B	382	VAL
1	B	385	LEU
1	B	388	LYS
1	B	390	ASP
1	B	398	LEU
1	B	402	ASN
1	B	404	LYS
1	B	407	LYS
1	B	408	LEU
1	B	410	GLU
1	C	2	ASP

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Mol	Chain	Res	Type
1	C	3	LYS
1	C	4	LEU
1	C	7	LYS
1	C	13	LEU
1	C	27	GLU
1	C	33	ARG
1	C	39	SER
1	C	41	SER
1	C	53	LEU
1	C	73	VAL
1	C	83	THR
1	C	84	GLN
1	C	93	LYS
1	C	98	VAL
1	C	110	LEU
1	C	120	LYS
1	C	121	ASP
1	C	134	LEU
1	C	135	THR
1	C	136	ASN
1	C	144	GLN
1	C	145	LEU
1	C	146	LEU
1	C	147	SER
1	C	150	ARG
1	C	153	SER
1	C	155	GLU
1	C	156	THR
1	C	158	THR
1	C	162	ASN
1	C	165	LYS
1	C	167	MET
1	C	169	ASN
1	C	172	LEU
1	C	174	VAL
1	C	177	ILE
1	C	180	ASN
1	C	184	THR
1	C	185	LYS
1	C	186	SER
1	C	187	LYS
1	C	200	ASP

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Mol	Chain	Res	Type
1	C	207	ASP
1	C	209	MET
1	C	232	ARG
1	C	240	ILE
1	C	243	ILE
1	C	259	THR
1	C	266	LYS
1	C	282	LEU
1	C	288	GLN
1	C	304	GLU
1	C	308	LYS
1	C	315	VAL
1	C	321	LYS
1	C	326	ARG
1	C	337	LEU
1	C	343	LEU
1	C	364	GLN
1	C	371	LEU
1	C	382	VAL
1	C	385	LEU
1	C	388	LYS
1	C	390	ASP
1	C	398	LEU
1	C	402	ASN
1	C	408	LEU
1	C	410	GLU
1	C	411	LYS
1	D	2	ASP
1	D	3	LYS
1	D	4	LEU
1	D	7	LYS
1	D	11	ILE
1	D	13	LEU
1	D	27	GLU
1	D	33	ARG
1	D	37	MET
1	D	39	SER
1	D	41	SER
1	D	53	LEU
1	D	73	VAL
1	D	83	THR
1	D	84	GLN

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Mol	Chain	Res	Type
1	D	86	HIS
1	D	93	LYS
1	D	110	LEU
1	D	120	LYS
1	D	121	ASP
1	D	134	LEU
1	D	135	THR
1	D	136	ASN
1	D	140	THR
1	D	141	LYS
1	D	144	GLN
1	D	145	LEU
1	D	146	LEU
1	D	147	SER
1	D	153	SER
1	D	155	GLU
1	D	156	THR
1	D	158	THR
1	D	162	ASN
1	D	165	LYS
1	D	169	ASN
1	D	172	LEU
1	D	174	VAL
1	D	180	ASN
1	D	182	SER
1	D	184	THR
1	D	185	LYS
1	D	186	SER
1	D	187	LYS
1	D	200	ASP
1	D	204	ARG
1	D	207	ASP
1	D	232	ARG
1	D	240	ILE
1	D	243	ILE
1	D	259	THR
1	D	266	LYS
1	D	282	LEU
1	D	288	GLN
1	D	304	GLU
1	D	308	LYS
1	D	315	VAL

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Mol	Chain	Res	Type
1	D	321	LYS
1	D	326	ARG
1	D	337	LEU
1	D	343	LEU
1	D	359	ASN
1	D	364	GLN
1	D	371	LEU
1	D	382	VAL
1	D	385	LEU
1	D	387	LYS
1	D	388	LYS
1	D	390	ASP
1	D	398	LEU
1	D	402	ASN
1	D	404	LYS
1	D	408	LEU
1	D	409	THR
1	D	410	GLU
1	E	4	LEU
1	E	7	LYS
1	E	13	LEU
1	E	26	ASN
1	E	32	MET
1	E	33	ARG
1	E	39	SER
1	E	45	LYS
1	E	53	LEU
1	E	55	MET
1	E	62	LEU
1	E	86	HIS
1	E	91	ILE
1	E	93	LYS
1	E	110	LEU
1	E	116	THR
1	E	120	LYS
1	E	121	ASP
1	E	124	LEU
1	E	134	LEU
1	E	135	THR
1	E	136	ASN
1	E	140	THR
1	E	144	GLN

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Mol	Chain	Res	Type
1	E	146	LEU
1	E	153	SER
1	E	154	GLU
1	E	155	GLU
1	E	157	THR
1	E	158	THR
1	E	162	ASN
1	E	163	LEU
1	E	165	LYS
1	E	167	MET
1	E	169	ASN
1	E	172	LEU
1	E	174	VAL
1	E	185	LYS
1	E	186	SER
1	E	204	ARG
1	E	207	ASP
1	E	213	LYS
1	E	241	THR
1	E	243	ILE
1	E	259	THR
1	E	266	LYS
1	E	281	ILE
1	E	282	LEU
1	E	288	GLN
1	E	304	GLU
1	E	308	LYS
1	E	315	VAL
1	E	317	LYS
1	E	319	ASN
1	E	326	ARG
1	E	328	LEU
1	E	334	ARG
1	E	337	LEU
1	E	342	ARG
1	E	343	LEU
1	E	359	ASN
1	E	360	SER
1	E	370	GLU
1	E	371	LEU
1	E	382	VAL
1	E	385	LEU

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Mol	Chain	Res	Type
1	E	387	LYS
1	E	388	LYS
1	E	390	ASP
1	E	398	LEU
1	E	402	ASN
1	E	408	LEU
1	E	409	THR
1	E	410	GLU
1	E	412	GLN
1	E	414	GLN
1	F	2	ASP
1	F	3	LYS
1	F	4	LEU
1	F	7	LYS
1	F	13	LEU
1	F	26	ASN
1	F	33	ARG
1	F	39	SER
1	F	41	SER
1	F	53	LEU
1	F	69	LEU
1	F	73	VAL
1	F	74	ARG
1	F	76	SER
1	F	84	GLN
1	F	96	ILE
1	F	98	VAL
1	F	110	LEU
1	F	120	LYS
1	F	121	ASP
1	F	128	LEU
1	F	134	LEU
1	F	135	THR
1	F	136	ASN
1	F	140	THR
1	F	141	LYS
1	F	144	GLN
1	F	146	LEU
1	F	155	GLU
1	F	156	THR
1	F	157	THR
1	F	162	ASN

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Mol	Chain	Res	Type
1	F	165	LYS
1	F	167	MET
1	F	172	LEU
1	F	173	LYS
1	F	174	VAL
1	F	177	ILE
1	F	184	THR
1	F	185	LYS
1	F	198	LEU
1	F	203	LYS
1	F	206	THR
1	F	207	ASP
1	F	209	MET
1	F	213	LYS
1	F	234	PHE
1	F	240	ILE
1	F	243	ILE
1	F	259	THR
1	F	272	VAL
1	F	278	VAL
1	F	280	ILE
1	F	282	LEU
1	F	284	ARG
1	F	288	GLN
1	F	292	ASP
1	F	297	ASN
1	F	304	GLU
1	F	308	LYS
1	F	320	ILE
1	F	326	ARG
1	F	330	LYS
1	F	337	LEU
1	F	340	GLU
1	F	342	ARG
1	F	344	VAL
1	F	371	LEU
1	F	382	VAL
1	F	385	LEU
1	F	388	LYS
1	F	390	ASP
1	F	401	LEU
1	F	402	ASN

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Mol	Chain	Res	Type
1	F	407	LYS
1	F	408	LEU
1	F	410	GLU
1	G	2	ASP
1	G	3	LYS
1	G	4	LEU
1	G	7	LYS
1	G	13	LEU
1	G	27	GLU
1	G	32	MET
1	G	33	ARG
1	G	37	MET
1	G	39	SER
1	G	41	SER
1	G	45	LYS
1	G	53	LEU
1	G	64	GLU
1	G	91	ILE
1	G	93	LYS
1	G	99	PHE
1	G	104	GLU
1	G	110	LEU
1	G	119	PHE
1	G	120	LYS
1	G	121	ASP
1	G	128	LEU
1	G	134	LEU
1	G	135	THR
1	G	136	ASN
1	G	139	HIS
1	G	141	LYS
1	G	144	GLN
1	G	146	LEU
1	G	147	SER
1	G	153	SER
1	G	155	GLU
1	G	156	THR
1	G	158	THR
1	G	160	VAL
1	G	162	ASN
1	G	165	LYS
1	G	167	MET

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Mol	Chain	Res	Type
1	G	172	LEU
1	G	174	VAL
1	G	180	ASN
1	G	185	LYS
1	G	186	SER
1	G	187	LYS
1	G	190	ASN
1	G	197	SER
1	G	200	ASP
1	G	207	ASP
1	G	209	MET
1	G	240	ILE
1	G	241	THR
1	G	259	THR
1	G	266	LYS
1	G	272	VAL
1	G	273	THR
1	G	279	ASP
1	G	281	ILE
1	G	282	LEU
1	G	295	VAL
1	G	297	ASN
1	G	304	GLU
1	G	308	LYS
1	G	321	LYS
1	G	324	VAL
1	G	326	ARG
1	G	334	ARG
1	G	337	LEU
1	G	342	ARG
1	G	371	LEU
1	G	377	LYS
1	G	382	VAL
1	G	385	LEU
1	G	387	LYS
1	G	388	LYS
1	G	390	ASP
1	G	395	GLU
1	G	397	HIS
1	G	400	LYS
1	G	402	ASN
1	G	403	VAL

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Mol	Chain	Res	Type
1	G	410	GLU
1	G	414	GLN
1	G	418	MET
1	H	3	LYS
1	H	4	LEU
1	H	7	LYS
1	H	13	LEU
1	H	18	ARG
1	H	21	LEU
1	H	26	ASN
1	H	33	ARG
1	H	34	MET
1	H	36	GLU
1	H	39	SER
1	H	41	SER
1	H	44	LEU
1	H	53	LEU
1	H	61	VAL
1	H	62	LEU
1	H	65	THR
1	H	74	ARG
1	H	84	GLN
1	H	86	HIS
1	H	93	LYS
1	H	104	GLU
1	H	110	LEU
1	H	116	THR
1	H	119	PHE
1	H	120	LYS
1	H	121	ASP
1	H	134	LEU
1	H	135	THR
1	H	138	ILE
1	H	140	THR
1	H	141	LYS
1	H	142	HIS
1	H	144	GLN
1	H	147	SER
1	H	153	SER
1	H	154	GLU
1	H	155	GLU
1	H	157	THR

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Mol	Chain	Res	Type
1	H	158	THR
1	H	162	ASN
1	H	163	LEU
1	H	165	LYS
1	H	167	MET
1	H	169	ASN
1	H	172	LEU
1	H	173	LYS
1	H	174	VAL
1	H	177	ILE
1	H	182	SER
1	H	185	LYS
1	H	186	SER
1	H	187	LYS
1	H	196	GLU
1	H	198	LEU
1	H	199	ILE
1	H	204	ARG
1	H	207	ASP
1	H	232	ARG
1	H	240	ILE
1	H	243	ILE
1	H	259	THR
1	H	277	CYS
1	H	279	ASP
1	H	281	ILE
1	H	282	LEU
1	H	288	GLN
1	H	295	VAL
1	H	297	ASN
1	H	304	GLU
1	H	308	LYS
1	H	315	VAL
1	H	317	LYS
1	H	321	LYS
1	H	324	VAL
1	H	325	ASP
1	H	326	ARG
1	H	342	ARG
1	H	343	LEU
1	H	346	LEU
1	H	356	VAL

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Mol	Chain	Res	Type
1	H	362	THR
1	H	364	GLN
1	H	371	LEU
1	H	377	LYS
1	H	382	VAL
1	H	385	LEU
1	H	388	LYS
1	H	390	ASP
1	H	398	LEU
1	H	402	ASN
1	H	409	THR
1	H	410	GLU
1	H	418	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (106) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	26	ASN
1	A	79	ASN
1	A	84	GLN
1	A	144	GLN
1	A	247	ASN
1	A	250	GLN
1	A	269	ASN
1	A	359	ASN
1	A	364	GLN
1	A	374	HIS
1	A	383	HIS
1	A	412	GLN
1	A	414	GLN
1	B	26	ASN
1	B	79	ASN
1	B	84	GLN
1	B	118	HIS
1	B	144	GLN
1	B	247	ASN
1	B	250	GLN
1	B	269	ASN
1	B	364	GLN
1	B	383	HIS
1	B	412	GLN
1	B	414	GLN

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Mol	Chain	Res	Type
1	C	26	ASN
1	C	79	ASN
1	C	84	GLN
1	C	118	HIS
1	C	144	GLN
1	C	247	ASN
1	C	250	GLN
1	C	269	ASN
1	C	352	HIS
1	C	359	ASN
1	C	364	GLN
1	C	383	HIS
1	C	412	GLN
1	C	414	GLN
1	D	26	ASN
1	D	79	ASN
1	D	84	GLN
1	D	144	GLN
1	D	247	ASN
1	D	250	GLN
1	D	269	ASN
1	D	288	GLN
1	D	364	GLN
1	D	383	HIS
1	D	412	GLN
1	D	414	GLN
1	E	26	ASN
1	E	84	GLN
1	E	115	GLN
1	E	118	HIS
1	E	144	GLN
1	E	229	GLN
1	E	269	ASN
1	E	288	GLN
1	E	319	ASN
1	E	333	HIS
1	E	352	HIS
1	E	364	GLN
1	E	383	HIS
1	E	402	ASN
1	E	412	GLN
1	E	414	GLN

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Mol	Chain	Res	Type
1	F	26	ASN
1	F	84	GLN
1	F	136	ASN
1	F	144	GLN
1	F	247	ASN
1	F	250	GLN
1	F	313	ASN
1	F	319	ASN
1	F	383	HIS
1	F	414	GLN
1	G	26	ASN
1	G	84	GLN
1	G	115	GLN
1	G	144	GLN
1	G	161	HIS
1	G	229	GLN
1	G	250	GLN
1	G	269	ASN
1	G	319	ASN
1	G	364	GLN
1	G	368	GLN
1	G	412	GLN
1	G	414	GLN
1	H	26	ASN
1	H	115	GLN
1	H	118	HIS
1	H	136	ASN
1	H	144	GLN
1	H	247	ASN
1	H	250	GLN
1	H	269	ASN
1	H	352	HIS
1	H	364	GLN
1	H	374	HIS
1	H	383	HIS
1	H	412	GLN
1	H	414	GLN
1	H	421	ASN
1	H	428	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

16 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	DEA	F	6433	-	19,19,19	0.95	0	24,27,27	0.73	0
2	NAD	B	2432	-	46,48,48	2.24	9 (19%)	64,73,73	1.54	8 (12%)
3	DEA	E	5433	-	19,19,19	1.00	0	24,27,27	0.73	0
2	NAD	A	1432	-	46,48,48	2.36	11 (23%)	64,73,73	1.51	8 (12%)
2	NAD	E	5432	-	46,48,48	2.18	9 (19%)	64,73,73	1.50	8 (12%)
3	DEA	B	2433	-	19,19,19	0.96	0	24,27,27	0.74	1 (4%)
3	DEA	D	4433	-	19,19,19	1.25	1 (5%)	24,27,27	0.77	0
3	DEA	G	7433	-	19,19,19	1.01	1 (5%)	24,27,27	0.77	1 (4%)
2	NAD	F	6432	-	46,48,48	2.29	11 (23%)	64,73,73	1.46	7 (10%)
2	NAD	D	4432	-	46,48,48	2.36	9 (19%)	64,73,73	1.53	8 (12%)
2	NAD	C	3432	-	46,48,48	2.27	9 (19%)	64,73,73	1.51	8 (12%)
2	NAD	G	7432	-	46,48,48	2.37	10 (21%)	64,73,73	1.53	7 (10%)
2	NAD	H	8432	-	46,48,48	2.21	11 (23%)	64,73,73	1.51	7 (10%)
3	DEA	C	3433	-	19,19,19	1.03	0	24,27,27	0.74	0
3	DEA	A	1433	-	19,19,19	1.04	0	24,27,27	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	DEA	H	8433	-	19,19,19	1.06	0	24,27,27	0.73	0

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	DEA	F	6433	-	-	4/12/12/12	0/2/2/2
2	NAD	B	2432	-	-	5/30/62/62	0/5/5/5
3	DEA	E	5433	-	-	4/12/12/12	0/2/2/2
2	NAD	A	1432	-	-	5/30/62/62	0/5/5/5
2	NAD	E	5432	-	-	5/30/62/62	0/5/5/5
3	DEA	B	2433	-	-	4/12/12/12	0/2/2/2
3	DEA	D	4433	-	-	4/12/12/12	0/2/2/2
3	DEA	G	7433	-	-	4/12/12/12	0/2/2/2
2	NAD	F	6432	-	-	6/30/62/62	0/5/5/5
2	NAD	D	4432	-	-	5/30/62/62	0/5/5/5
2	NAD	C	3432	-	-	5/30/62/62	0/5/5/5
2	NAD	G	7432	-	-	7/30/62/62	0/5/5/5
2	NAD	H	8432	-	-	6/30/62/62	0/5/5/5
3	DEA	C	3433	-	-	4/12/12/12	0/2/2/2
3	DEA	A	1433	-	-	4/12/12/12	0/2/2/2
3	DEA	H	8433	-	-	4/12/12/12	0/2/2/2

All (81) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	4432	NAD	C5N-C4N	8.22	1.53	1.38
2	F	6432	NAD	C5N-C4N	7.99	1.52	1.38
2	A	1432	NAD	C5N-C4N	7.98	1.52	1.38
2	H	8432	NAD	C5N-C4N	7.97	1.52	1.38
2	B	2432	NAD	C5N-C4N	7.79	1.52	1.38
2	E	5432	NAD	C5N-C4N	7.75	1.52	1.38
2	G	7432	NAD	C5N-C4N	7.74	1.52	1.38
2	C	3432	NAD	C5N-C4N	7.71	1.52	1.38
2	D	4432	NAD	C2N-N1N	6.96	1.42	1.35
2	G	7432	NAD	C2N-N1N	6.95	1.42	1.35
2	B	2432	NAD	C2N-N1N	6.73	1.42	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1432	NAD	C4N-C3N	6.64	1.49	1.39
2	D	4432	NAD	C4N-C3N	6.58	1.49	1.39
2	F	6432	NAD	C4N-C3N	6.57	1.49	1.39
2	G	7432	NAD	C4N-C3N	6.48	1.49	1.39
2	A	1432	NAD	C2N-N1N	6.43	1.42	1.35
2	C	3432	NAD	C2N-N1N	6.38	1.42	1.35
2	C	3432	NAD	C4N-C3N	6.23	1.48	1.39
2	B	2432	NAD	C4N-C3N	6.19	1.48	1.39
2	H	8432	NAD	C2N-N1N	6.18	1.41	1.35
2	E	5432	NAD	C4N-C3N	6.08	1.48	1.39
2	D	4432	NAD	C2N-C3N	5.98	1.48	1.39
2	H	8432	NAD	C4N-C3N	5.91	1.48	1.39
2	F	6432	NAD	C2N-N1N	5.90	1.41	1.35
2	G	7432	NAD	C2N-C3N	5.82	1.48	1.39
2	H	8432	NAD	C2N-C3N	5.70	1.48	1.39
2	C	3432	NAD	C2N-C3N	5.63	1.47	1.39
2	E	5432	NAD	C2N-N1N	5.60	1.41	1.35
2	B	2432	NAD	C2N-C3N	5.44	1.47	1.39
2	A	1432	NAD	C2N-C3N	5.30	1.47	1.39
2	E	5432	NAD	C2N-C3N	4.92	1.46	1.39
2	F	6432	NAD	C2N-C3N	4.89	1.46	1.39
2	C	3432	NAD	C6N-N1N	4.45	1.45	1.35
2	D	4432	NAD	C6N-N1N	4.41	1.45	1.35
2	G	7432	NAD	C6N-N1N	4.34	1.45	1.35
2	A	1432	NAD	C6N-N1N	4.24	1.45	1.35
2	E	5432	NAD	C6N-N1N	4.17	1.44	1.35
2	F	6432	NAD	C6N-N1N	4.15	1.44	1.35
2	B	2432	NAD	C6N-N1N	4.09	1.44	1.35
2	H	8432	NAD	C6N-N1N	3.85	1.44	1.35
2	A	1432	NAD	PN-O3	3.72	1.63	1.59
2	G	7432	NAD	PN-O3	3.46	1.63	1.59
2	F	6432	NAD	PN-O3	3.27	1.63	1.59
2	E	5432	NAD	PN-O3	3.14	1.62	1.59
2	E	5432	NAD	O4B-C1B	-2.95	1.35	1.42
2	G	7432	NAD	O4B-C1B	-2.87	1.35	1.42
2	D	4432	NAD	C2A-N1A	2.75	1.38	1.33
2	F	6432	NAD	O4B-C1B	-2.74	1.35	1.42
2	C	3432	NAD	O4B-C1B	-2.64	1.35	1.42
2	A	1432	NAD	O4B-C1B	-2.63	1.35	1.42
2	A	1432	NAD	C7N-N7N	2.62	1.37	1.33
2	F	6432	NAD	C2A-N1A	2.62	1.38	1.33
2	F	6432	NAD	C7N-N7N	2.62	1.37	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1432	NAD	C2A-N1A	2.59	1.38	1.33
2	G	7432	NAD	C2A-N1A	2.55	1.38	1.33
2	B	2432	NAD	O4B-C1B	-2.52	1.36	1.42
2	H	8432	NAD	PN-O3	2.44	1.62	1.59
2	B	2432	NAD	C7N-N7N	2.43	1.37	1.33
2	C	3432	NAD	C2A-N1A	2.41	1.38	1.33
2	C	3432	NAD	C7N-N7N	2.40	1.37	1.33
2	F	6432	NAD	C6N-C5N	-2.39	1.33	1.38
2	A	1432	NAD	C6N-C5N	-2.35	1.33	1.38
2	B	2432	NAD	C2A-N1A	2.32	1.38	1.33
2	C	3432	NAD	C6N-C5N	-2.31	1.33	1.38
2	D	4432	NAD	O4B-C1B	-2.30	1.36	1.42
2	G	7432	NAD	C6N-C5N	-2.27	1.33	1.38
2	A	1432	NAD	PA-O3	2.26	1.61	1.59
2	E	5432	NAD	C2A-N1A	2.26	1.37	1.33
2	D	4432	NAD	C7N-N7N	2.20	1.37	1.33
2	B	2432	NAD	PN-O3	2.18	1.61	1.59
2	G	7432	NAD	C7N-N7N	2.16	1.36	1.33
2	H	8432	NAD	O4D-C1D	2.16	1.43	1.40
2	D	4432	NAD	PN-O3	2.15	1.61	1.59
2	F	6432	NAD	O4D-C1D	2.13	1.43	1.40
2	H	8432	NAD	C7N-N7N	2.12	1.36	1.33
3	D	4433	DEA	C2'-C3'	2.10	1.55	1.53
3	G	7433	DEA	C2'-C3'	2.09	1.55	1.53
2	H	8432	NAD	O4B-C1B	-2.08	1.37	1.42
2	E	5432	NAD	C6N-C5N	-2.07	1.34	1.38
2	H	8432	NAD	C6N-C5N	-2.06	1.34	1.38
2	H	8432	NAD	C2A-N1A	2.04	1.37	1.33

All (63) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	7432	NAD	C3N-C7N-N7N	5.83	124.92	117.74
2	B	2432	NAD	C3N-C7N-N7N	5.74	124.81	117.74
2	D	4432	NAD	C3N-C7N-N7N	5.72	124.79	117.74
2	A	1432	NAD	C3N-C7N-N7N	5.65	124.69	117.74
2	H	8432	NAD	C3N-C7N-N7N	5.59	124.63	117.74
2	C	3432	NAD	C3N-C7N-N7N	5.54	124.56	117.74
2	G	7432	NAD	O7N-C7N-C3N	-5.50	112.88	119.60
2	F	6432	NAD	C3N-C7N-N7N	5.46	124.46	117.74
2	A	1432	NAD	O7N-C7N-C3N	-5.32	113.09	119.60
2	D	4432	NAD	O7N-C7N-C3N	-5.29	113.13	119.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2432	NAD	O7N-C7N-C3N	-5.29	113.13	119.60
2	C	3432	NAD	O7N-C7N-C3N	-5.27	113.16	119.60
2	E	5432	NAD	C3N-C7N-N7N	5.22	124.17	117.74
2	H	8432	NAD	O7N-C7N-C3N	-5.17	113.28	119.60
2	F	6432	NAD	O7N-C7N-C3N	-5.16	113.28	119.60
2	E	5432	NAD	O7N-C7N-C3N	-5.08	113.38	119.60
2	D	4432	NAD	C6N-N1N-C2N	-4.99	117.64	121.88
2	G	7432	NAD	C6N-N1N-C2N	-4.98	117.64	121.88
2	C	3432	NAD	C6N-N1N-C2N	-4.93	117.68	121.88
2	B	2432	NAD	C6N-N1N-C2N	-4.88	117.73	121.88
2	H	8432	NAD	C6N-N1N-C2N	-4.85	117.75	121.88
2	E	5432	NAD	C6N-N1N-C2N	-4.84	117.76	121.88
2	A	1432	NAD	C6N-N1N-C2N	-4.52	118.03	121.88
2	D	4432	NAD	C5N-C4N-C3N	-4.24	116.19	120.36
2	H	8432	NAD	C5N-C4N-C3N	-4.20	116.23	120.36
2	B	2432	NAD	C5N-C4N-C3N	-4.19	116.25	120.36
2	E	5432	NAD	C5N-C4N-C3N	-4.18	116.26	120.36
2	F	6432	NAD	C6N-N1N-C2N	-4.07	118.42	121.88
2	G	7432	NAD	C5N-C4N-C3N	-4.05	116.39	120.36
2	F	6432	NAD	C5N-C4N-C3N	-4.00	116.44	120.36
2	A	1432	NAD	C5N-C4N-C3N	-3.94	116.49	120.36
2	C	3432	NAD	C5N-C4N-C3N	-3.91	116.52	120.36
2	G	7432	NAD	C5N-C6N-N1N	3.24	124.80	120.38
2	C	3432	NAD	C5N-C6N-N1N	3.09	124.60	120.38
2	A	1432	NAD	O4B-C1B-C2B	-2.97	100.25	106.62
2	E	5432	NAD	C5N-C6N-N1N	2.97	124.43	120.38
2	A	1432	NAD	C5N-C6N-N1N	2.96	124.42	120.38
2	H	8432	NAD	C5N-C6N-N1N	2.94	124.39	120.38
2	H	8432	NAD	O4B-C1B-C2B	-2.94	100.33	106.62
2	D	4432	NAD	C5N-C6N-N1N	2.93	124.38	120.38
2	B	2432	NAD	C5N-C6N-N1N	2.90	124.34	120.38
2	F	6432	NAD	C5N-C6N-N1N	2.77	124.16	120.38
2	C	3432	NAD	O4B-C1B-C2B	-2.75	100.73	106.62
2	B	2432	NAD	O4B-C1B-C2B	-2.70	100.84	106.62
2	E	5432	NAD	O4B-C1B-C2B	-2.67	100.90	106.62
2	G	7432	NAD	O4B-C1B-C2B	-2.61	101.02	106.62
2	D	4432	NAD	O4B-C1B-C2B	-2.54	101.19	106.62
2	G	7432	NAD	O2A-PA-O3	2.37	113.67	107.27
2	A	1432	NAD	O2A-PA-O3	2.36	113.66	107.27
2	A	1432	NAD	O5B-C5B-C4B	-2.28	101.24	108.99
2	F	6432	NAD	O4B-C1B-C2B	-2.27	101.75	106.62
2	F	6432	NAD	O5B-C5B-C4B	-2.26	101.29	108.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	4432	NAD	O5B-C5B-C4B	-2.23	101.41	108.99
2	C	3432	NAD	O5B-C5B-C4B	-2.18	101.58	108.99
3	G	7433	DEA	O-C4'-C3'	-2.11	115.99	121.62
2	B	2432	NAD	O5B-C5B-C4B	-2.11	101.81	108.99
2	E	5432	NAD	O2A-PA-O3	2.10	112.94	107.27
2	E	5432	NAD	C6N-N1N-C1D	2.10	123.84	119.73
2	C	3432	NAD	O2A-PA-O3	2.08	112.90	107.27
2	B	2432	NAD	O2A-PA-O3	2.05	112.81	107.27
2	H	8432	NAD	O5B-C5B-C4B	-2.03	102.08	108.99
2	D	4432	NAD	O2A-PA-O3	2.01	112.71	107.27
3	B	2433	DEA	O-C4'-C3'	-2.01	116.27	121.62

There are no chirality outliers.

All (76) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1432	NAD	O4D-C1D-N1N-C2N
2	A	1432	NAD	O4D-C1D-N1N-C6N
2	A	1432	NAD	C2D-C1D-N1N-C2N
2	A	1432	NAD	C2D-C1D-N1N-C6N
2	B	2432	NAD	O4D-C1D-N1N-C2N
2	B	2432	NAD	O4D-C1D-N1N-C6N
2	B	2432	NAD	C2D-C1D-N1N-C2N
2	B	2432	NAD	C2D-C1D-N1N-C6N
2	C	3432	NAD	O4D-C1D-N1N-C2N
2	C	3432	NAD	O4D-C1D-N1N-C6N
2	C	3432	NAD	C2D-C1D-N1N-C2N
2	C	3432	NAD	C2D-C1D-N1N-C6N
2	D	4432	NAD	O4D-C1D-N1N-C2N
2	D	4432	NAD	O4D-C1D-N1N-C6N
2	D	4432	NAD	C2D-C1D-N1N-C2N
2	D	4432	NAD	C2D-C1D-N1N-C6N
2	E	5432	NAD	O4D-C1D-N1N-C2N
2	E	5432	NAD	O4D-C1D-N1N-C6N
2	E	5432	NAD	C2D-C1D-N1N-C2N
2	E	5432	NAD	C2D-C1D-N1N-C6N
2	F	6432	NAD	O4D-C1D-N1N-C2N
2	F	6432	NAD	O4D-C1D-N1N-C6N
2	F	6432	NAD	C2D-C1D-N1N-C2N
2	F	6432	NAD	C2D-C1D-N1N-C6N
2	G	7432	NAD	O4D-C1D-N1N-C2N
2	G	7432	NAD	O4D-C1D-N1N-C6N

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Mol	Chain	Res	Type	Atoms
2	G	7432	NAD	C2D-C1D-N1N-C2N
2	G	7432	NAD	C2D-C1D-N1N-C6N
2	H	8432	NAD	O4D-C1D-N1N-C2N
2	H	8432	NAD	O4D-C1D-N1N-C6N
2	H	8432	NAD	C2D-C1D-N1N-C2N
2	H	8432	NAD	C2D-C1D-N1N-C6N
3	A	1433	DEA	O3'-C3'-C4'-O
3	A	1433	DEA	O3'-C3'-C4'-OXT
3	B	2433	DEA	O3'-C3'-C4'-O
3	B	2433	DEA	O3'-C3'-C4'-OXT
3	C	3433	DEA	O3'-C3'-C4'-O
3	C	3433	DEA	O3'-C3'-C4'-OXT
3	D	4433	DEA	O3'-C3'-C4'-O
3	D	4433	DEA	O3'-C3'-C4'-OXT
3	E	5433	DEA	O3'-C3'-C4'-O
3	E	5433	DEA	O3'-C3'-C4'-OXT
3	F	6433	DEA	O3'-C3'-C4'-O
3	F	6433	DEA	O3'-C3'-C4'-OXT
3	G	7433	DEA	O3'-C3'-C4'-O
3	G	7433	DEA	O3'-C3'-C4'-OXT
3	H	8433	DEA	O3'-C3'-C4'-O
3	H	8433	DEA	O3'-C3'-C4'-OXT
3	A	1433	DEA	C2'-C3'-C4'-O
3	A	1433	DEA	C2'-C3'-C4'-OXT
3	B	2433	DEA	C2'-C3'-C4'-OXT
3	C	3433	DEA	C2'-C3'-C4'-OXT
3	D	4433	DEA	C2'-C3'-C4'-OXT
3	E	5433	DEA	C2'-C3'-C4'-OXT
3	F	6433	DEA	C2'-C3'-C4'-O
3	F	6433	DEA	C2'-C3'-C4'-OXT
3	G	7433	DEA	C2'-C3'-C4'-OXT
3	H	8433	DEA	C2'-C3'-C4'-O
3	H	8433	DEA	C2'-C3'-C4'-OXT
3	B	2433	DEA	C2'-C3'-C4'-O
3	C	3433	DEA	C2'-C3'-C4'-O
3	D	4433	DEA	C2'-C3'-C4'-O
3	G	7433	DEA	C2'-C3'-C4'-O
3	E	5433	DEA	C2'-C3'-C4'-O
2	G	7432	NAD	PN-O3-PA-O1A
2	H	8432	NAD	C2B-C1B-N9A-C8A
2	F	6432	NAD	O4B-C4B-C5B-O5B
2	A	1432	NAD	O4B-C4B-C5B-O5B

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Mol	Chain	Res	Type	Atoms
2	B	2432	NAD	O4B-C4B-C5B-O5B
2	D	4432	NAD	O4B-C4B-C5B-O5B
2	E	5432	NAD	O4B-C4B-C5B-O5B
2	H	8432	NAD	O4B-C4B-C5B-O5B
2	G	7432	NAD	PN-O3-PA-O2A
2	C	3432	NAD	O4B-C4B-C5B-O5B
2	G	7432	NAD	O4B-C4B-C5B-O5B
2	F	6432	NAD	C2B-C1B-N9A-C8A

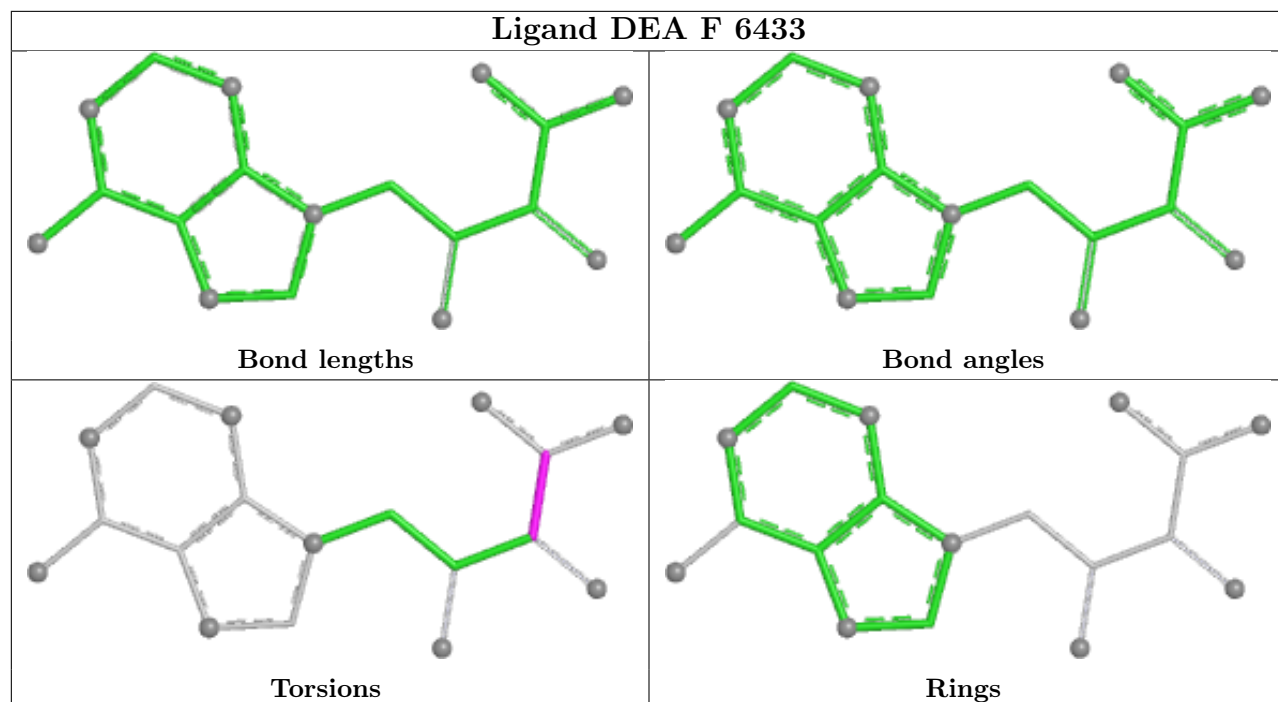
There are no ring outliers.

9 monomers are involved in 27 short contacts:

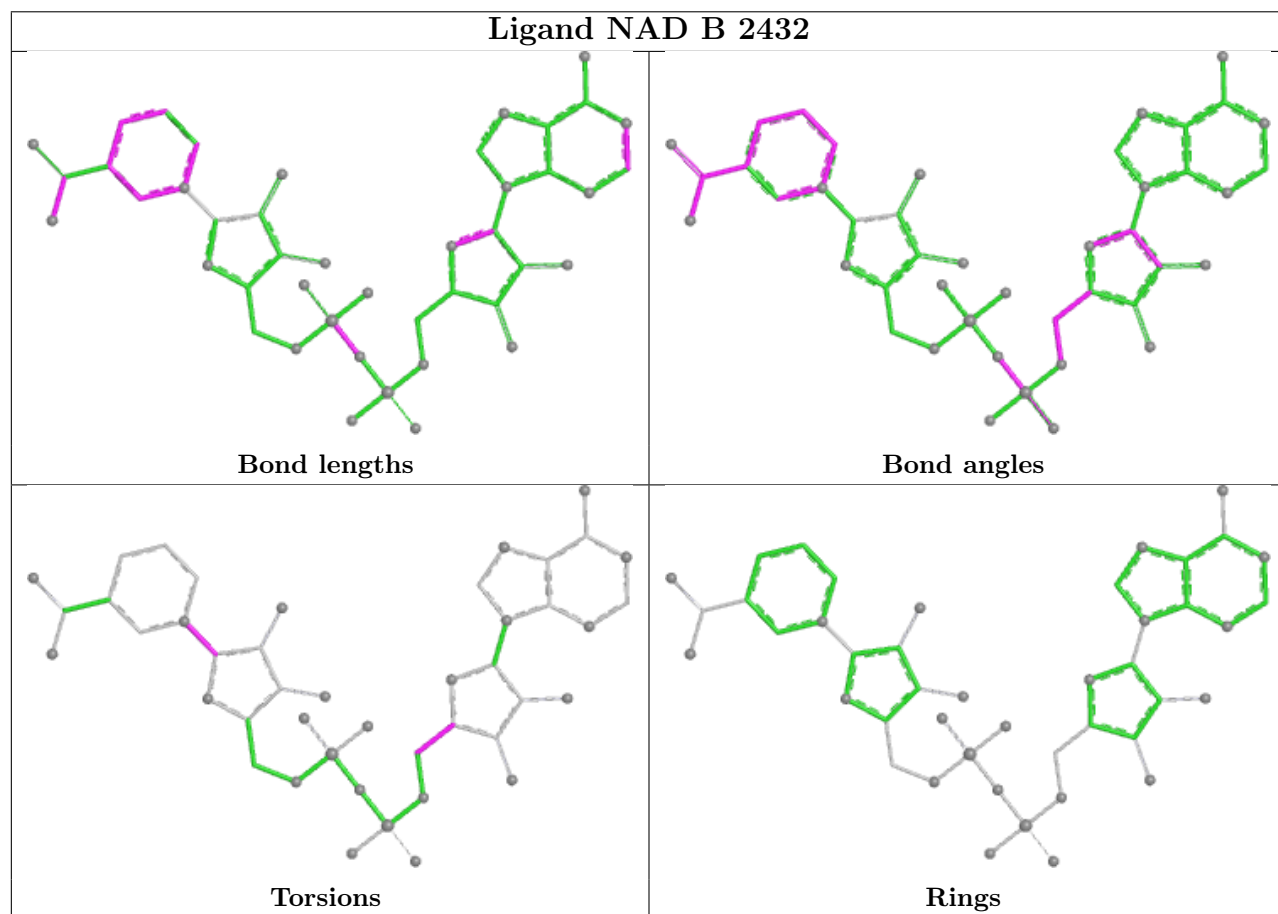
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	6433	DEA	1	0
2	B	2432	NAD	3	0
2	A	1432	NAD	2	0
2	E	5432	NAD	3	0
2	F	6432	NAD	2	0
2	D	4432	NAD	2	0
2	C	3432	NAD	3	0
2	G	7432	NAD	6	0
2	H	8432	NAD	5	0

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.

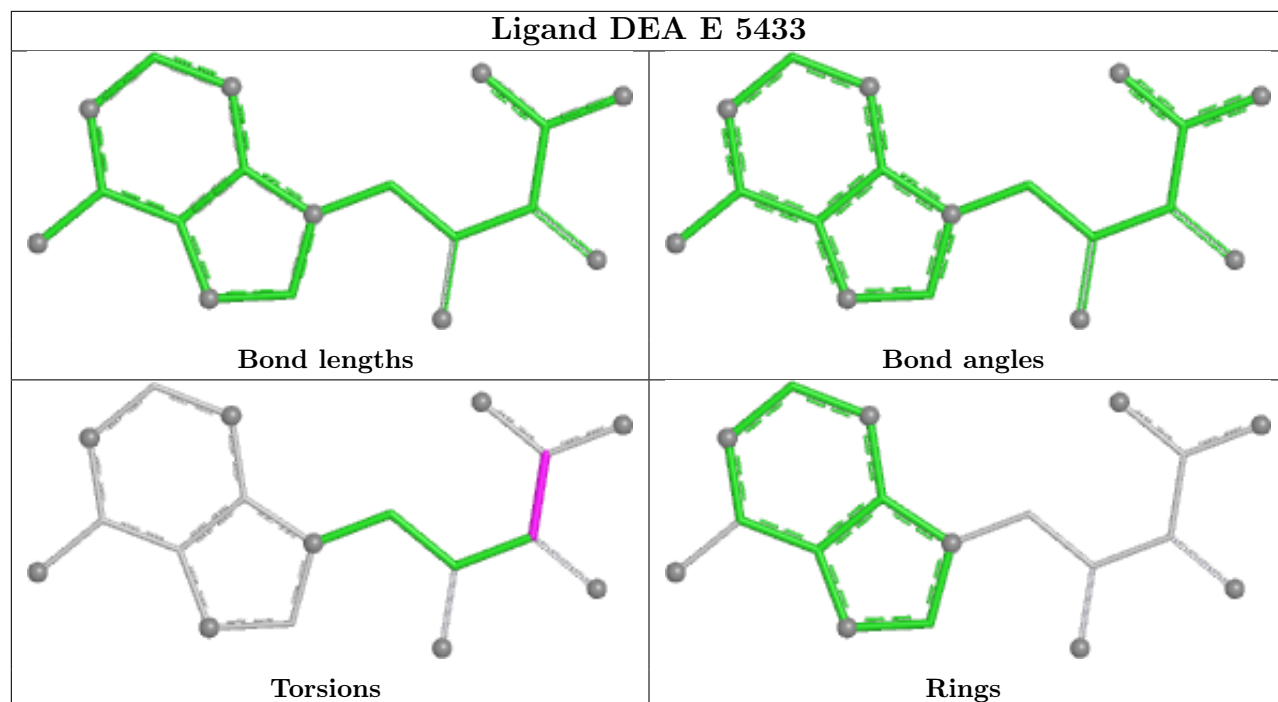
Ligand DEA F 6433



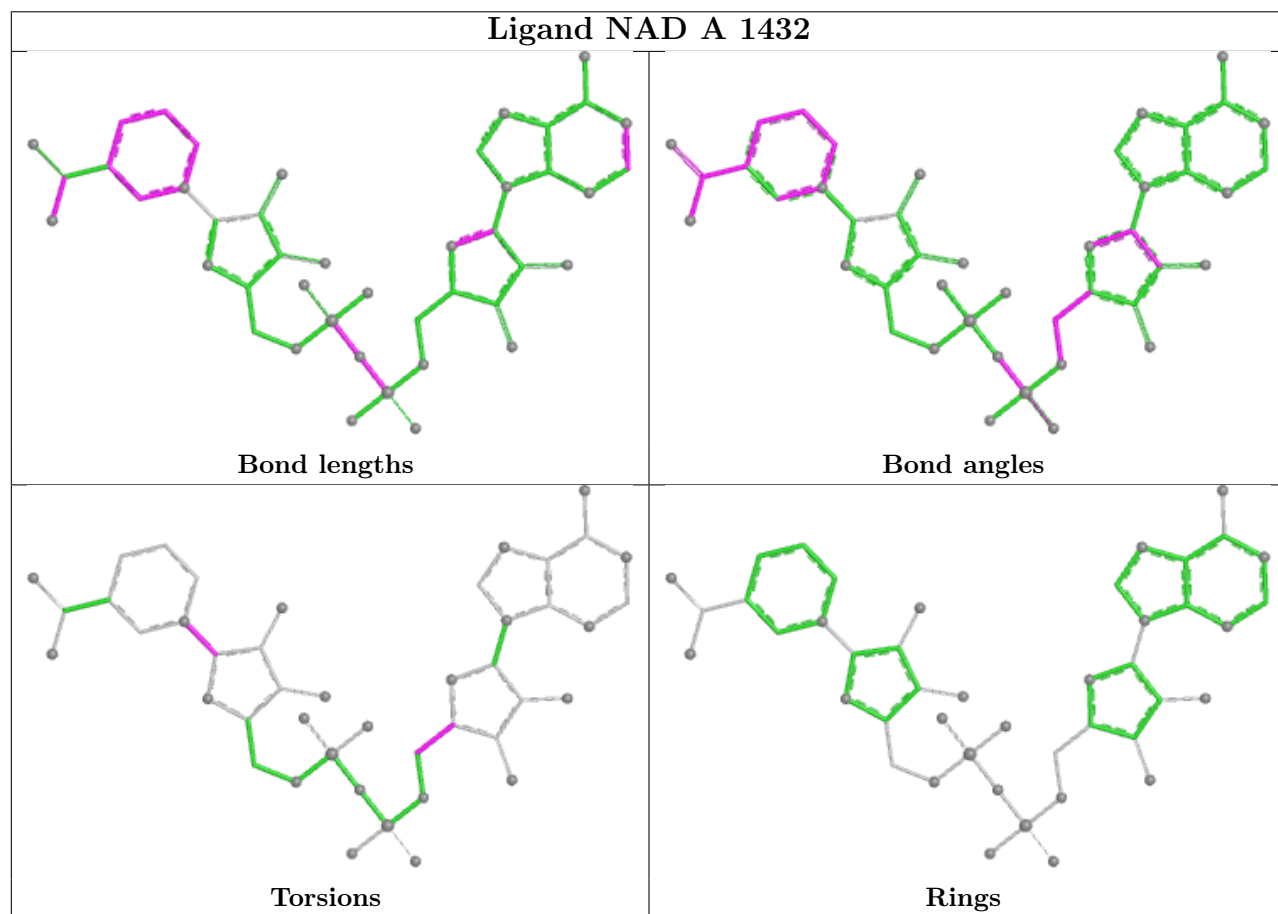
Ligand NAD B 2432



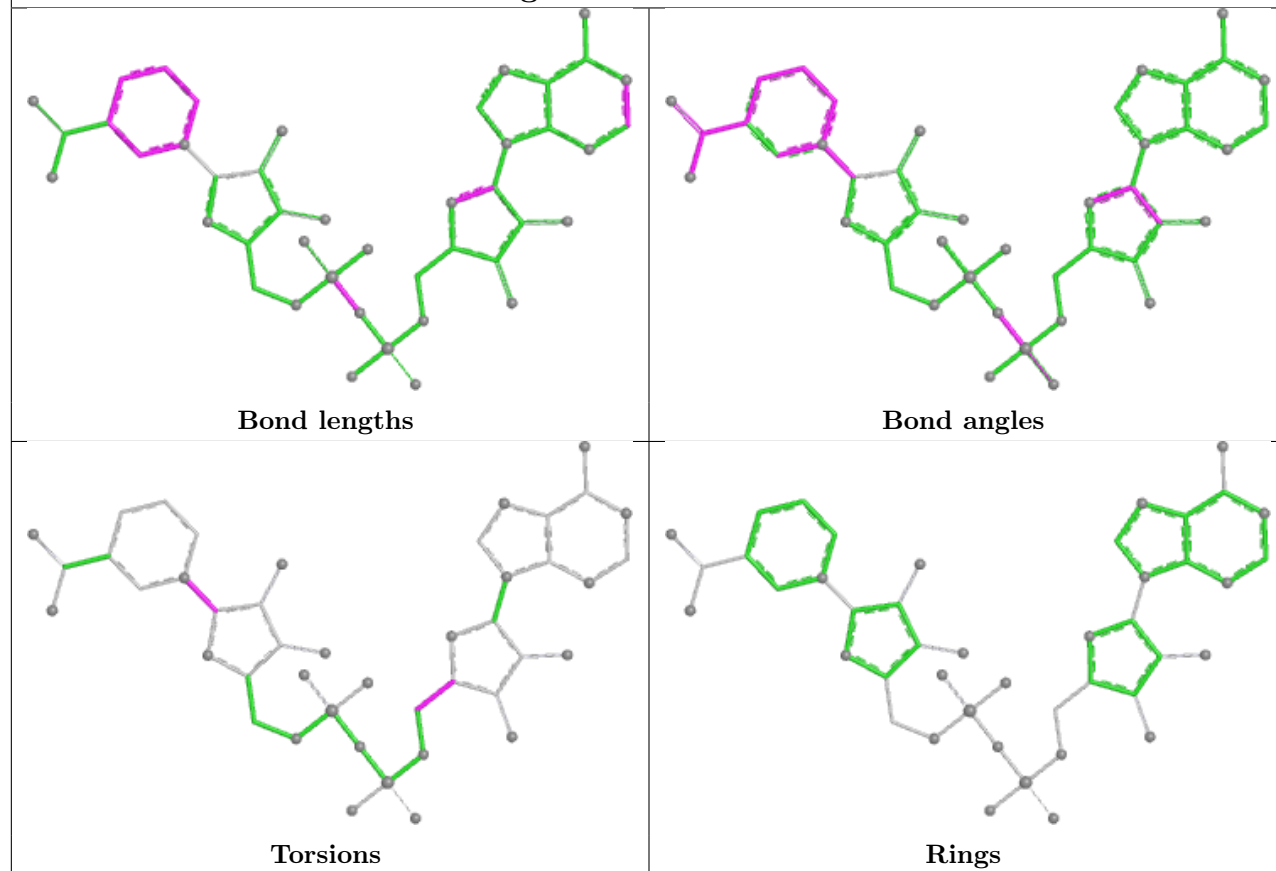
Ligand DEA E 5433



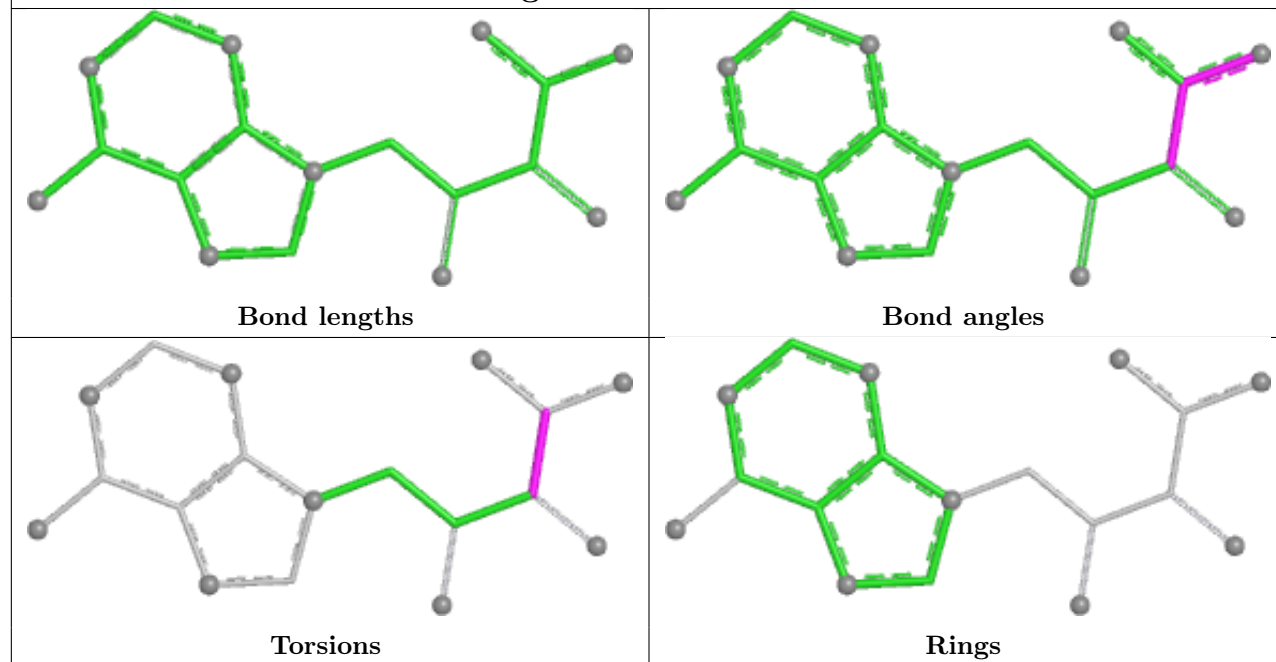
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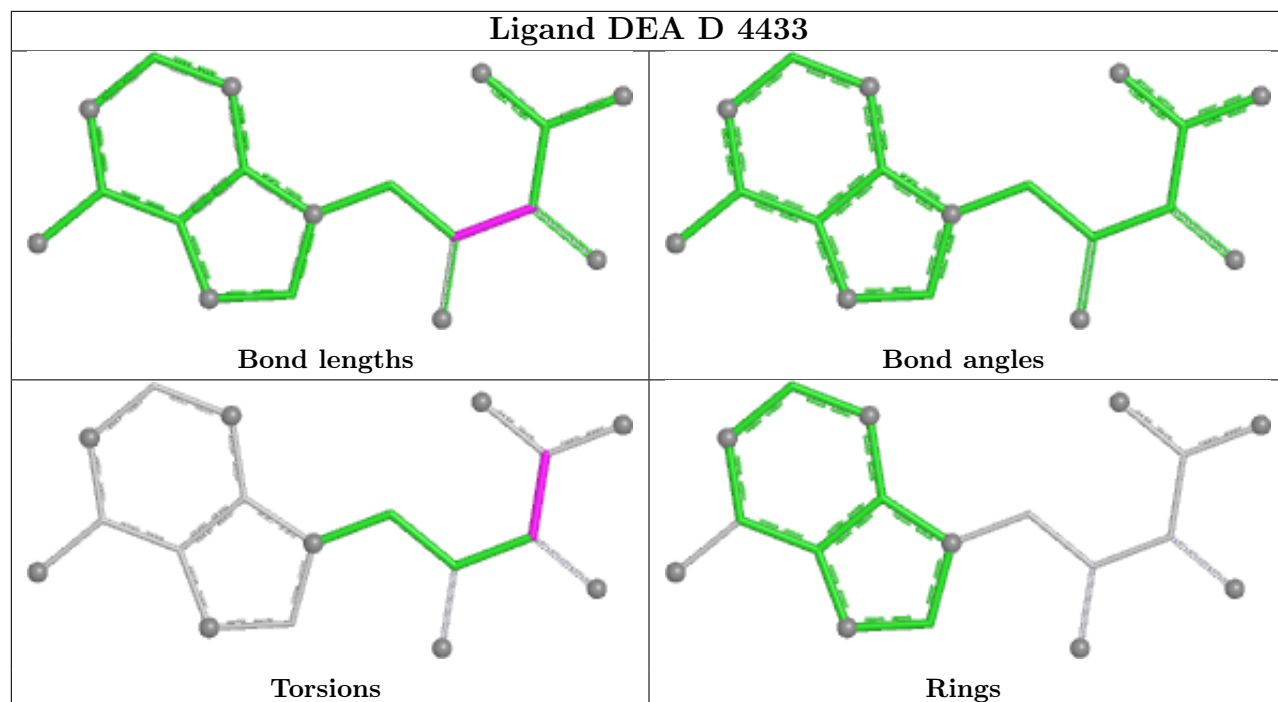
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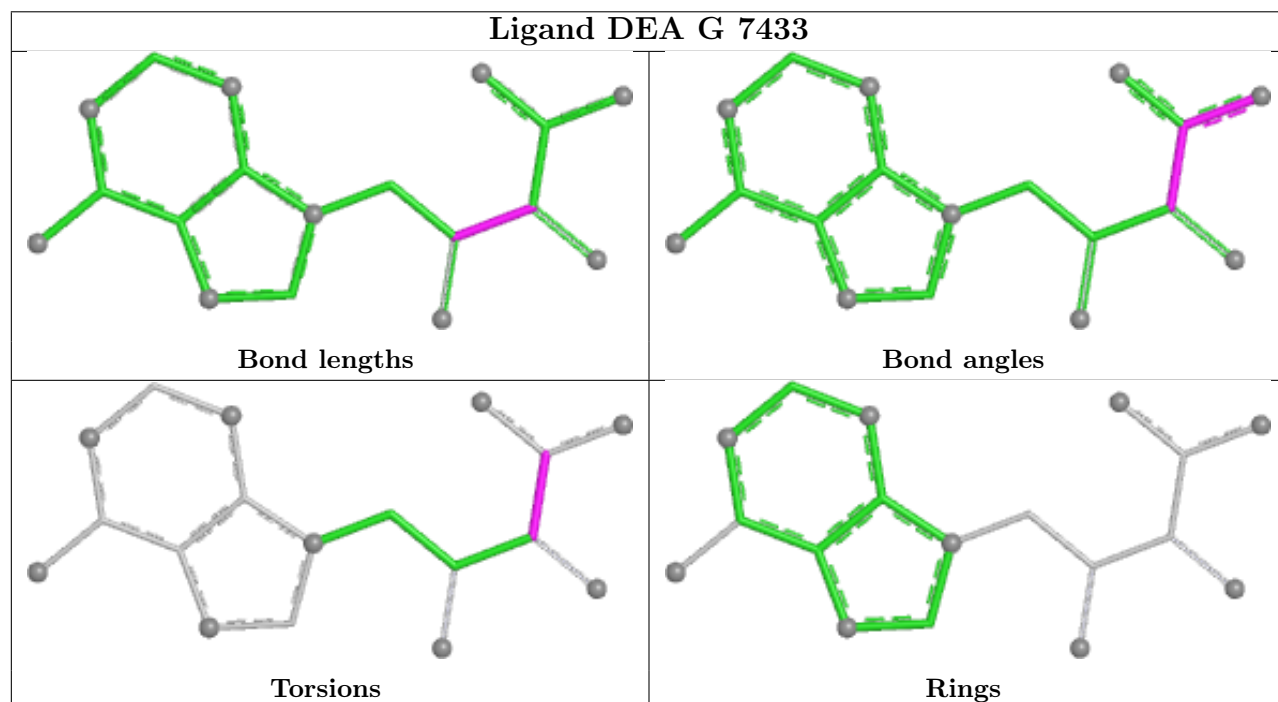
Ligand DEA B 2433

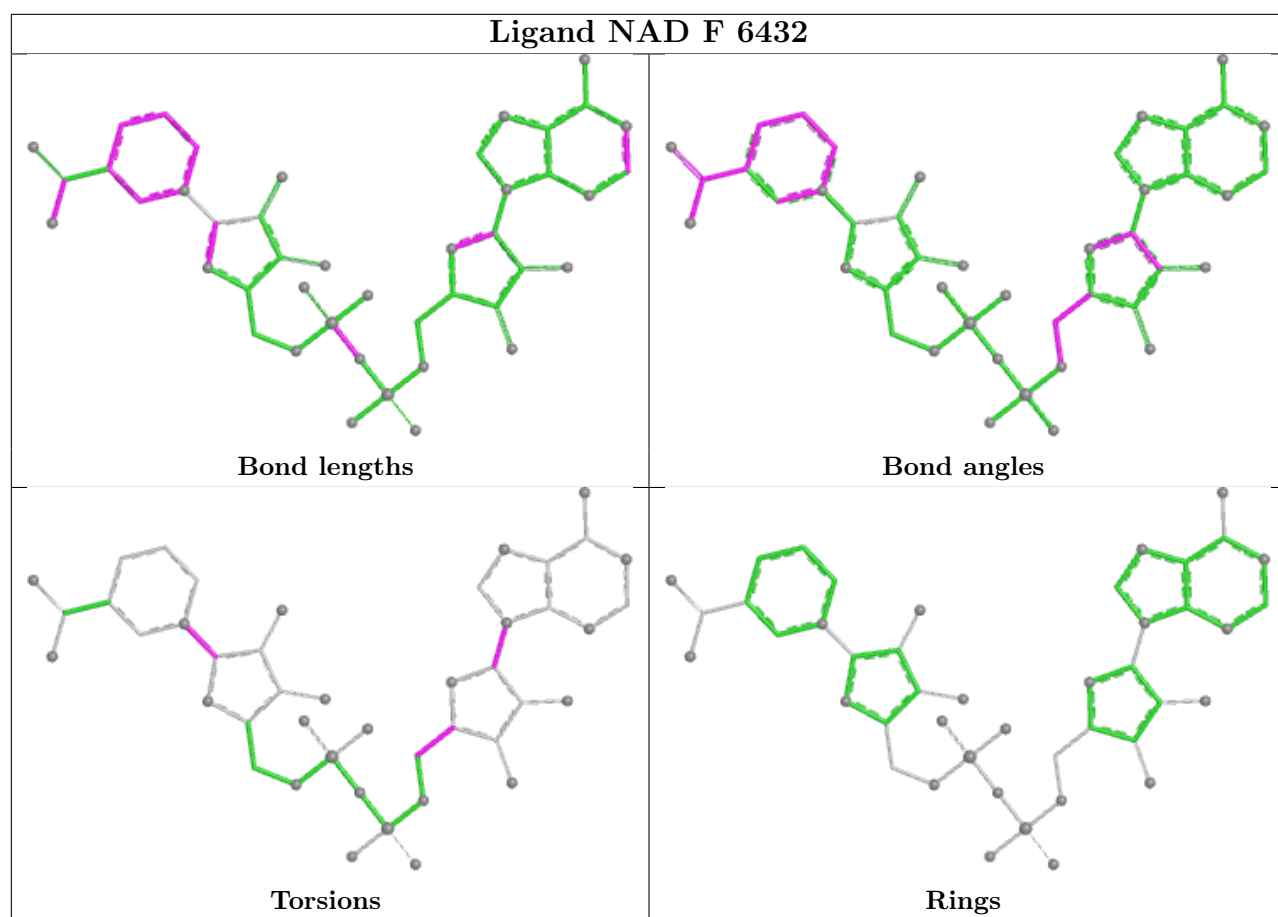


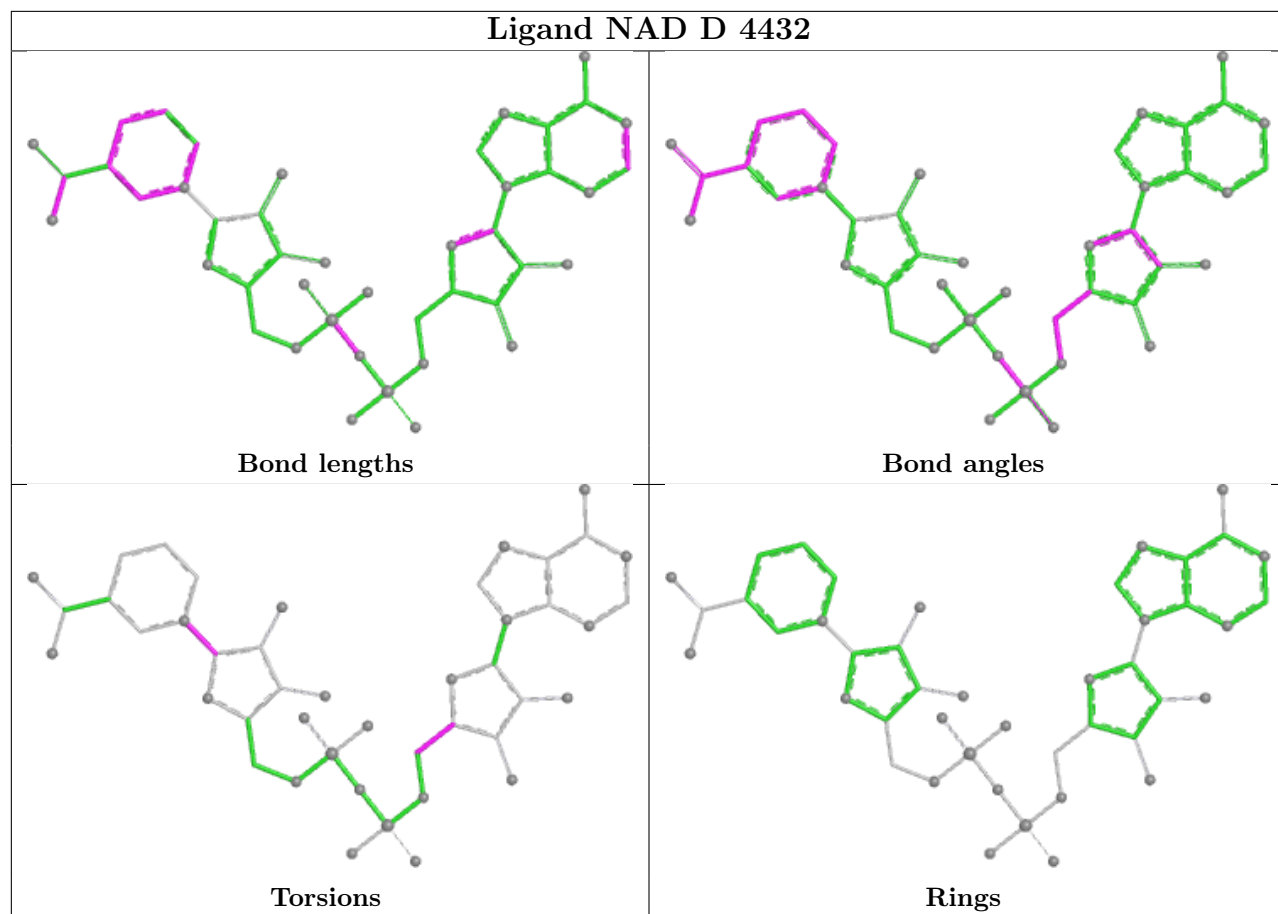
Ligand DEA D 4433

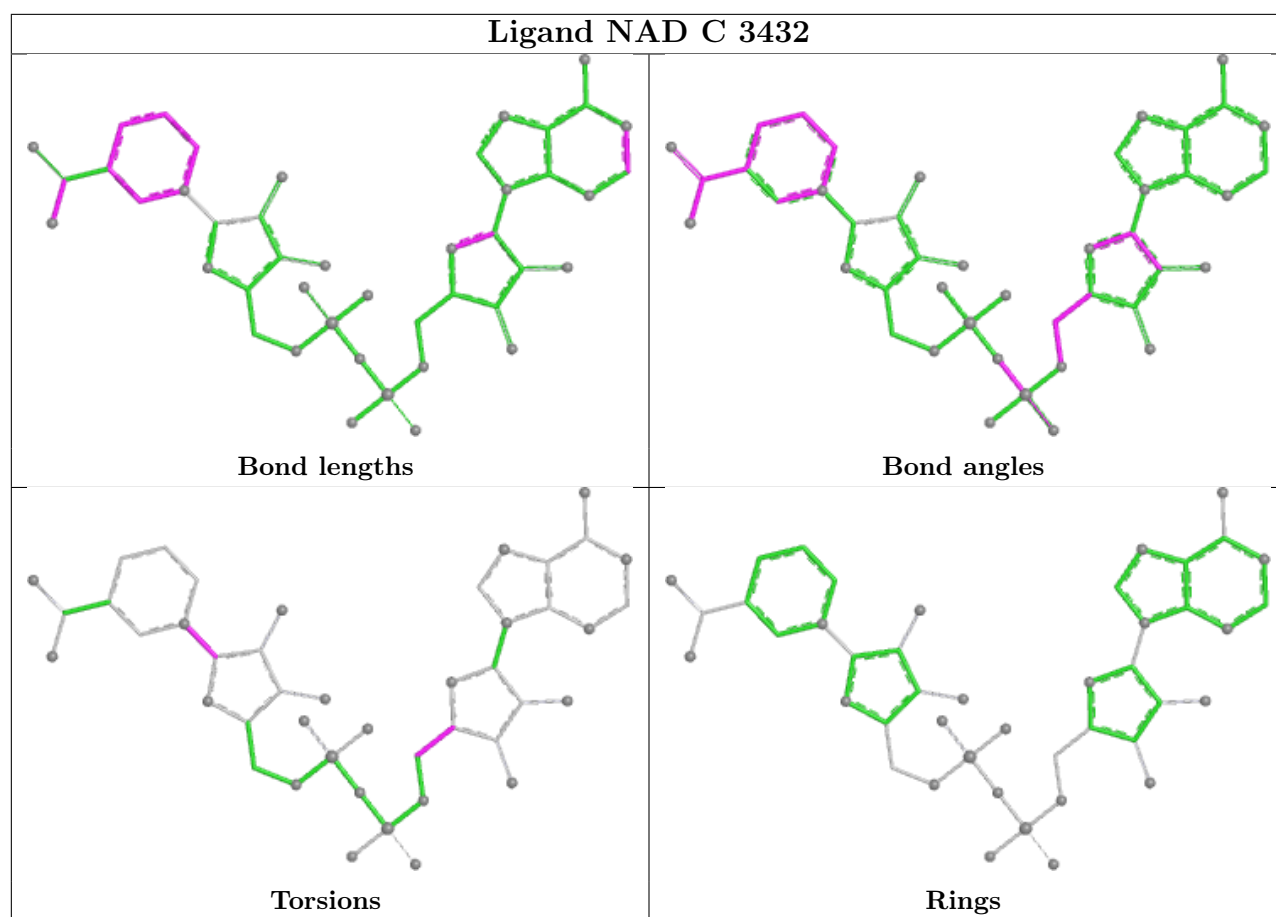


Ligand DEA G 7433

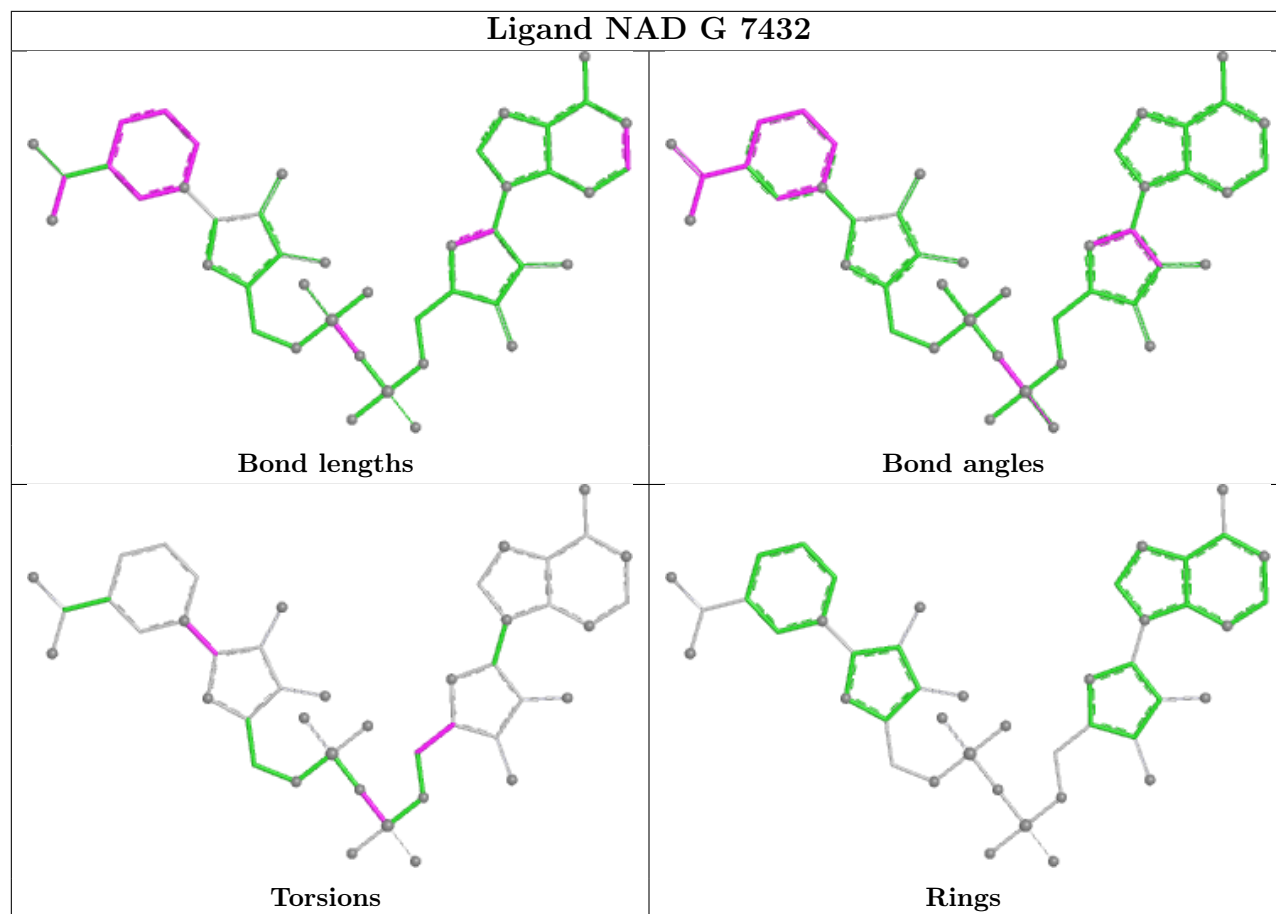




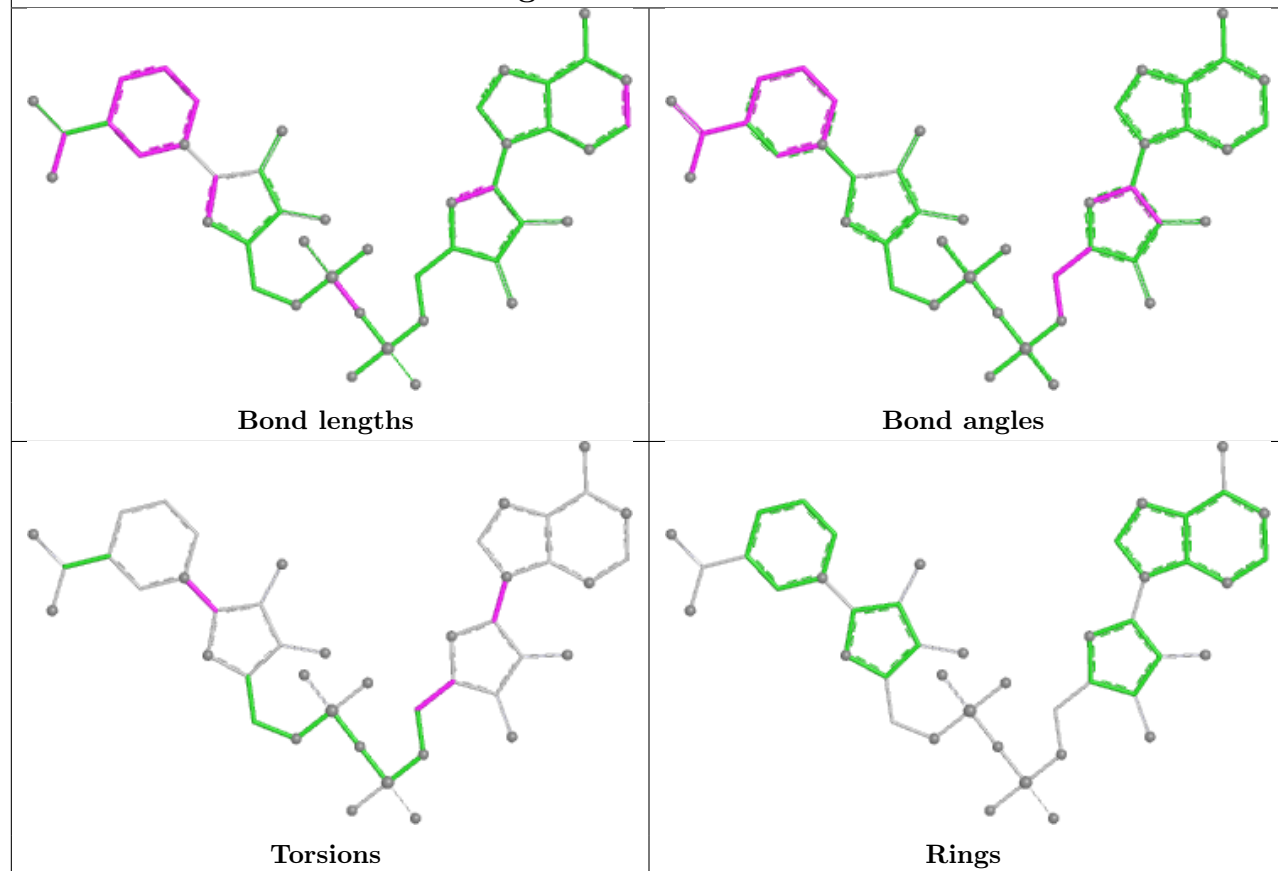




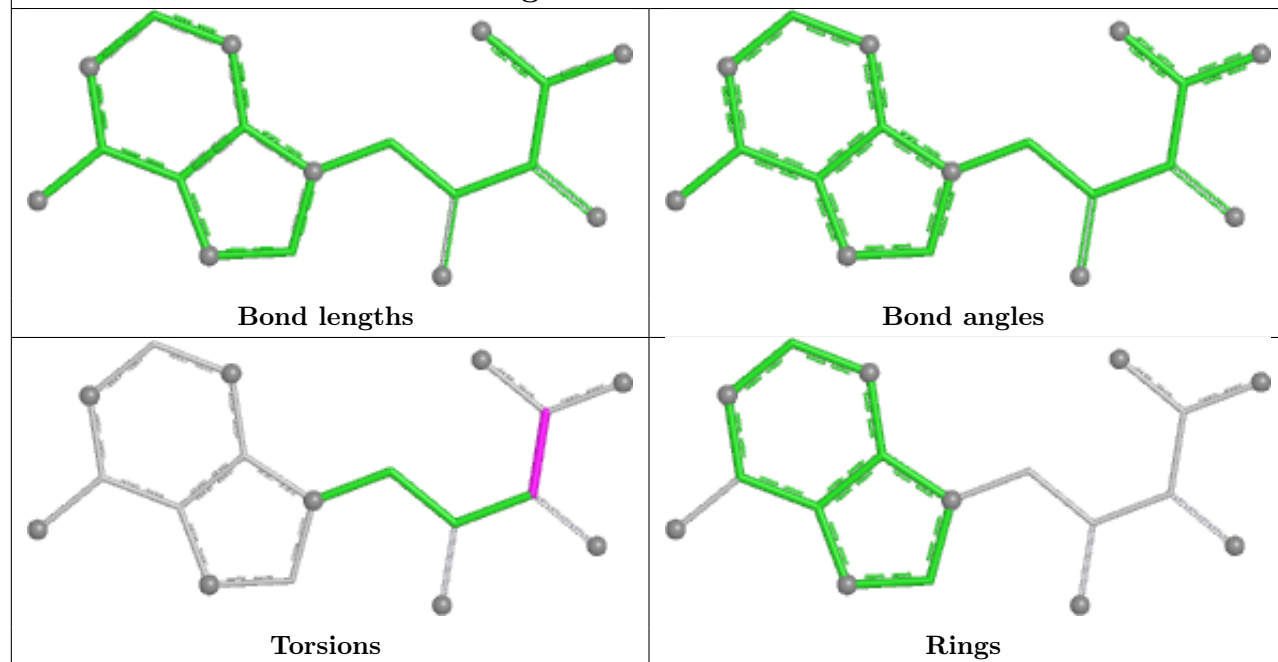
Ligand NAD G 7432

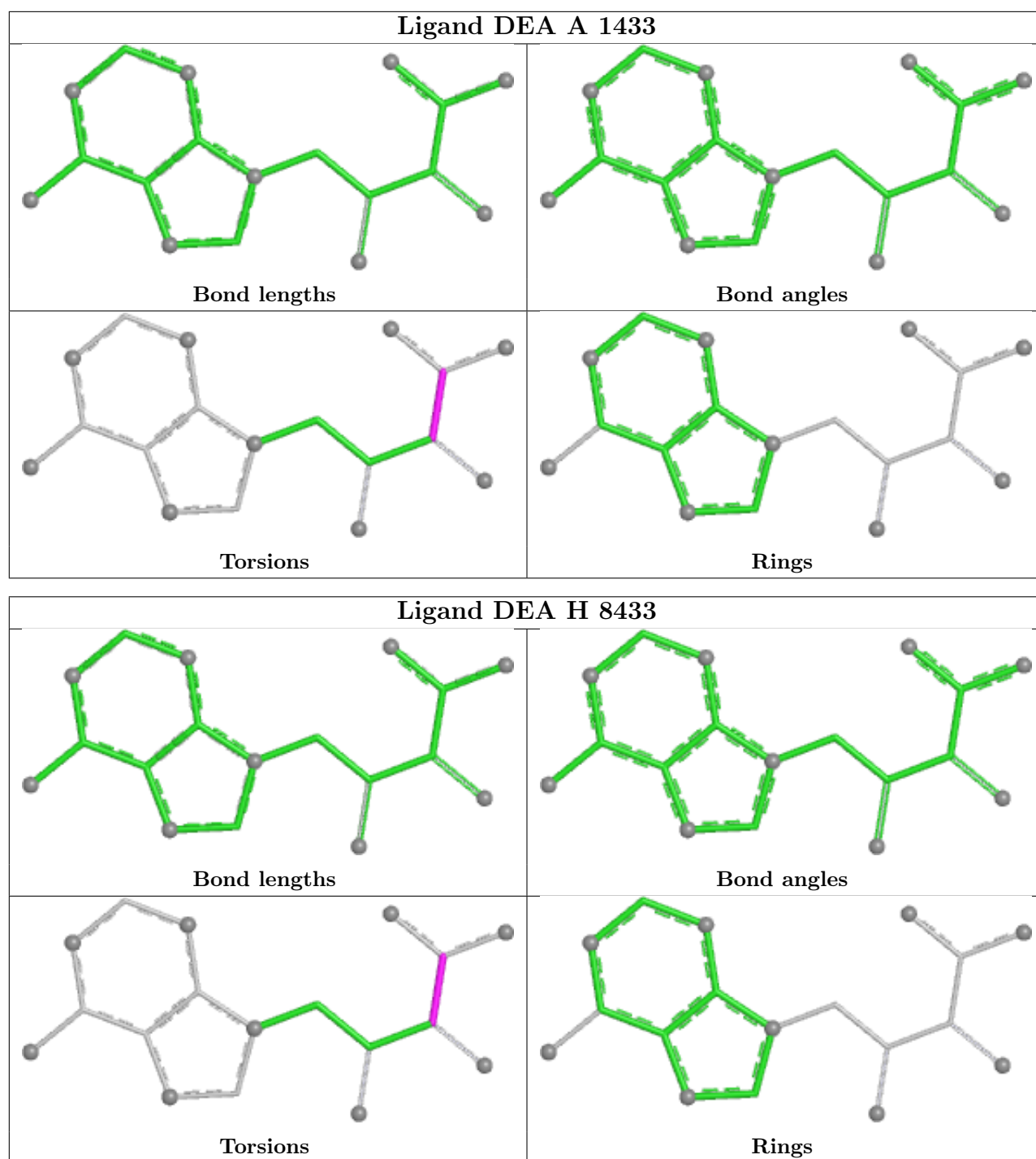


Ligand NAD H 8432



Ligand DEA C 3433





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	430/431 (99%)	0.20	10 (2%) 61 38	2, 3, 4, 6	0
1	B	430/431 (99%)	0.25	12 (2%) 55 32	2, 3, 4, 7	0
1	C	430/431 (99%)	0.19	11 (2%) 57 34	2, 3, 4, 6	0
1	D	430/431 (99%)	0.22	13 (3%) 52 30	2, 3, 4, 7	0
1	E	430/431 (99%)	0.13	4 (0%) 81 61	2, 2, 4, 5	0
1	F	430/431 (99%)	0.13	8 (1%) 66 43	2, 2, 4, 7	0
1	G	430/431 (99%)	0.10	6 (1%) 73 51	2, 2, 4, 6	0
1	H	430/431 (99%)	0.14	11 (2%) 57 34	2, 2, 4, 7	0
All	All	3440/3448 (99%)	0.17	75 (2%) 62 39	2, 2, 4, 7	0

All (75) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	2	ASP	7.4
1	D	2	ASP	5.9
1	A	2	ASP	5.9
1	E	2	ASP	4.8
1	B	376	ASP	4.5
1	F	2	ASP	4.5
1	F	375	PRO	4.2
1	D	381	GLY	4.2
1	E	33	ARG	3.9
1	B	2	ASP	3.6
1	C	3	LYS	3.4
1	H	376	ASP	3.4
1	E	41	SER	3.4
1	B	373	THR	3.2
1	H	33	ARG	3.2
1	A	122	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	376	ASP	3.1
1	C	381	GLY	3.0
1	D	410	GLU	2.9
1	B	308	LYS	2.9
1	H	410	GLU	2.9
1	G	381	GLY	2.9
1	H	121	ASP	2.8
1	G	410	GLU	2.8
1	A	376	ASP	2.8
1	H	381	GLY	2.8
1	H	162	ASN	2.7
1	H	7	LYS	2.7
1	H	72	GLU	2.6
1	C	376	ASP	2.6
1	F	3	LYS	2.6
1	G	2	ASP	2.6
1	A	312	GLU	2.6
1	A	33	ARG	2.6
1	D	168	ALA	2.5
1	G	3	LYS	2.5
1	D	279	ASP	2.5
1	E	375	PRO	2.5
1	A	316	GLU	2.4
1	A	262	ASP	2.4
1	B	3	LYS	2.4
1	D	167	MET	2.4
1	D	421	ASN	2.4
1	B	207	ASP	2.4
1	C	2	ASP	2.4
1	F	308	LYS	2.4
1	H	169	ASN	2.3
1	B	33	ARG	2.3
1	F	107	GLU	2.3
1	D	151	GLY	2.3
1	F	376	ASP	2.3
1	H	275	THR	2.3
1	B	37	MET	2.3
1	F	410	GLU	2.3
1	B	30	GLY	2.3
1	C	7	LYS	2.2
1	G	373	THR	2.2
1	A	41	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	4	LEU	2.2
1	C	155	GLU	2.2
1	D	3	LYS	2.2
1	D	41	SER	2.1
1	C	72	GLU	2.1
1	F	33	ARG	2.1
1	B	72	GLU	2.1
1	C	375	PRO	2.1
1	D	95	GLY	2.1
1	G	136	ASN	2.1
1	D	414	GLN	2.1
1	A	308	LYS	2.0
1	C	356	VAL	2.0
1	C	45	LYS	2.0
1	B	162	ASN	2.0
1	C	156	THR	2.0
1	B	422	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

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

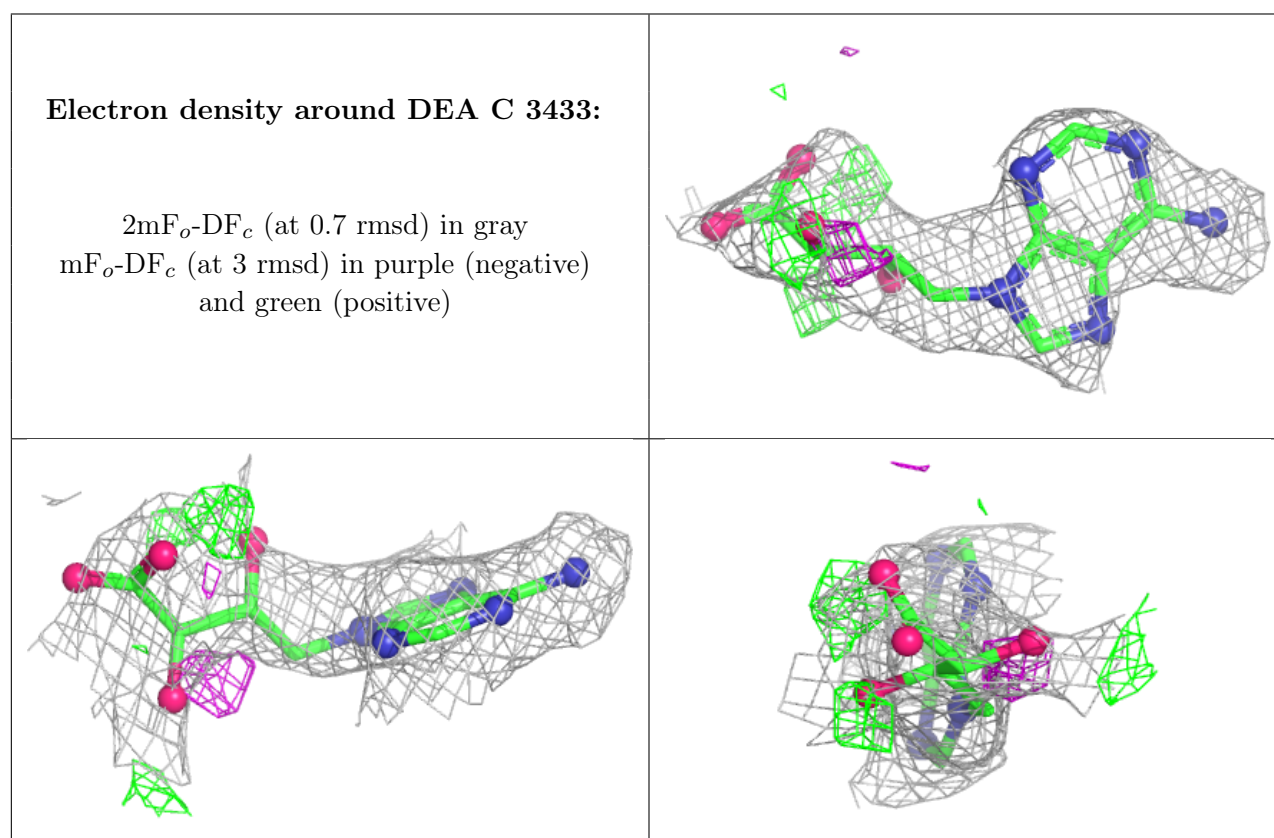
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	DEA	C	3433	18/18	0.76	0.17	2,2,5,5	0
3	DEA	B	2433	18/18	0.84	0.14	2,2,4,5	0
3	DEA	D	4433	18/18	0.84	0.12	2,2,3,4	0
3	DEA	H	8433	18/18	0.85	0.13	2,2,3,3	0
3	DEA	G	7433	18/18	0.88	0.14	2,2,5,6	0
3	DEA	A	1433	18/18	0.89	0.11	2,2,4,5	0

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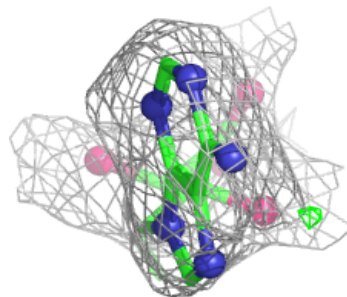
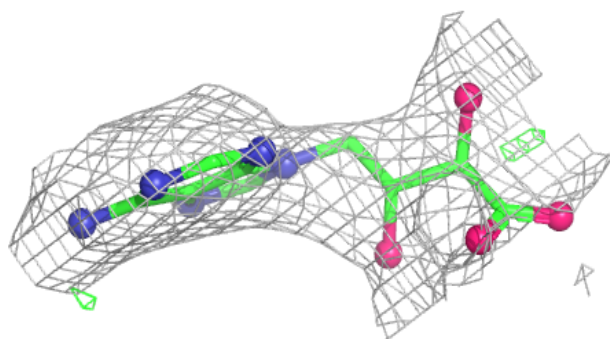
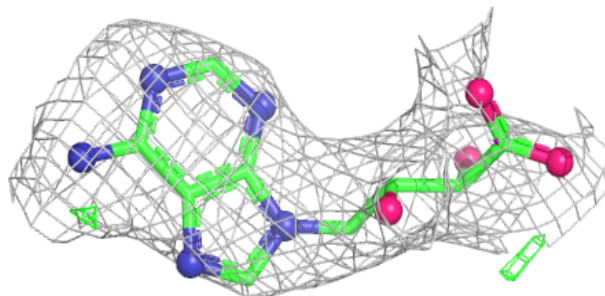
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	DEA	F	6433	18/18	0.89	0.10	2,2,4,4	0
3	DEA	E	5433	18/18	0.90	0.09	2,2,3,3	0
2	NAD	A	1432	44/44	0.92	0.10	2,2,3,4	0
2	NAD	H	8432	44/44	0.92	0.10	2,2,4,5	0
2	NAD	B	2432	44/44	0.93	0.10	2,2,3,4	0
2	NAD	C	3432	44/44	0.93	0.10	2,2,3,3	0
2	NAD	D	4432	44/44	0.93	0.09	2,2,3,3	0
2	NAD	G	7432	44/44	0.94	0.08	2,2,3,3	0
2	NAD	F	6432	44/44	0.94	0.09	2,2,3,4	0
2	NAD	E	5432	44/44	0.95	0.09	2,2,3,4	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.

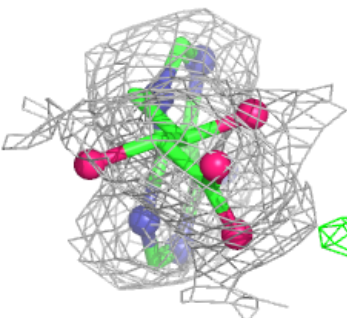
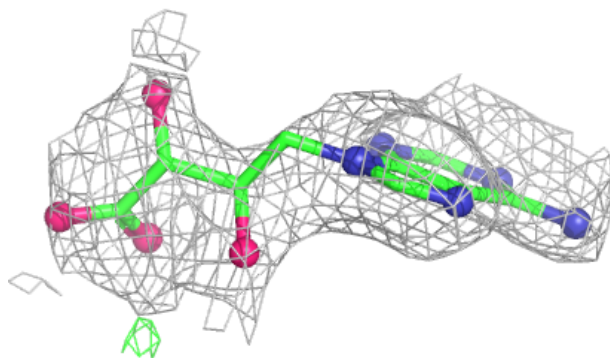
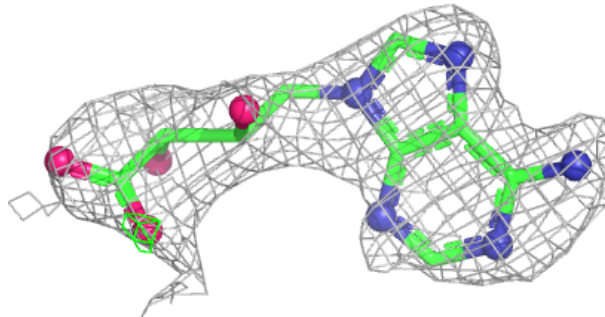


Electron density around DEA B 2433:

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

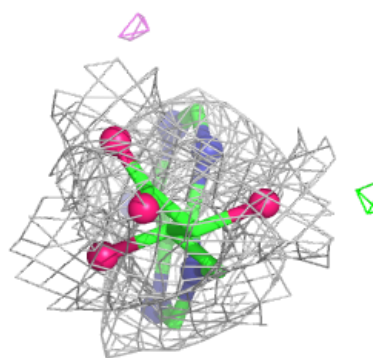
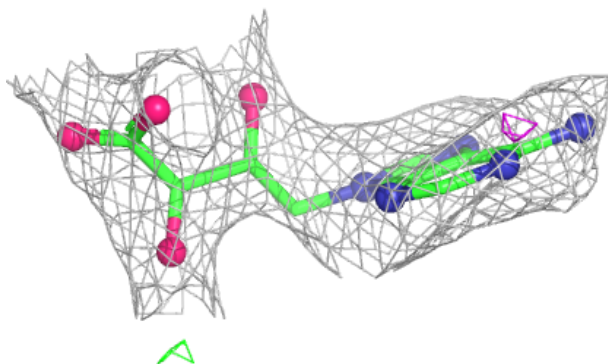
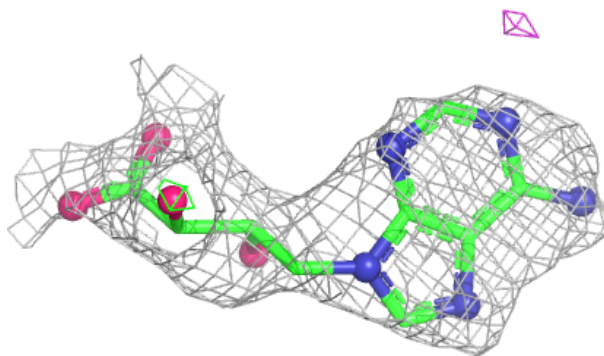
**Electron density around DEA D 4433:**

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

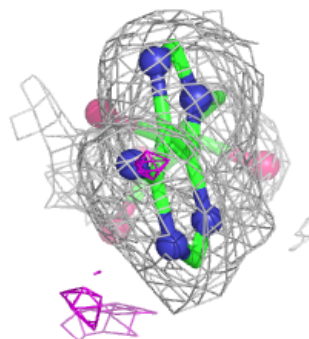
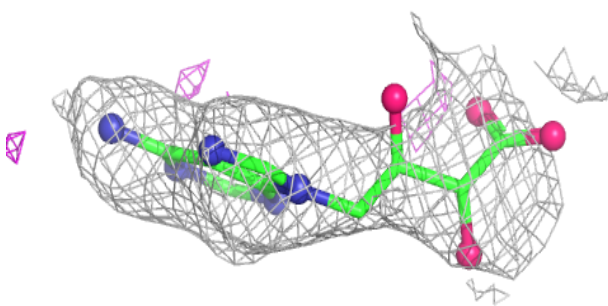
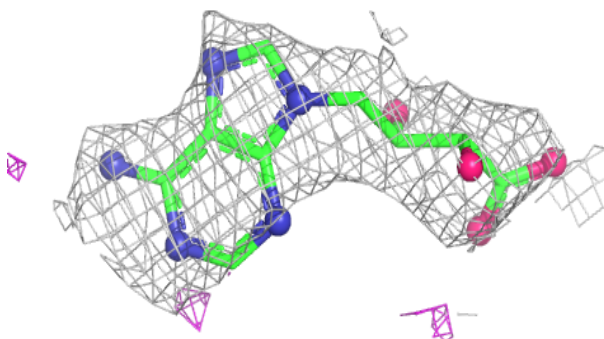


Electron density around DEA H 8433:

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

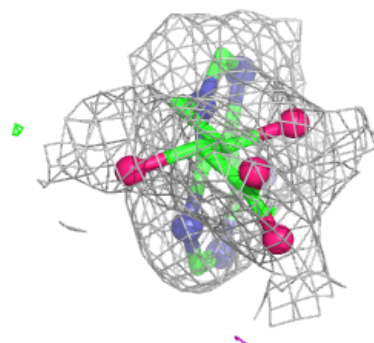
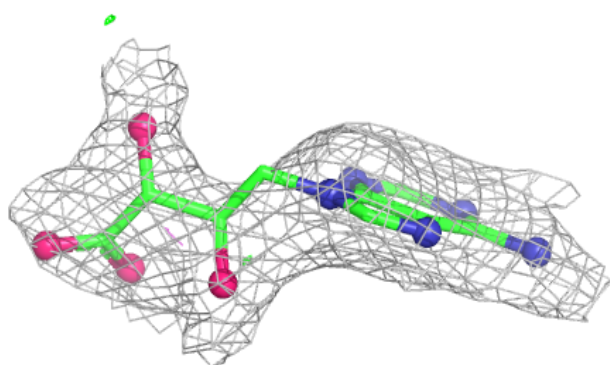
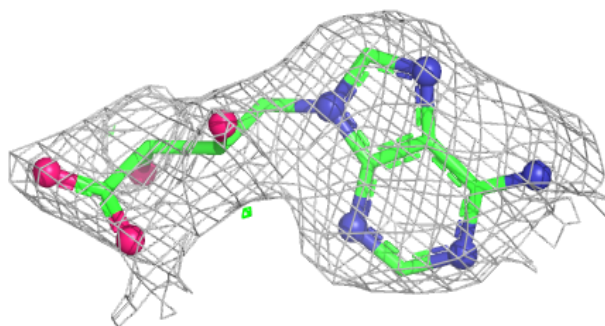
**Electron density around DEA G 7433:**

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

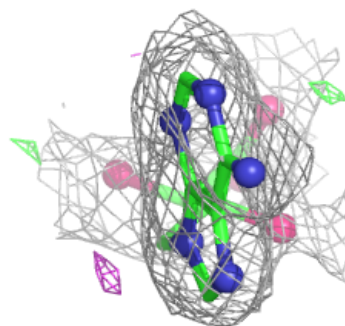
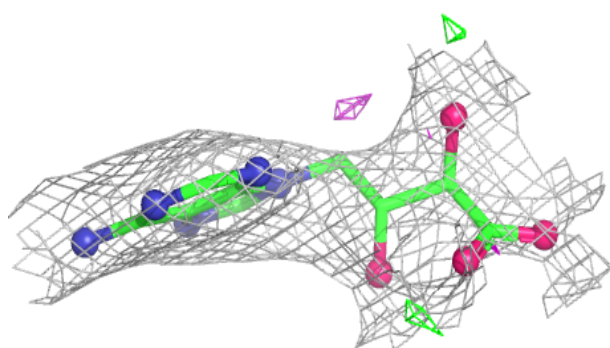
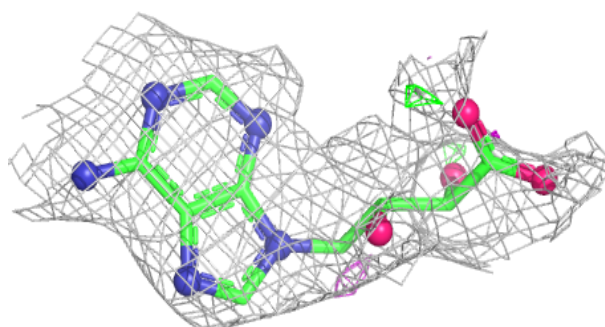


Electron density around DEA A 1433:

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

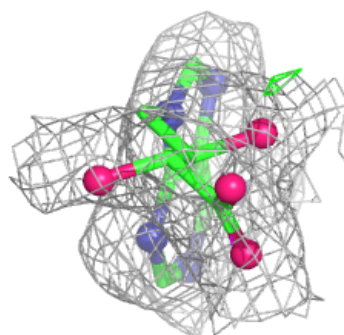
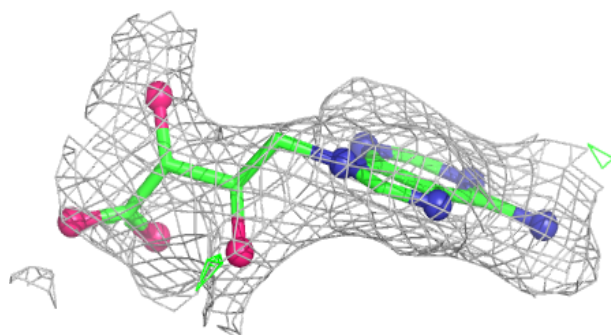
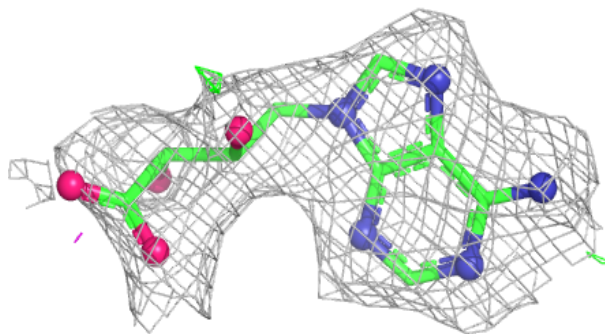
**Electron density around DEA F 6433:**

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

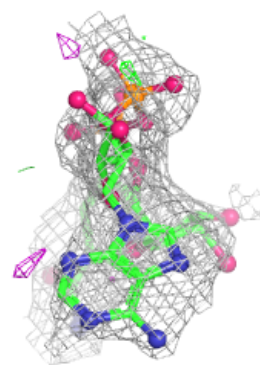
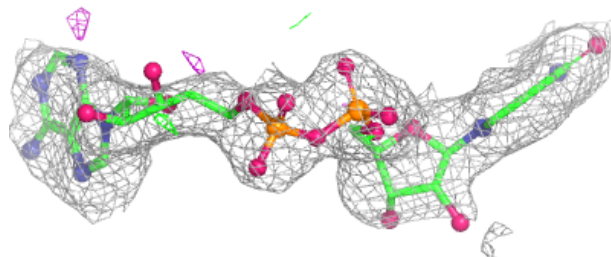
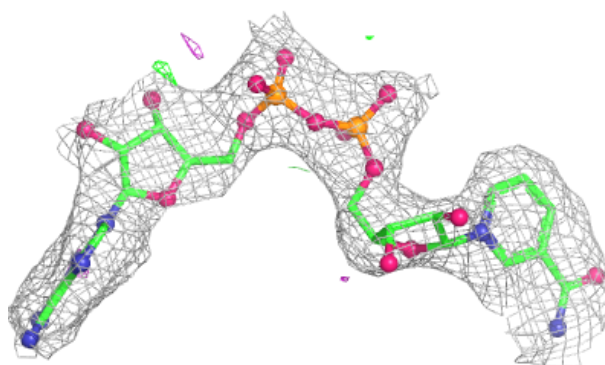


Electron density around DEA E 5433:

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

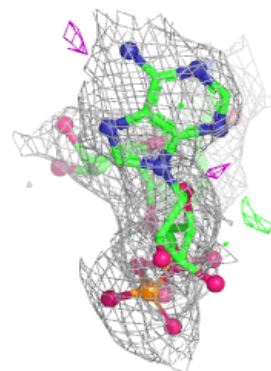
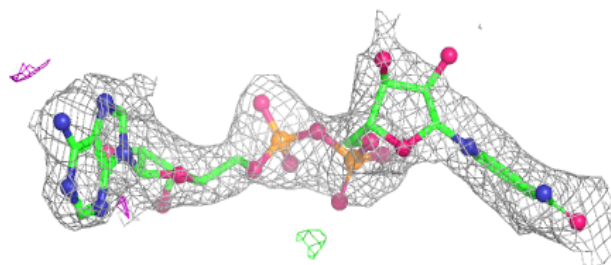
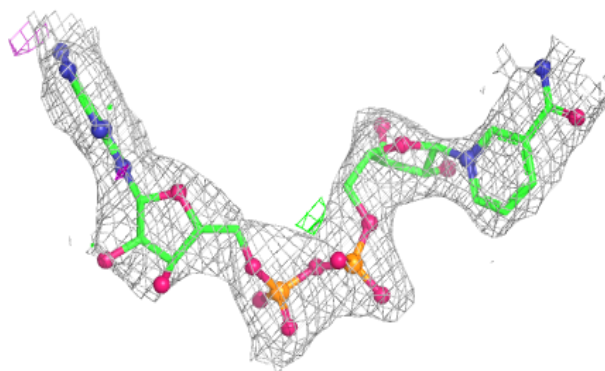
**Electron density around NAD A 1432:**

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

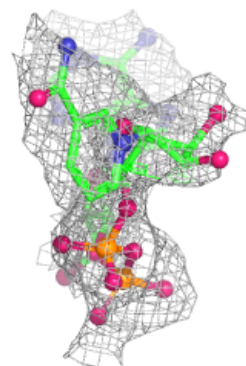
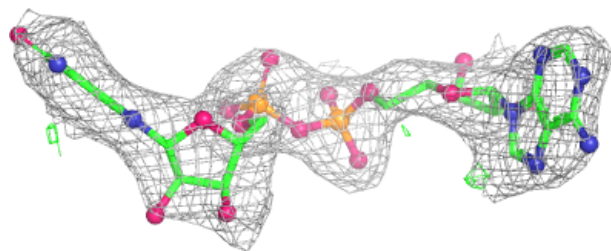
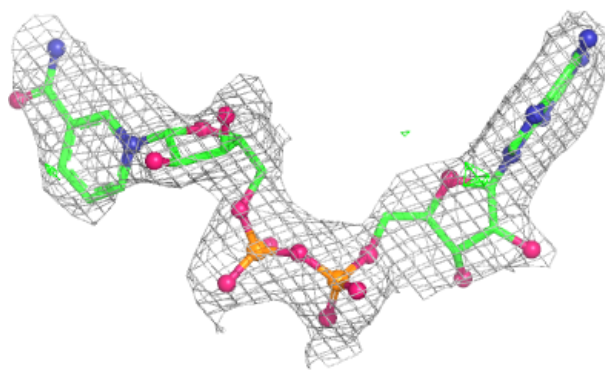


Electron density around NAD H 8432:

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

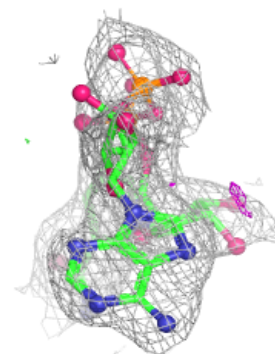
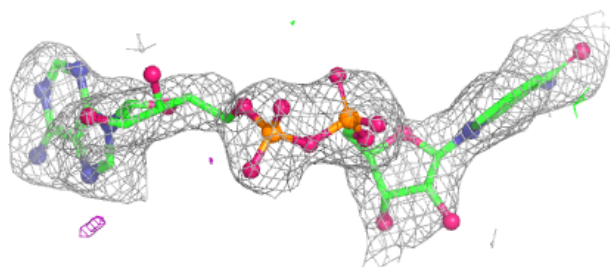
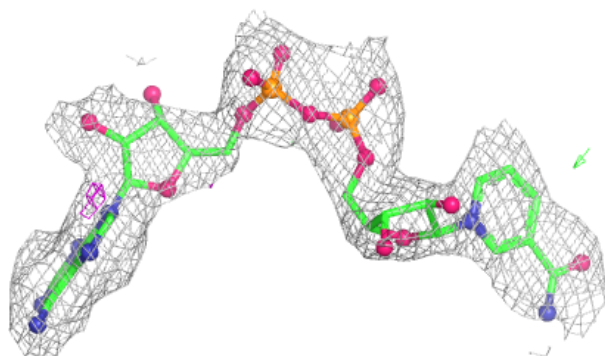
**Electron density around NAD B 2432:**

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

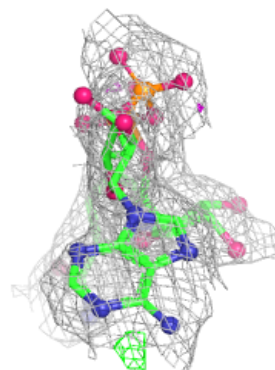
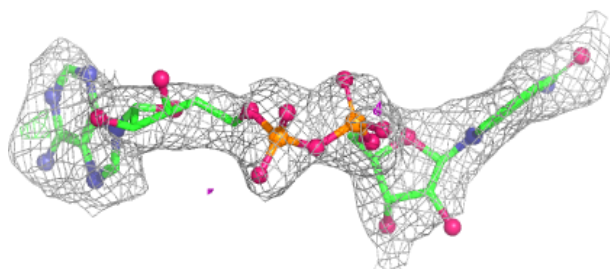
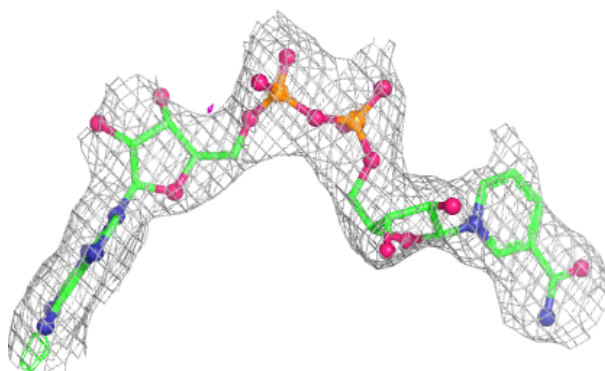


Electron density around NAD C 3432:

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

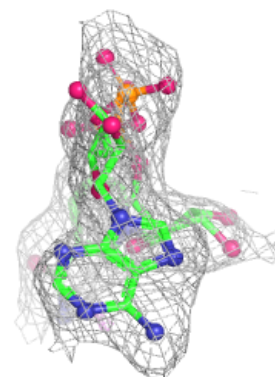
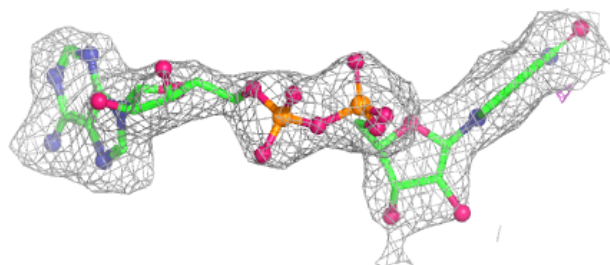
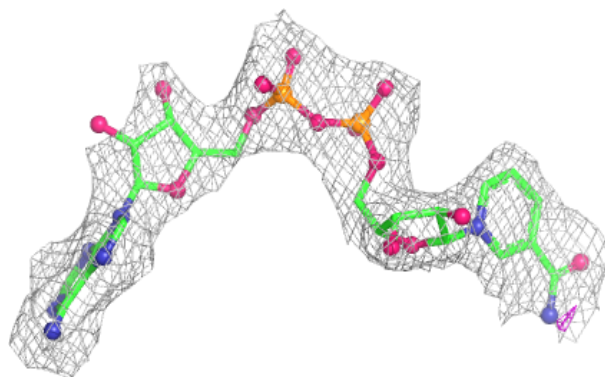
**Electron density around NAD D 4432:**

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

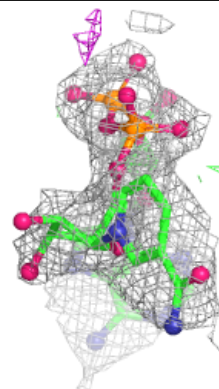
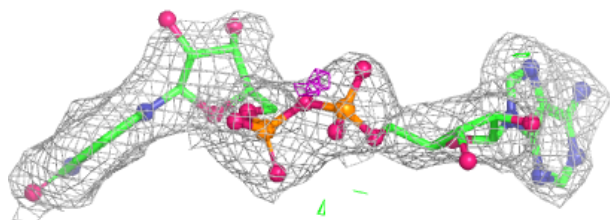
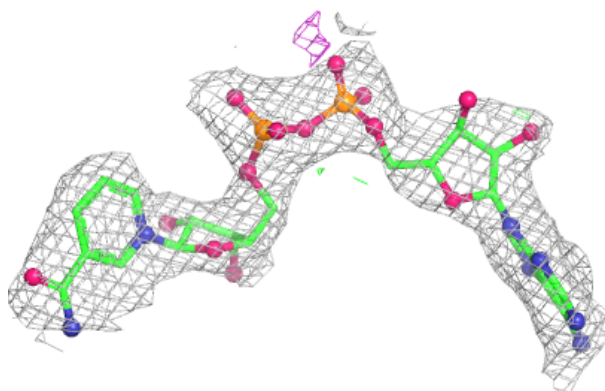


Electron density around NAD G 7432:

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

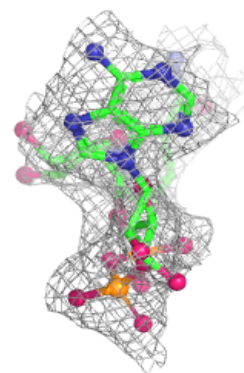
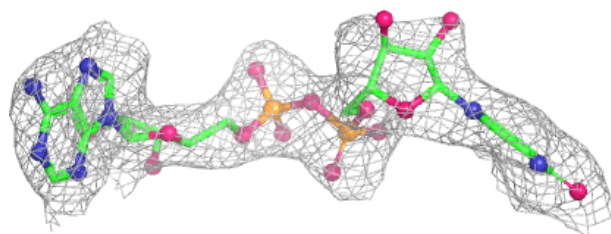
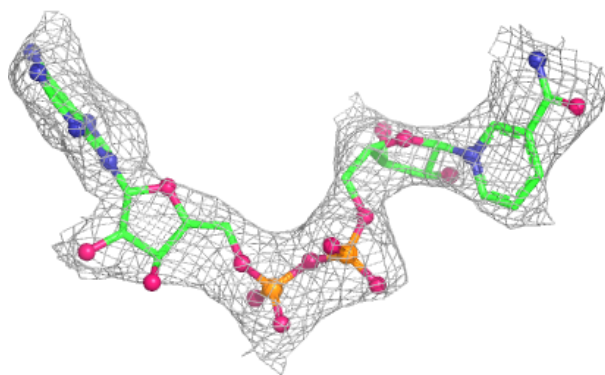
**Electron density around NAD F 6432:**

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



Electron density around NAD E 5432:

$2mF_o - DF_c$ (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.