



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 09:41 PM UTC

PDB ID : 8ARP / pdb_00008arp
Title : Crystal structure of DEAD-box protein Dbp2 in complex with ADP
Authors : Song, Q.X.; Rety, S.; Xi, X.G.
Deposited on : 2022-08-17
Resolution : 3.05 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

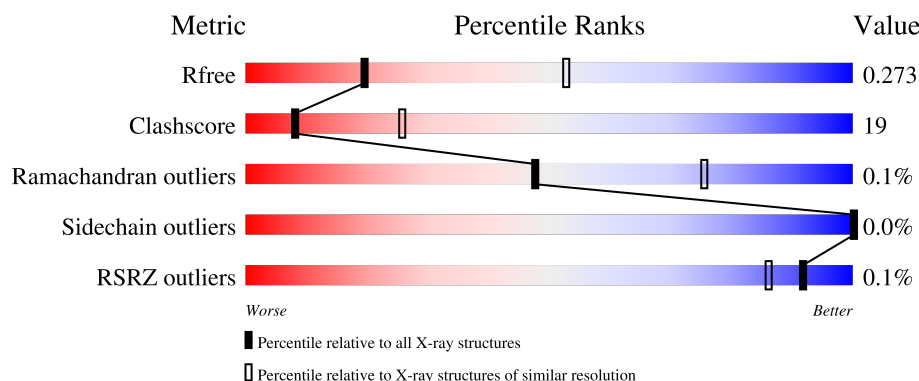
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.05 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	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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	546	
1	B	546	
1	C	546	
1	D	546	
1	E	546	

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Mol	Chain	Length	Quality of chain
1	F	546	53% 28% 19%

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	E	2002	-	-	X	-

2 Entry composition [i](#)

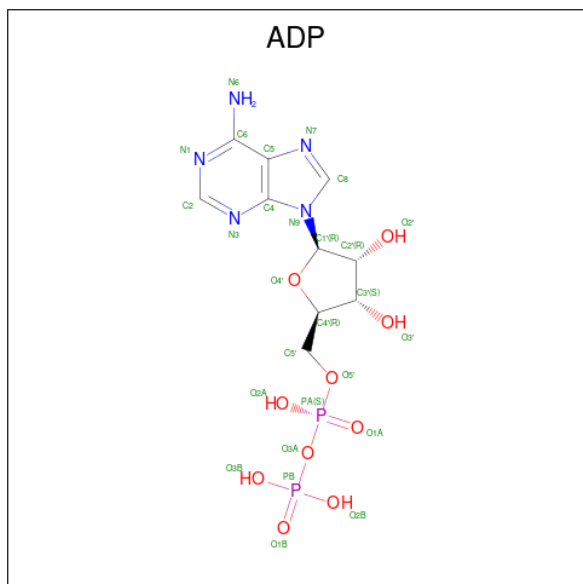
There are 4 unique types of molecules in this entry. The entry contains 21294 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ATP-dependent RNA helicase DBP2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	443	Total	C	N	O	S	0	0	0
			3505	2202	616	671	16			
1	B	444	Total	C	N	O	S	0	0	0
			3516	2208	620	672	16			
1	C	445	Total	C	N	O	S	0	0	0
			3528	2217	621	674	16			
1	D	444	Total	C	N	O	S	0	0	0
			3516	2208	620	672	16			
1	E	444	Total	C	N	O	S	0	0	0
			3516	2208	620	672	16			
1	F	443	Total	C	N	O	S	0	0	0
			3508	2204	618	670	16			

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	O S	0	0
			5 4 1			
3	B	1	Total	O S	0	0
			5 4 1			
3	C	1	Total	O S	0	0
			5 4 1			
3	D	1	Total	O S	0	0
			5 4 1			
3	E	1	Total	O S	0	0
			5 4 1			
3	E	1	Total	O S	0	0
			5 4 1			

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	E	1	Total	O	S	0	0
			5	4	1		
3	F	1	Total	O	S	0	0
			5	4	1		

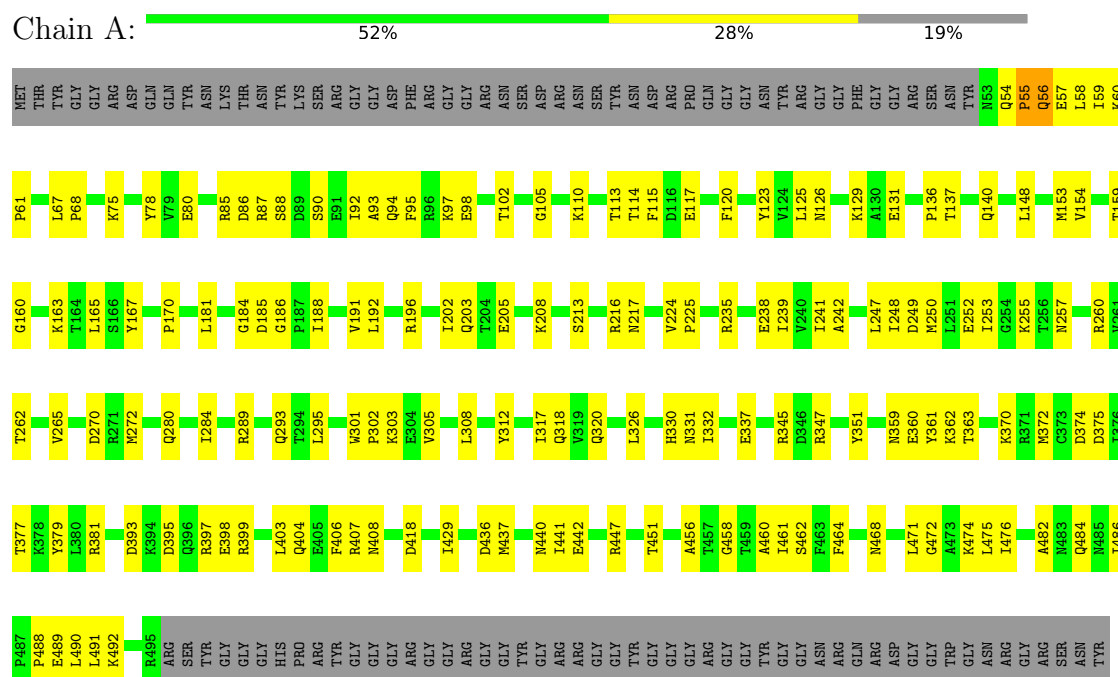
- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		
4	C	1	Total	Mg	0	0
			1	1		
4	E	1	Total	Mg	0	0
			1	1		

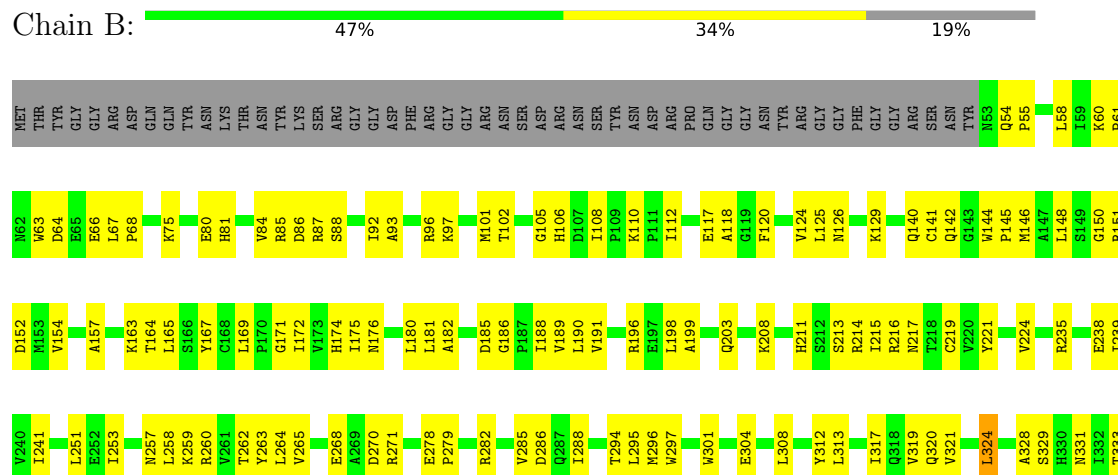
3 Residue-property plots

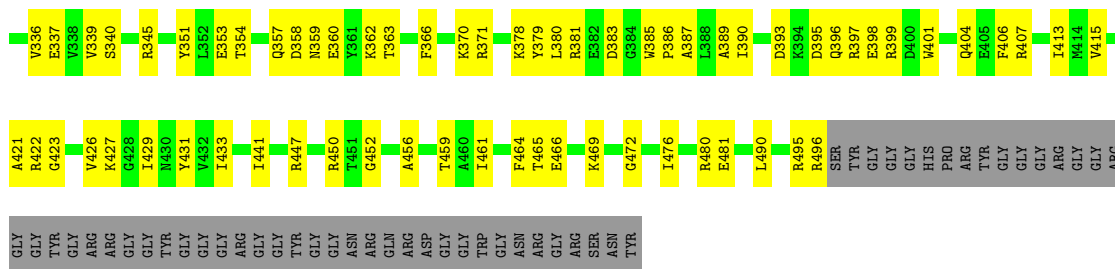
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: ATP-dependent RNA helicase DBP2

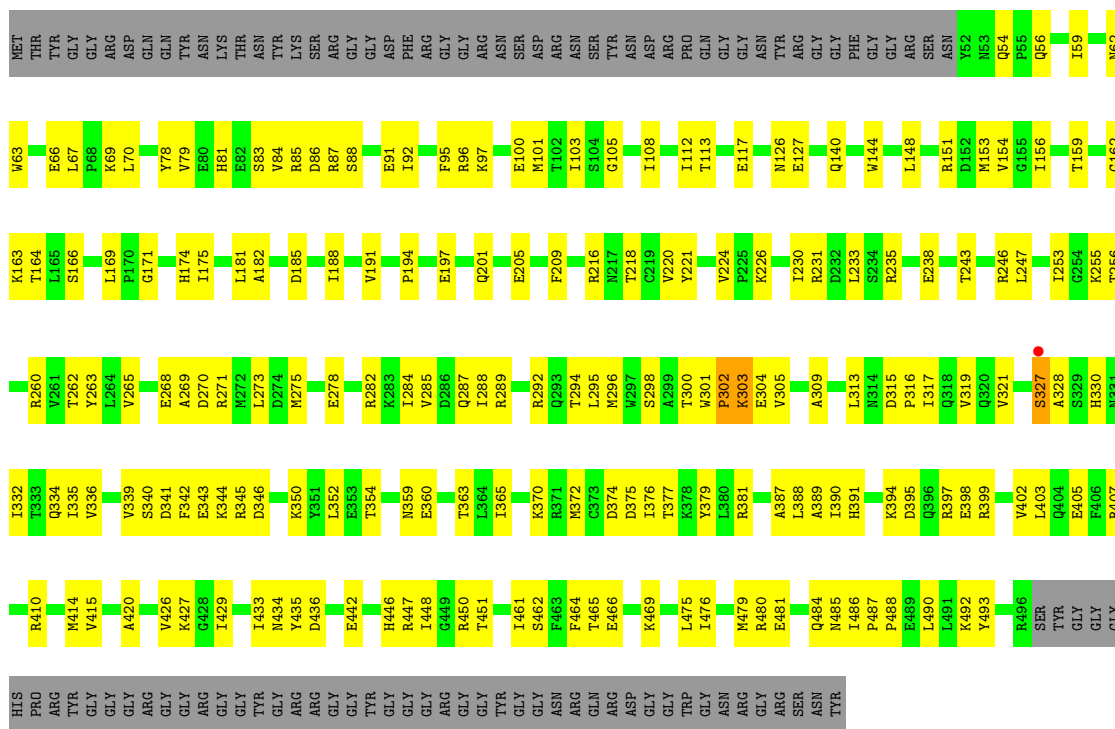


• Molecule 1: ATP-dependent RNA helicase DBP2

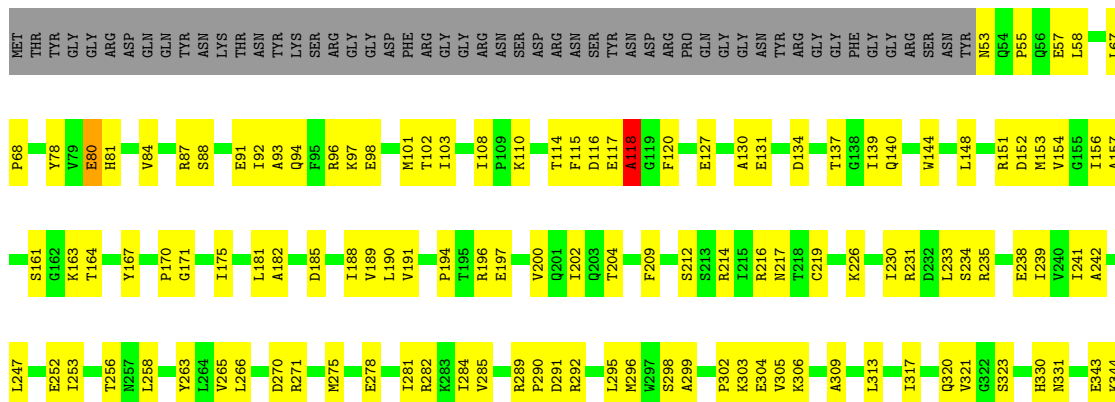


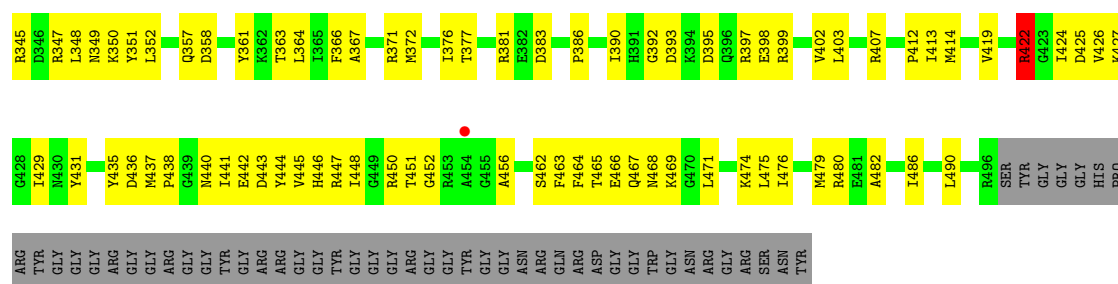


- Molecule 1: ATP-dependent RNA helicase DBP2



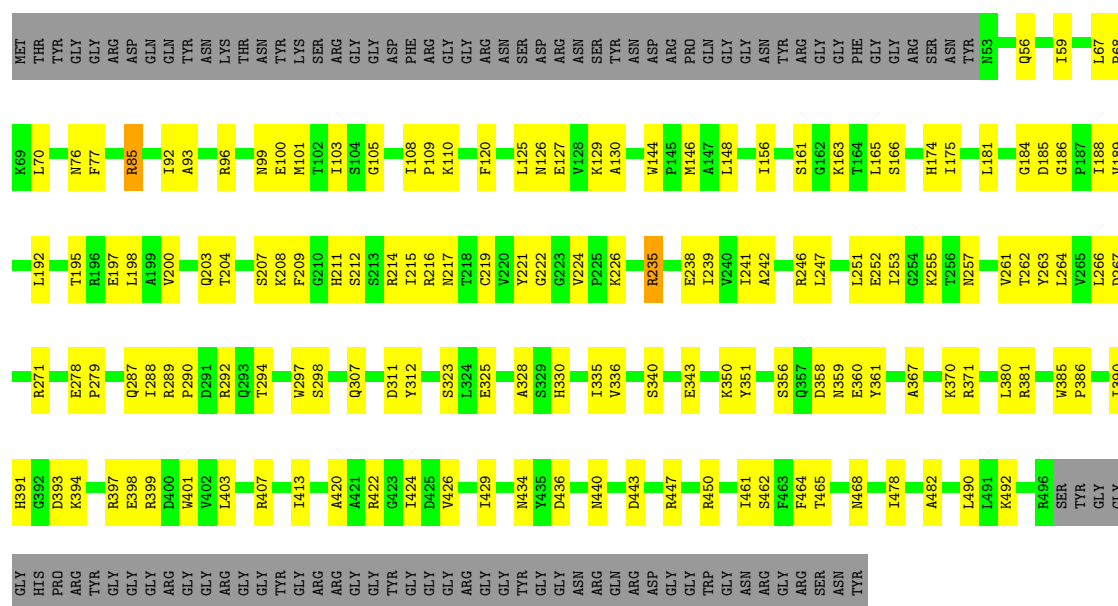
- Molecule 1: ATP-dependent RNA helicase DBP2





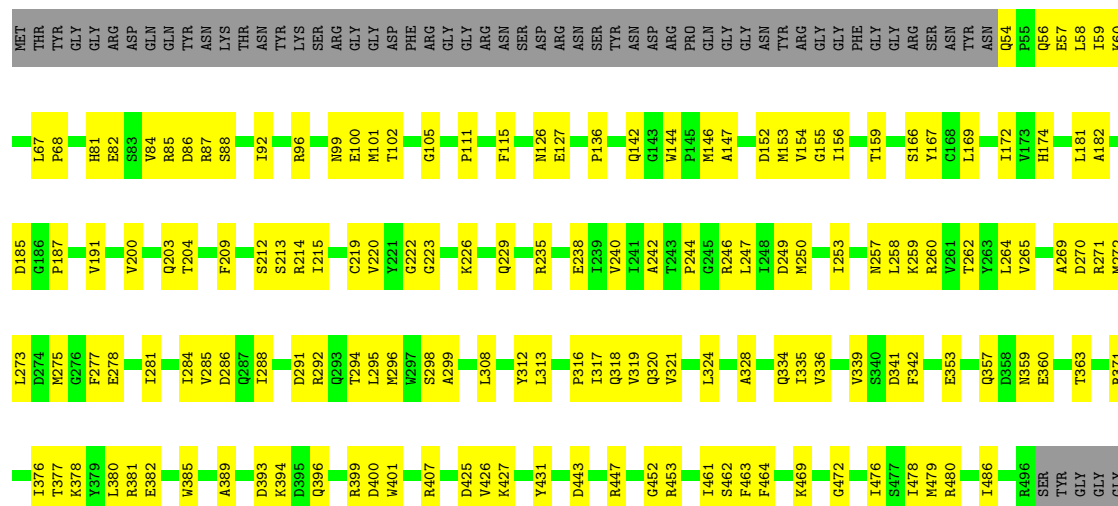
• Molecule 1: ATP-dependent RNA helicase DBP2

Chain E: 54% 27% 19%



• Molecule 1: ATP-dependent RNA helicase DBP2

Chain F: 53% 28% 19%



HIS
PRO
ARG
TYR
GLY
GLY
GLY
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ASN
ARG
GLN
ARG
ASP
GLY
GLY
TRP
GLY
ASN
ASN
ARG
GLY
ARG
SER
ASN
TYR

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	145.94Å 168.84Å 168.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	119.40 – 3.05 119.40 – 3.05	Depositor EDS
% Data completeness (in resolution range)	96.2 (119.40-3.05) 96.1 (119.40-3.05)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 3.07Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.223 , 0.270 0.227 , 0.273	Depositor DCC
R_{free} test set	3779 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	77.6	Xtriage
Anisotropy	0.481	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 125.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.22$	Xtriage
Estimated twinning fraction	0.428 for -h,l,k	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	21294	wwPDB-VP
Average B, all atoms (Å ²)	110.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.01% 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: SO4, ADP, MG

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	0.18	0/3574	0.50	2/4840 (0.0%)
1	B	0.22	0/3585	0.55	0/4854
1	C	0.22	0/3598	0.61	2/4872 (0.0%)
1	D	0.20	0/3585	0.59	1/4854 (0.0%)
1	E	0.21	0/3585	0.53	0/4854
1	F	0.19	0/3577	0.50	0/4843
All	All	0.20	0/21504	0.55	5/29117 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	3
1	E	0	2
1	F	0	2
All	All	0	13

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	302	PRO	CA-C-N	8.13	136.33	121.70
1	C	302	PRO	C-N-CA	8.13	136.33	121.70
1	A	55	PRO	CA-C-N	7.25	137.78	125.02
1	A	55	PRO	C-N-CA	7.25	137.78	125.02

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Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	D	118	ALA	N-CA-C	-5.30	100.27	108.90

There are no chirality outliers.

All (13) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	56	GLN	Peptide
1	A	58	LEU	Peptide
1	B	324	LEU	Peptide
1	B	81	HIS	Peptide
1	C	303	LYS	Peptide
1	C	56	GLN	Peptide
1	D	118	ALA	Peptide
1	D	323	SER	Peptide
1	D	422	ARG	Sidechain
1	E	235	ARG	Sidechain
1	E	85	ARG	Peptide
1	F	324	LEU	Peptide
1	F	56	GLN	Peptide

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	3505	0	3485	113	0
1	B	3516	0	3498	163	0
1	C	3528	0	3508	170	0
1	D	3516	0	3498	175	0
1	E	3516	0	3497	118	0
1	F	3508	0	3493	122	0
2	A	27	0	12	5	0
2	B	27	0	12	0	0
2	C	27	0	12	1	0
2	D	27	0	12	2	0
2	E	27	0	12	0	0
2	F	27	0	12	1	0
3	A	5	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	5	0	0	0	0
3	C	5	0	0	0	0
3	D	5	0	0	0	0
3	E	15	0	0	3	0
3	F	5	0	0	0	0
4	A	1	0	0	0	0
4	C	1	0	0	0	0
4	E	1	0	0	0	0
All	All	21294	0	21051	821	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 19.

All (821) 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:D:78:TYR:OH	1:D:110:LYS:NZ	1.95	0.98
1:C:330:HIS:NE2	1:C:481:GLU:OE2	2.08	0.87
1:C:302:PRO:HB2	1:C:304:GLU:H	1.39	0.87
1:C:397:ARG:NH1	1:F:213:SER:O	2.09	0.85
1:E:59:ILE:O	1:E:287:GLN:NE2	2.14	0.80
1:D:427:LYS:HZ3	1:D:451:THR:HA	1.46	0.80
1:F:57:GLU:OE2	1:F:59:ILE:N	2.15	0.80
1:E:307:GLN:NE2	1:E:311:ASP:OD2	2.15	0.79
1:D:152:ASP:HB3	1:D:313:LEU:HD23	1.65	0.78
1:B:60:LYS:NZ	1:B:61:PRO:O	2.15	0.78
1:C:156:ILE:HG21	1:C:301:TRP:HB2	1.65	0.78
1:D:437:MET:HE2	1:D:462:SER:HB3	1.65	0.78
1:B:336:VAL:HG11	1:B:490:LEU:HD13	1.64	0.78
1:C:66:GLU:OE1	1:C:69:LYS:NZ	2.17	0.77
1:B:196:ARG:NH2	1:B:393:ASP:OD2	2.17	0.77
1:A:148:LEU:HD22	1:A:170:PRO:HB3	1.66	0.77
1:D:235:ARG:HG3	1:D:235:ARG:HH11	1.50	0.77
1:F:147:ALA:HB2	1:F:153:MET:HE1	1.67	0.77
1:B:397:ARG:NH1	1:E:214:ARG:O	2.17	0.76
1:A:404:GLN:O	1:A:408:ASN:ND2	2.17	0.76
1:C:390:ILE:HG22	1:C:420:ALA:HB1	1.68	0.76
1:D:426:VAL:HG13	1:D:429:ILE:HD11	1.68	0.76
1:F:57:GLU:OE2	1:F:59:ILE:HG13	1.86	0.76
1:D:87:ARG:HG2	1:D:92:ILE:HG23	1.68	0.75
1:F:380:LEU:HB3	1:F:385:TRP:HB2	1.69	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:196:ARG:NH1	1:D:371:ARG:HD2	2.01	0.75
1:A:440:ASN:ND2	1:A:442:GLU:OE1	2.17	0.75
1:F:127:GLU:OE2	1:F:212:SER:OG	2.05	0.74
1:C:334:GLN:O	1:C:485:ASN:ND2	2.18	0.74
1:E:371:ARG:HG2	1:E:371:ARG:HH11	1.53	0.73
1:A:196:ARG:NH2	1:A:393:ASP:OD2	2.20	0.73
1:F:335:ILE:HD11	1:F:461:ILE:HA	1.70	0.73
1:D:139:ILE:HG13	1:D:321:VAL:HG21	1.71	0.73
1:A:192:LEU:HB3	1:A:272:MET:HE1	1.68	0.73
1:E:267:ASP:HA	1:E:297:TRP:HB2	1.70	0.73
1:B:188:ILE:HD13	1:B:260:ARG:O	1.89	0.73
1:D:175:ILE:HG23	1:D:188:ILE:HD11	1.71	0.72
1:A:105:GLY:HA3	1:A:317:ILE:HG22	1.71	0.72
1:D:372:MET:HE3	1:D:436:ASP:OD2	1.89	0.72
1:A:476:ILE:HG23	1:A:486:ILE:HG12	1.71	0.72
1:D:171:GLY:HA2	1:D:263:TYR:CE2	2.24	0.72
1:A:203:GLN:HB2	1:A:241:ILE:HD13	1.72	0.71
1:D:67:LEU:HD22	1:D:290:PRO:HG2	1.73	0.71
1:F:389:ALA:O	1:F:394:LYS:NZ	2.21	0.71
1:A:160:GLY:HA2	2:A:2001:ADP:O1A	1.92	0.70
1:C:153:MET:HG2	1:C:295:LEU:HD22	1.73	0.70
1:C:182:ALA:HB3	1:C:185:ASP:OD2	1.92	0.70
1:A:332:ILE:HD11	1:A:460:ALA:HB2	1.74	0.69
1:B:358:ASP:OD1	1:B:359:ASN:N	2.25	0.69
1:D:156:ILE:HD11	1:D:320:GLN:HA	1.75	0.69
1:E:424:ILE:HD13	1:E:426:VAL:HG12	1.75	0.69
1:C:436:ASP:O	1:C:447:ARG:NH1	2.23	0.69
1:A:262:THR:HG22	1:A:289:ARG:HD3	1.75	0.69
1:B:407:ARG:HD2	1:B:426:VAL:HG23	1.73	0.69
1:A:205:GLU:OE2	2:A:2001:ADP:H3'	1.92	0.69
1:F:174:HIS:NE2	1:F:262:THR:OG1	2.25	0.68
1:C:484:GLN:HG2	1:C:485:ASN:O	1.92	0.68
1:B:54:GLN:HG2	1:B:253:ILE:HG22	1.76	0.68
1:C:247:LEU:HD23	1:C:284:ILE:HD13	1.75	0.68
1:C:402:VAL:HG12	1:C:414:MET:HE2	1.76	0.68
1:B:464:PHE:HD1	1:B:465:THR:N	1.92	0.67
1:B:58:LEU:HD21	1:B:251:LEU:HD12	1.75	0.67
1:F:54:GLN:N	1:F:249:ASP:OD1	2.28	0.67
1:F:242:ALA:HB1	1:F:247:LEU:HB2	1.76	0.67
1:B:58:LEU:HD11	1:B:251:LEU:HB2	1.76	0.67
1:F:102:THR:OG1	1:F:320:GLN:NE2	2.27	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:67:LEU:HD23	1:E:70:LEU:HD12	1.77	0.67
1:F:288:ILE:HD13	1:F:292:ARG:HD2	1.78	0.66
1:E:288:ILE:HD13	1:E:292:ARG:HD3	1.75	0.66
1:B:380:LEU:HD11	1:B:387:ALA:HB2	1.76	0.66
1:D:197:GLU:OE2	1:D:392:GLY:N	2.28	0.66
1:B:60:LYS:HZ1	1:B:63:TRP:CD1	2.14	0.66
1:C:372:MET:O	1:C:376:ILE:HG13	1.96	0.66
1:C:442:GLU:O	1:C:446:HIS:ND1	2.28	0.66
1:C:78:TYR:HB2	1:C:148:LEU:HB3	1.78	0.66
1:A:55:PRO:HB2	1:A:56:GLN:HG3	1.77	0.66
1:B:259:LYS:NZ	1:C:342:PHE:O	2.28	0.66
1:C:377:THR:HG21	1:C:389:ALA:HB2	1.78	0.66
1:F:476:ILE:HG23	1:F:486:ILE:HG12	1.78	0.66
1:F:215:ILE:HG23	1:F:238:GLU:HB2	1.77	0.65
1:D:81:HIS:CD2	1:D:117:GLU:HG2	2.30	0.65
1:E:358:ASP:OD1	1:E:361:TYR:HB3	1.96	0.65
1:A:488:PRO:HA	1:A:491:LEU:HD13	1.79	0.65
1:C:345:ARG:NH2	1:C:379:TYR:O	2.28	0.65
1:A:54:GLN:HB3	1:A:253:ILE:HG22	1.79	0.65
1:B:87:ARG:N	1:B:88:SER:OG	2.24	0.65
1:D:190:LEU:HD11	1:D:258:LEU:HD22	1.77	0.65
1:A:437:MET:SD	1:A:462:SER:OG	2.55	0.64
1:D:427:LYS:HE2	1:D:452:GLY:H	1.62	0.64
1:C:426:VAL:HG13	1:C:429:ILE:HD11	1.78	0.64
1:D:357:GLN:OE1	1:D:357:GLN:N	2.30	0.64
1:D:402:VAL:HG12	1:D:414:MET:HE2	1.79	0.64
1:C:391:HIS:HE1	1:C:394:LYS:HB2	1.63	0.64
1:D:78:TYR:HH	1:D:110:LYS:NZ	1.95	0.64
1:C:390:ILE:HD11	1:C:402:VAL:HB	1.79	0.64
1:A:472:GLY:O	1:A:476:ILE:HD12	1.98	0.64
1:B:221:TYR:HE1	1:B:224:VAL:HG11	1.62	0.64
1:F:100:GLU:HG3	1:F:321:VAL:O	1.97	0.64
1:F:182:ALA:HB3	1:F:185:ASP:OD2	1.98	0.63
1:B:215:ILE:HG23	1:B:238:GLU:HB2	1.79	0.63
1:B:165:LEU:HD12	1:B:169:LEU:HD11	1.78	0.63
1:D:467:GLN:OE1	1:D:469:LYS:NZ	2.30	0.63
1:A:440:ASN:OD1	1:A:441:ILE:N	2.32	0.63
1:F:222:GLY:HA2	1:F:246:ARG:HE	1.62	0.63
1:D:442:GLU:O	1:D:446:HIS:ND1	2.32	0.63
1:B:216:ARG:NH1	1:B:235:ARG:O	2.32	0.63
1:C:302:PRO:HB2	1:C:304:GLU:N	2.13	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:264:LEU:HB3	1:E:294:THR:HG22	1.80	0.63
1:F:226:LYS:HG3	1:F:246:ARG:HH11	1.64	0.62
1:C:151:ARG:NH2	1:C:315:ASP:O	2.30	0.62
1:C:103:ILE:HG22	1:C:319:VAL:HG22	1.80	0.62
1:D:196:ARG:HH12	1:D:371:ARG:HD2	1.64	0.62
1:E:188:ILE:HA	1:E:261:VAL:HA	1.81	0.62
1:A:137:THR:N	1:A:140:GLN:OE1	2.32	0.62
1:C:218:THR:HG21	1:C:233:LEU:HD12	1.81	0.62
1:B:203:GLN:HB3	1:B:241:ILE:HG13	1.82	0.62
1:B:214:ARG:O	1:E:397:ARG:NH2	2.33	0.62
1:C:83:SER:OG	1:C:117:GLU:OE2	2.14	0.62
1:D:464:PHE:HD1	1:D:465:THR:N	1.97	0.62
1:E:271:ARG:HD2	1:E:440:ASN:HB3	1.82	0.62
1:A:92:ILE:HG12	1:A:110:LYS:HZ1	1.64	0.61
1:D:464:PHE:CE1	1:D:468:ASN:HB2	2.34	0.61
1:A:249:ASP:O	1:A:253:ILE:HG23	2.00	0.61
1:D:242:ALA:HB1	1:D:247:LEU:HB2	1.82	0.61
1:D:427:LYS:NZ	1:D:451:THR:HA	2.15	0.61
1:A:120:PHE:HE1	1:A:148:LEU:HD21	1.64	0.61
1:A:395:ASP:HA	1:A:398:GLU:HG3	1.83	0.61
1:B:106:HIS:O	1:B:151:ARG:NH2	2.34	0.61
1:C:96:ARG:O	1:C:100:GLU:N	2.34	0.61
1:D:331:ASN:ND2	1:D:456:ALA:HB1	2.16	0.61
1:A:78:TYR:HB2	1:A:148:LEU:HB3	1.83	0.60
1:A:126:ASN:HB2	1:D:130:ALA:HB2	1.83	0.60
1:A:337:GLU:OE2	1:A:351:TYR:OH	2.11	0.60
1:D:118:ALA:O	1:D:120:PHE:N	2.29	0.60
1:C:327:SER:OG	1:C:328:ALA:N	2.35	0.60
1:C:101:MET:HB3	1:C:321:VAL:HG22	1.83	0.60
1:C:171:GLY:HA2	1:C:263:TYR:CE2	2.35	0.60
1:D:171:GLY:HA2	1:D:263:TYR:HE2	1.62	0.60
1:E:290:PRO:HA	1:E:292:ARG:NH1	2.17	0.60
1:F:377:THR:HG21	1:F:389:ALA:HB2	1.82	0.60
1:C:216:ARG:NH1	1:C:235:ARG:O	2.35	0.60
1:B:112:ILE:HD11	1:B:145:PRO:HD3	1.84	0.60
1:D:372:MET:O	1:D:376:ILE:HD12	2.01	0.60
1:F:407:ARG:HG2	1:F:426:VAL:HG13	1.84	0.60
1:C:235:ARG:NH1	1:F:393:ASP:O	2.31	0.60
1:D:443:ASP:O	1:D:447:ARG:HG3	2.02	0.60
1:E:424:ILE:HD11	1:E:450:ARG:HD2	1.82	0.60
1:B:54:GLN:N	1:B:55:PRO:HD3	2.18	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:57:GLU:HG3	1:D:252:GLU:HG2	1.84	0.59
1:C:230:ILE:HD12	1:C:231:ARG:N	2.18	0.59
1:D:361:TYR:HD2	1:D:363:THR:HG23	1.68	0.59
1:B:92:ILE:HD12	1:B:110:LYS:HG2	1.83	0.59
1:F:60:LYS:HE2	1:F:286:ASP:HB3	1.84	0.59
1:A:451:THR:HG22	1:A:458:GLY:HA3	1.84	0.59
1:B:386:PRO:HD3	1:D:386:PRO:HB3	1.84	0.59
1:D:358:ASP:OD1	1:D:361:TYR:HB3	2.03	0.59
1:B:112:ILE:N	1:B:141:CYS:O	2.33	0.59
1:D:157:ALA:HB3	1:D:163:LYS:HD3	1.84	0.59
1:F:269:ALA:N	1:F:298:SER:OG	2.35	0.59
1:A:331:ASN:OD1	1:A:456:ALA:HB1	2.03	0.59
1:D:367:ALA:HA	1:D:436:ASP:HB2	1.84	0.59
1:B:191:VAL:HG12	1:B:265:VAL:HB	1.84	0.58
1:C:96:ARG:HD3	1:C:101:MET:HE3	1.85	0.58
1:E:464:PHE:CE1	1:E:468:ASN:HB2	2.37	0.58
1:E:127:GLU:OE2	1:E:212:SER:HB2	2.03	0.58
1:D:270:ASP:OD1	1:D:271:ARG:N	2.34	0.58
1:A:482:ALA:O	1:A:484:GLN:NE2	2.35	0.58
1:C:475:LEU:HD12	1:C:476:ILE:N	2.19	0.58
1:F:353:GLU:O	1:F:357:GLN:NE2	2.35	0.58
1:E:323:SER:HB3	1:E:325:GLU:HG3	1.86	0.58
1:B:345:ARG:NH2	1:B:379:TYR:O	2.36	0.58
1:B:381:ARG:NH2	1:B:387:ALA:O	2.34	0.58
1:B:120:PHE:CE1	1:B:148:LEU:HD11	2.39	0.57
1:D:226:LYS:O	1:D:230:ILE:HG23	2.04	0.57
1:D:115:PHE:HE2	1:D:134:ASP:HA	1.68	0.57
1:E:189:VAL:HG22	1:E:263:TYR:HB3	1.86	0.57
1:B:87:ARG:HB2	1:B:88:SER:HA	1.85	0.57
1:F:318:GLN:OE1	1:F:318:GLN:N	2.32	0.57
1:B:363:THR:OG1	1:B:431:TYR:O	2.11	0.57
1:C:163:LYS:NZ	1:C:268:GLU:OE2	2.31	0.57
1:D:110:LYS:H	1:D:110:LYS:HD3	1.67	0.57
1:A:395:ASP:O	1:A:399:ARG:HB2	2.03	0.57
1:B:84:VAL:HG22	1:B:117:GLU:OE2	2.04	0.57
1:B:214:ARG:NH2	1:E:208:LYS:NZ	2.53	0.57
1:B:378:LYS:HG2	1:B:381:ARG:HD2	1.86	0.57
1:F:87:ARG:H	1:F:88:SER:HB2	1.69	0.57
1:A:95:PHE:HA	1:A:98:GLU:CD	2.29	0.57
1:F:142:GLN:HG3	1:F:146:MET:HE3	1.87	0.57
1:C:194:PRO:HB2	1:C:275:MET:HE1	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:422:ARG:HE	1:B:423:GLY:N	2.03	0.56
1:D:395:ASP:HA	1:D:398:GLU:HB2	1.86	0.56
1:E:381:ARG:NH2	3:E:2002:SO4:O1	2.37	0.56
1:E:99:ASN:HB2	1:E:101:MET:SD	2.45	0.56
1:F:167:TYR:CG	1:F:265:VAL:HG21	2.40	0.56
1:D:57:GLU:CD	1:D:58:LEU:H	2.13	0.56
1:C:159:THR:HG22	1:C:163:LYS:NZ	2.21	0.56
1:A:436:ASP:O	1:A:447:ARG:NH2	2.38	0.56
1:C:54:GLN:HB2	1:C:253:ILE:HG23	1.87	0.56
1:D:299:ALA:HB1	1:D:442:GLU:OE2	2.06	0.56
1:E:371:ARG:HH11	1:E:371:ARG:CG	2.17	0.56
1:A:362:LYS:NZ	1:A:406:PHE:O	2.36	0.56
1:E:340:SER:N	1:E:343:GLU:OE2	2.37	0.56
1:B:217:ASN:HA	1:B:239:ILE:O	2.06	0.56
1:F:376:ILE:O	1:F:380:LEU:HD12	2.05	0.56
1:A:92:ILE:HG12	1:A:110:LYS:NZ	2.21	0.55
1:C:221:TYR:HA	1:C:243:THR:HG22	1.87	0.55
1:D:151:ARG:HH11	1:D:317:ILE:HD11	1.71	0.55
1:C:344:LYS:HB3	1:C:435:TYR:CE1	2.41	0.55
1:D:153:MET:HG2	1:D:295:LEU:HD22	1.87	0.55
1:E:288:ILE:HD13	1:E:292:ARG:CD	2.36	0.55
1:D:200:VAL:O	1:D:204:THR:N	2.33	0.55
1:C:388:LEU:HD13	1:C:402:VAL:HG13	1.88	0.55
1:E:103:ILE:HG22	1:E:108:ILE:HD13	1.89	0.55
1:A:181:LEU:O	1:A:185:ASP:HB2	2.06	0.55
1:B:182:ALA:HA	1:E:401:TRP:CE2	2.42	0.55
1:C:175:ILE:HD12	1:C:238:GLU:HB3	1.89	0.55
1:D:127:GLU:OE2	1:D:212:SER:OG	2.23	0.55
1:D:343:GLU:O	1:D:347:ARG:N	2.31	0.55
1:D:427:LYS:NZ	1:D:429:ILE:O	2.40	0.55
1:F:99:ASN:O	1:F:101:MET:HG3	2.06	0.55
1:C:87:ARG:H	1:C:88:SER:HA	1.72	0.54
1:A:113:THR:OG1	1:A:117:GLU:OE1	2.26	0.54
1:B:476:ILE:O	1:B:480:ARG:N	2.35	0.54
1:C:395:ASP:O	1:C:399:ARG:NE	2.41	0.54
1:F:181:LEU:O	1:F:185:ASP:HB2	2.07	0.54
1:C:375:ASP:HB3	1:C:379:TYR:CZ	2.42	0.54
1:E:492:LYS:N	1:E:492:LYS:HD2	2.22	0.54
1:F:472:GLY:O	1:F:476:ILE:HD12	2.08	0.54
1:A:429:ILE:O	1:A:451:THR:HG23	2.07	0.54
1:B:380:LEU:HD11	1:B:387:ALA:CB	2.38	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:395:ASP:O	1:C:399:ARG:HG2	2.07	0.54
1:D:436:ASP:O	1:D:447:ARG:NH1	2.40	0.54
1:A:102:THR:HB	1:A:320:GLN:HB3	1.89	0.54
1:A:318:GLN:OE1	1:A:318:GLN:N	2.41	0.54
1:B:96:ARG:HB2	1:B:97:LYS:HD3	1.88	0.54
1:D:424:ILE:H	1:D:450:ARG:HH21	1.55	0.54
1:B:164:THR:HA	1:B:167:TYR:CE2	2.43	0.54
1:B:366:PHE:HB3	1:B:447:ARG:HH21	1.72	0.54
1:D:114:THR:HG22	1:D:116:ASP:H	1.73	0.54
1:D:196:ARG:HH12	1:D:371:ARG:HH11	1.56	0.54
1:D:422:ARG:HH11	2:D:2001:ADP:H4'	1.73	0.54
1:B:380:LEU:HD12	1:B:381:ARG:N	2.22	0.54
1:C:487:PRO:HB2	1:C:490:LEU:HB3	1.89	0.53
1:D:486:ILE:HG23	1:D:490:LEU:HD23	1.91	0.53
1:E:380:LEU:HB3	1:E:385:TRP:HB2	1.90	0.53
1:E:186:GLY:N	1:E:257:ASN:OD1	2.39	0.53
1:F:363:THR:HG23	1:F:431:TYR:O	2.09	0.53
1:D:347:ARG:HH21	1:D:350:LYS:HD3	1.74	0.53
1:F:376:ILE:HG22	1:F:380:LEU:HD11	1.91	0.53
1:B:176:ASN:OD1	1:B:213:SER:OG	2.26	0.53
1:C:480:ARG:HG2	1:C:484:GLN:OE1	2.08	0.53
1:D:191:VAL:HG22	1:D:265:VAL:HB	1.90	0.53
1:A:120:PHE:CE1	1:A:148:LEU:HD21	2.42	0.53
1:C:100:GLU:HG3	1:C:321:VAL:O	2.08	0.53
1:A:381:ARG:HD3	1:F:381:ARG:HB3	1.89	0.53
1:B:174:HIS:HD2	1:B:263:TYR:HB2	1.73	0.53
1:A:253:ILE:HG13	1:A:255:LYS:HG2	1.91	0.53
1:D:182:ALA:HB3	1:D:185:ASP:OD2	2.09	0.53
1:F:152:ASP:OD1	1:F:294:THR:N	2.38	0.53
1:F:273:LEU:HD21	1:F:308:LEU:HD22	1.91	0.53
1:B:151:ARG:NH2	1:B:317:ILE:HG13	2.24	0.53
1:B:398:GLU:OE2	1:E:235:ARG:HD3	2.09	0.53
1:C:96:ARG:HH12	1:C:103:ILE:CD1	2.21	0.53
1:D:345:ARG:O	1:D:349:ASN:ND2	2.42	0.53
1:F:285:VAL:HG11	1:F:312:TYR:CD2	2.44	0.53
1:F:427:LYS:HZ1	1:F:452:GLY:HA2	1.73	0.53
1:B:196:ARG:HH22	1:B:371:ARG:HH21	1.55	0.53
1:C:159:THR:HG22	1:C:163:LYS:HZ3	1.72	0.53
1:C:253:ILE:CG2	1:C:255:LYS:NZ	2.72	0.53
1:C:191:VAL:HG22	1:C:265:VAL:HB	1.91	0.52
1:C:233:LEU:HD23	1:C:256:THR:HB	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:391:HIS:CE1	1:C:394:LYS:HB2	2.42	0.52
1:F:87:ARG:N	1:F:88:SER:HB2	2.24	0.52
1:F:105:GLY:HA3	1:F:317:ILE:HD13	1.91	0.52
1:C:174:HIS:NE2	1:C:262:THR:OG1	2.30	0.52
1:D:263:TYR:HE1	1:D:295:LEU:HD11	1.74	0.52
1:A:90:SER:O	1:A:94:GLN:HG2	2.09	0.52
1:A:184:GLY:HA3	1:B:345:ARG:NH1	2.25	0.52
1:D:330:HIS:ND1	1:D:482:ALA:HA	2.25	0.52
1:E:434:ASN:HB2	1:E:462:SER:HA	1.90	0.52
1:B:125:LEU:O	1:B:129:LYS:HG3	2.10	0.52
1:C:375:ASP:HB3	1:C:379:TYR:CE2	2.44	0.52
1:C:59:ILE:O	1:C:287:GLN:NE2	2.43	0.52
1:E:125:LEU:O	1:E:129:LYS:HG2	2.10	0.52
1:A:247:LEU:HD23	1:A:284:ILE:HD13	1.92	0.52
1:C:63:TRP:HZ3	1:C:70:LEU:HD11	1.75	0.52
1:E:221:TYR:HE1	1:E:224:VAL:HG21	1.74	0.52
1:F:153:MET:HE2	1:F:295:LEU:HD23	1.91	0.52
1:A:224:VAL:HG22	1:A:225:PRO:HD2	1.91	0.52
1:A:238:GLU:OE2	1:D:397:ARG:HD3	2.10	0.52
1:F:152:ASP:HB3	1:F:313:LEU:HD22	1.92	0.52
1:B:397:ARG:NH1	1:E:238:GLU:CD	2.67	0.51
1:E:67:LEU:HD21	1:E:289:ARG:HB2	1.93	0.51
1:E:335:ILE:HG23	1:E:461:ILE:HD13	1.90	0.51
1:A:248:ILE:O	1:A:252:GLU:HG3	2.11	0.51
1:C:335:ILE:HD11	1:C:461:ILE:HG23	1.91	0.51
1:C:343:GLU:O	1:C:346:ASP:N	2.42	0.51
1:E:426:VAL:HG13	1:E:429:ILE:HD11	1.91	0.51
1:C:103:ILE:HD12	1:C:108:ILE:HD12	1.92	0.51
1:D:87:ARG:H	1:D:88:SER:HB2	1.76	0.51
1:F:96:ARG:HH21	1:F:111:PRO:HD3	1.75	0.51
1:A:250:MET:HA	1:A:253:ILE:HG12	1.91	0.51
1:A:489:GLU:O	1:A:492:LYS:NZ	2.25	0.51
1:D:191:VAL:HG23	1:D:239:ILE:HD11	1.92	0.51
1:B:301:TRP:O	1:B:301:TRP:CG	2.64	0.51
1:F:278:GLU:HA	1:F:281:ILE:HG12	1.93	0.51
1:B:64:ASP:N	1:B:64:ASP:OD1	2.43	0.51
1:B:151:ARG:HH21	1:B:317:ILE:HG13	1.75	0.51
1:C:296:MET:HE1	1:C:305:VAL:HG23	1.92	0.51
1:C:330:HIS:CE1	1:C:481:GLU:OE2	2.64	0.51
1:B:175:ILE:HD11	1:B:189:VAL:HG23	1.92	0.51
1:B:219:CYS:HA	1:B:241:ILE:HB	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:226:LYS:HE3	1:F:246:ARG:NH1	2.25	0.51
1:F:320:GLN:OE1	1:F:320:GLN:N	2.39	0.51
1:A:270:ASP:OD1	1:A:270:ASP:N	2.43	0.51
1:D:96:ARG:HH21	1:D:97:LYS:NZ	2.09	0.51
1:D:217:ASN:HB3	1:D:239:ILE:HG23	1.92	0.51
1:E:253:ILE:HG22	1:E:255:LYS:HD3	1.93	0.51
1:A:93:ALA:O	1:A:97:LYS:HG2	2.11	0.51
1:C:253:ILE:HG22	1:C:255:LYS:HZ2	1.75	0.51
1:D:296:MET:HE3	1:D:313:LEU:HD11	1.93	0.51
1:B:171:GLY:O	1:B:175:ILE:HG12	2.10	0.50
1:D:438:PRO:HG3	1:D:443:ASP:HB2	1.93	0.50
1:F:115:PHE:CE1	1:F:136:PRO:HB3	2.46	0.50
1:F:264:LEU:O	1:F:294:THR:HA	2.11	0.50
1:A:377:THR:O	1:A:381:ARG:HG3	2.12	0.50
1:C:91:GLU:HB3	1:C:95:PHE:CE2	2.47	0.50
1:D:196:ARG:NE	1:D:393:ASP:OD2	2.44	0.50
1:D:247:LEU:HD23	1:D:284:ILE:HD13	1.92	0.50
1:F:226:LYS:CG	1:F:246:ARG:HH11	2.24	0.50
1:C:253:ILE:HG22	1:C:255:LYS:NZ	2.26	0.50
1:E:92:ILE:O	1:E:96:ARG:HG3	2.10	0.50
1:D:191:VAL:HG11	1:D:202:ILE:HG21	1.94	0.50
1:A:67:LEU:N	1:A:68:PRO:HD2	2.27	0.50
1:D:403:LEU:HA	1:D:414:MET:HE1	1.93	0.50
1:B:189:VAL:HG22	1:B:263:TYR:HB3	1.93	0.50
1:D:422:ARG:NH2	2:D:2001:ADP:O3B	2.44	0.50
1:E:67:LEU:N	1:E:68:PRO:HD2	2.25	0.50
1:B:198:LEU:HD13	1:B:268:GLU:OE1	2.12	0.50
1:B:495:ARG:HG2	1:B:496:ARG:H	1.77	0.50
1:C:185:ASP:HB3	1:C:260:ARG:HD3	1.94	0.50
1:D:148:LEU:HD12	1:D:170:PRO:HB3	1.94	0.50
1:F:172:ILE:HD12	1:F:215:ILE:HD12	1.94	0.50
1:F:425:ASP:OD1	1:F:453:ARG:NH1	2.44	0.50
1:B:66:GLU:OE2	1:C:339:VAL:HG11	2.12	0.50
1:B:112:ILE:HD13	1:B:118:ALA:HB2	1.94	0.50
1:C:171:GLY:HA2	1:C:263:TYR:HE2	1.76	0.50
1:C:479:MET:HG2	1:C:484:GLN:HB2	1.93	0.50
1:D:55:PRO:HG2	1:D:253:ILE:HA	1.94	0.50
1:D:361:TYR:CD2	1:D:363:THR:HG23	2.47	0.50
1:C:269:ALA:N	1:C:298:SER:OG	2.45	0.50
1:D:93:ALA:HA	1:D:96:ARG:NH1	2.27	0.50
1:D:140:GLN:HG2	1:D:144:TRP:CZ2	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:395:ASP:O	1:D:399:ARG:NE	2.44	0.50
1:D:464:PHE:HD1	1:D:465:THR:H	1.57	0.50
1:C:289:ARG:O	1:C:292:ARG:HG2	2.11	0.49
1:E:181:LEU:O	1:E:185:ASP:HB2	2.12	0.49
1:F:155:GLY:HA2	1:F:319:VAL:HG22	1.94	0.49
1:B:144:TRP:NE1	1:B:165:LEU:O	2.43	0.49
1:A:351:TYR:CE1	1:A:461:ILE:HG12	2.47	0.49
1:B:67:LEU:N	1:B:68:PRO:HD2	2.27	0.49
1:D:53:ASN:OD1	1:F:371:ARG:NH1	2.45	0.49
1:D:57:GLU:CG	1:D:58:LEU:H	2.25	0.49
1:D:377:THR:HG22	1:D:381:ARG:HH21	1.77	0.49
1:D:386:PRO:O	1:D:413:ILE:HB	2.12	0.49
1:E:56:GLN:HG3	1:E:252:GLU:O	2.12	0.49
1:B:169:LEU:O	1:B:172:ILE:HG13	2.12	0.49
1:C:221:TYR:HE1	1:C:224:VAL:HG11	1.77	0.49
1:C:433:ILE:HA	1:C:461:ILE:O	2.12	0.49
1:D:103:ILE:HG21	1:D:108:ILE:HG21	1.93	0.49
1:E:184:GLY:O	1:E:257:ASN:ND2	2.45	0.49
1:A:395:ASP:O	1:A:399:ARG:NE	2.46	0.49
1:B:397:ARG:NE	1:E:214:ARG:HB3	2.27	0.49
1:D:219:CYS:HA	1:D:241:ILE:O	2.12	0.49
1:E:105:GLY:CA	1:E:108:ILE:HD11	2.42	0.49
1:F:378:LYS:O	1:F:382:GLU:HG3	2.11	0.49
1:B:126:ASN:O	1:E:126:ASN:HB3	2.11	0.49
1:B:268:GLU:N	1:B:297:TRP:O	2.46	0.49
1:C:309:ALA:O	1:C:313:LEU:HB2	2.12	0.49
1:D:87:ARG:HB3	1:D:88:SER:HA	1.94	0.49
1:D:363:THR:HG22	1:D:431:TYR:HB2	1.93	0.49
1:F:144:TRP:NE1	1:F:166:SER:HA	2.27	0.49
1:C:292:ARG:NH1	1:C:294:THR:OG1	2.46	0.49
1:C:224:VAL:H	1:C:246:ARG:NH2	2.11	0.49
1:D:78:TYR:OH	1:D:80:GLU:HG2	2.13	0.49
1:D:137:THR:HB	1:D:140:GLN:HB2	1.95	0.49
1:E:393:ASP:O	1:E:394:LYS:HG3	2.13	0.49
1:F:154:VAL:HG13	1:F:296:MET:HE2	1.95	0.49
1:B:370:LYS:HD3	1:B:393:ASP:OD2	2.12	0.49
1:A:217:ASN:HA	1:A:239:ILE:O	2.13	0.49
1:A:372:MET:HA	1:A:375:ASP:HB2	1.93	0.49
1:C:395:ASP:HA	1:C:398:GLU:HB2	1.94	0.49
1:D:235:ARG:HH11	1:D:235:ARG:CG	2.24	0.49
1:A:56:GLN:C	1:A:57:GLU:HG3	2.38	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:79:VAL:HG12	1:C:79:VAL:O	2.13	0.48
1:E:185:ASP:HA	1:E:257:ASN:HD21	1.77	0.48
1:E:197:GLU:OE2	1:E:370:LYS:HB2	2.13	0.48
1:F:142:GLN:O	1:F:146:MET:HG3	2.13	0.48
1:F:144:TRP:CZ2	1:F:169:LEU:HD12	2.48	0.48
1:B:258:LEU:HB3	1:B:288:ILE:HG22	1.95	0.48
1:E:188:ILE:HD12	1:E:189:VAL:HG23	1.95	0.48
1:F:313:LEU:HD13	1:F:316:PRO:HB3	1.94	0.48
1:F:335:ILE:CD1	1:F:461:ILE:HA	2.42	0.48
1:A:148:LEU:CD2	1:A:170:PRO:HB3	2.41	0.48
1:B:60:LYS:CD	1:B:286:ASP:HB3	2.43	0.48
1:B:101:MET:SD	1:B:321:VAL:HG23	2.53	0.48
1:B:214:ARG:NH2	1:E:208:LYS:HZ1	2.10	0.48
1:C:350:LYS:O	1:C:354:THR:HG23	2.14	0.48
1:C:405:GLU:HB3	1:C:410:ARG:HB3	1.94	0.48
1:E:203:GLN:HB2	1:E:241:ILE:HD12	1.96	0.48
1:E:311:ASP:C	1:E:312:TYR:HD1	2.21	0.48
1:C:465:THR:HG22	1:C:466:GLU:OE1	2.14	0.48
1:F:92:ILE:O	1:F:96:ARG:N	2.42	0.48
1:A:153:MET:HG2	1:A:295:LEU:HD22	1.96	0.48
1:B:214:ARG:O	1:E:397:ARG:NE	2.46	0.48
1:F:159:THR:HG23	1:F:299:ALA:HB2	1.96	0.48
1:A:123:TYR:CE2	1:A:213:SER:HB3	2.48	0.48
1:A:191:VAL:HG11	1:A:202:ILE:HG21	1.96	0.48
1:D:194:PRO:HB2	1:D:275:MET:HE1	1.95	0.48
1:E:195:THR:OG1	1:E:198:LEU:HD23	2.13	0.48
1:C:175:ILE:HD13	1:C:188:ILE:HB	1.96	0.48
1:C:224:VAL:O	1:C:246:ARG:NH2	2.47	0.48
1:D:263:TYR:CE1	1:D:295:LEU:HD11	2.49	0.48
1:C:370:LYS:HE2	1:C:374:ASP:OD2	2.14	0.48
1:C:475:LEU:HD11	1:C:490:LEU:CD1	2.44	0.48
1:D:84:VAL:HA	1:D:87:ARG:NH2	2.29	0.48
1:F:271:ARG:HG3	1:F:275:MET:HE1	1.96	0.48
1:F:396:GLN:O	1:F:400:ASP:N	2.46	0.48
1:B:333:THR:OG1	1:B:459:THR:HA	2.14	0.48
1:C:253:ILE:CG2	1:C:255:LYS:HZ2	2.27	0.48
1:D:437:MET:HE3	1:D:463:PHE:C	2.39	0.48
1:E:219:CYS:SG	1:E:221:TYR:HE2	2.37	0.48
1:B:397:ARG:NH1	1:E:214:ARG:C	2.72	0.47
1:D:55:PRO:HG2	1:D:252:GLU:O	2.14	0.47
1:E:215:ILE:HD12	1:E:239:ILE:HD11	1.94	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:399:ARG:O	1:E:403:LEU:HG	2.14	0.47
1:F:81:HIS:ND1	1:F:82:GLU:HG2	2.28	0.47
1:B:75:LYS:HD3	1:B:150:GLY:O	2.13	0.47
1:E:381:ARG:NH2	3:E:2002:SO4:S	2.87	0.47
1:F:87:ARG:HD2	1:F:92:ILE:HD11	1.95	0.47
1:B:102:THR:HB	1:B:320:GLN:HB3	1.96	0.47
1:D:92:ILE:HD12	1:D:96:ARG:HH11	1.79	0.47
1:B:339:VAL:HG12	1:B:340:SER:O	2.14	0.47
1:D:96:ARG:HH21	1:D:97:LYS:HZ1	1.60	0.47
1:D:189:VAL:HG22	1:D:263:TYR:HB3	1.95	0.47
1:D:266:LEU:HD11	1:D:296:MET:HE2	1.96	0.47
1:F:156:ILE:HA	1:F:298:SER:O	2.13	0.47
1:B:140:GLN:NE2	1:B:165:LEU:HB2	2.29	0.47
1:B:142:GLN:O	1:B:146:MET:HG3	2.13	0.47
1:F:223:GLY:H	1:F:246:ARG:HH21	1.63	0.47
1:B:265:VAL:HG22	1:B:295:LEU:HB2	1.96	0.47
1:C:113:THR:N	1:C:117:GLU:OE1	2.31	0.47
1:E:207:SER:OG	1:E:217:ASN:ND2	2.46	0.47
1:E:359:ASN:HA	1:E:360:GLU:HA	1.56	0.47
1:F:67:LEU:N	1:F:68:PRO:HD2	2.30	0.47
1:A:345:ARG:CZ	1:A:379:TYR:HB3	2.44	0.47
1:B:188:ILE:HD11	1:B:260:ARG:HG2	1.97	0.47
1:B:270:ASP:OD1	1:B:271:ARG:N	2.46	0.47
1:B:339:VAL:HG12	1:B:340:SER:N	2.30	0.47
1:C:63:TRP:O	1:C:67:LEU:HG	2.14	0.47
1:C:197:GLU:HG2	1:C:370:LYS:HB3	1.97	0.47
1:C:397:ARG:HD2	1:F:214:ARG:O	2.15	0.47
1:D:216:ARG:NH1	1:D:238:GLU:OE2	2.47	0.47
1:D:345:ARG:NH2	1:D:383:ASP:OD1	2.46	0.47
1:E:367:ALA:HA	1:E:436:ASP:HB2	1.95	0.47
1:E:464:PHE:CD1	1:E:468:ASN:HB2	2.48	0.47
1:F:270:ASP:OD1	1:F:271:ARG:N	2.45	0.47
1:F:334:GLN:OE1	1:F:479:MET:HG2	2.15	0.47
1:A:159:THR:HA	1:A:163:LYS:NZ	2.29	0.47
1:A:216:ARG:NH1	1:A:235:ARG:O	2.47	0.47
1:A:397:ARG:NH1	1:D:214:ARG:HA	2.30	0.47
1:A:471:LEU:HD12	1:A:475:LEU:HB2	1.96	0.47
1:B:87:ARG:H	1:B:88:SER:HG	1.58	0.47
1:B:152:ASP:HB3	1:B:313:LEU:HD23	1.97	0.47
1:E:386:PRO:O	1:E:413:ILE:HB	2.14	0.47
1:F:153:MET:CE	1:F:295:LEU:HD23	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:80:GLU:OE2	1:B:84:VAL:HB	2.15	0.47
1:B:124:VAL:CG2	1:B:169:LEU:HD23	2.44	0.47
1:C:181:LEU:O	1:C:185:ASP:HB2	2.15	0.47
1:C:224:VAL:H	1:C:246:ARG:HH21	1.63	0.47
1:E:407:ARG:HG3	1:E:426:VAL:HG23	1.96	0.47
1:F:476:ILE:O	1:F:480:ARG:N	2.45	0.47
1:A:181:LEU:HD21	1:A:238:GLU:HG3	1.96	0.47
1:C:197:GLU:HG2	1:C:370:LYS:CB	2.44	0.47
1:F:285:VAL:HG11	1:F:312:TYR:HD2	1.78	0.47
1:A:114:THR:HG22	1:A:117:GLU:HG3	1.97	0.46
1:A:381:ARG:HB3	1:F:381:ARG:HD3	1.96	0.46
1:C:63:TRP:CZ3	1:C:70:LEU:HD11	2.50	0.46
1:D:278:GLU:OE1	1:D:282:ARG:NH2	2.47	0.46
1:D:348:LEU:HD21	1:D:352:LEU:HD12	1.97	0.46
1:D:476:ILE:O	1:D:480:ARG:HG3	2.14	0.46
1:F:127:GLU:OE1	1:F:209:PHE:HA	2.14	0.46
1:F:203:GLN:HG3	1:F:219:CYS:HB2	1.97	0.46
1:B:345:ARG:NH2	1:B:383:ASP:OD1	2.48	0.46
1:C:294:THR:O	1:C:295:LEU:HD23	2.15	0.46
1:D:474:LYS:N	1:D:474:LYS:HD2	2.30	0.46
1:E:292:ARG:HG3	1:E:294:THR:HG23	1.96	0.46
1:C:484:GLN:CG	1:C:485:ASN:N	2.79	0.46
1:D:289:ARG:NH1	1:D:291:ASP:OD1	2.49	0.46
1:E:390:ILE:HD12	1:E:420:ALA:HB1	1.96	0.46
1:F:427:LYS:HD2	1:F:427:LYS:HA	1.73	0.46
1:B:101:MET:HA	1:B:320:GLN:O	2.15	0.46
1:A:78:TYR:HB2	1:A:148:LEU:CB	2.44	0.46
1:A:140:GLN:HE21	1:A:165:LEU:HG	1.81	0.46
1:A:395:ASP:HA	1:A:398:GLU:CG	2.45	0.46
1:B:466:GLU:O	1:B:469:LYS:HG2	2.15	0.46
1:D:296:MET:HE1	1:D:309:ALA:HA	1.97	0.46
1:D:302:PRO:HB2	1:D:304:GLU:H	1.79	0.46
1:D:424:ILE:H	1:D:450:ARG:NH2	2.14	0.46
1:F:244:PRO:HG2	1:F:272:MET:HE1	1.95	0.46
1:F:250:MET:HA	1:F:253:ILE:HG22	1.97	0.46
1:B:164:THR:HA	1:B:167:TYR:CZ	2.50	0.46
1:B:282:ARG:HA	1:B:285:VAL:HG22	1.98	0.46
1:C:398:GLU:OE2	1:F:235:ARG:O	2.33	0.46
1:E:103:ILE:CG2	1:E:108:ILE:HD13	2.45	0.46
1:A:163:LYS:N	2:A:2001:ADP:O3B	2.46	0.46
1:C:85:ARG:HA	1:C:86:ASP:HA	1.65	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:127:GLU:OE1	1:C:209:PHE:HA	2.15	0.46
1:C:171:GLY:O	1:C:175:ILE:HG12	2.15	0.46
1:E:242:ALA:HB1	1:E:247:LEU:HB2	1.96	0.46
1:B:331:ASN:HD21	1:B:456:ALA:C	2.23	0.46
1:B:396:GLN:HA	1:B:399:ARG:NH2	2.31	0.46
1:C:340:SER:O	1:C:344:LYS:HG3	2.16	0.46
1:C:359:ASN:OD1	1:C:360:GLU:HA	2.16	0.46
1:E:174:HIS:NE2	1:E:262:THR:OG1	2.33	0.46
1:E:336:VAL:HG22	1:E:462:SER:HB2	1.97	0.46
1:A:75:LYS:HD2	1:A:293:GLN:HB2	1.97	0.46
1:A:160:GLY:HA2	2:A:2001:ADP:PA	2.56	0.46
1:B:60:LYS:NZ	1:B:63:TRP:CD1	2.84	0.46
1:B:154:VAL:HG23	1:B:296:MET:HB3	1.98	0.46
1:B:390:ILE:HD11	1:B:421:ALA:HB2	1.98	0.46
1:F:394:LYS:HB3	1:F:399:ARG:HG3	1.98	0.46
1:A:418:ASP:OD1	1:A:447:ARG:NH1	2.37	0.46
1:C:105:GLY:HA3	1:C:317:ILE:HD12	1.97	0.46
1:C:464:PHE:CZ	1:C:469:LYS:HA	2.51	0.46
1:F:191:VAL:HB	1:F:265:VAL:HG13	1.98	0.46
1:A:359:ASN:OD1	1:A:359:ASN:N	2.49	0.45
1:C:285:VAL:HG13	1:C:292:ARG:HH21	1.81	0.45
1:D:81:HIS:HD2	1:D:117:GLU:HG2	1.76	0.45
1:F:291:ASP:OD1	1:F:291:ASP:N	2.49	0.45
1:D:181:LEU:O	1:D:185:ASP:HB2	2.17	0.45
1:D:441:ILE:HB	1:D:471:LEU:HD11	1.98	0.45
1:F:57:GLU:O	1:F:58:LEU:HD12	2.15	0.45
1:A:85:ARG:HA	1:A:86:ASP:HA	1.54	0.45
1:D:103:ILE:HG21	1:D:108:ILE:HG13	1.98	0.45
1:D:344:LYS:HB3	1:D:435:TYR:CE1	2.52	0.45
1:D:443:ASP:O	1:D:447:ARG:N	2.39	0.45
1:A:125:LEU:HD21	1:A:129:LYS:NZ	2.32	0.45
1:A:303:LYS:HD3	1:A:303:LYS:N	2.32	0.45
1:C:226:LYS:HD3	1:C:226:LYS:H	1.81	0.45
1:D:281:ILE:O	1:D:285:VAL:HG23	2.16	0.45
1:E:120:PHE:CE1	1:E:148:LEU:HD11	2.52	0.45
1:F:181:LEU:HD12	1:F:181:LEU:HA	1.82	0.45
1:F:200:VAL:O	1:F:204:THR:HG23	2.15	0.45
1:A:60:LYS:HD2	1:A:61:PRO:HD2	1.98	0.45
1:C:144:TRP:NE1	1:C:166:SER:HA	2.32	0.45
1:A:59:ILE:HD12	1:B:340:SER:HB2	1.98	0.45
1:B:396:GLN:CD	1:B:396:GLN:H	2.25	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:156:ILE:HA	1:C:298:SER:O	2.17	0.45
1:C:220:VAL:HG11	1:C:233:LEU:HD11	1.98	0.45
1:C:305:VAL:O	1:C:309:ALA:N	2.30	0.45
1:C:332:ILE:HG12	1:C:451:THR:HG23	1.99	0.45
1:B:102:THR:O	1:B:319:VAL:HA	2.17	0.45
1:C:246:ARG:O	1:C:246:ARG:HG2	2.16	0.45
1:E:200:VAL:O	1:E:204:THR:HG23	2.17	0.45
1:B:157:ALA:HB3	1:B:163:LYS:CG	2.47	0.45
1:C:270:ASP:OD1	1:C:271:ARG:N	2.48	0.45
1:C:403:LEU:O	1:C:407:ARG:HG3	2.17	0.45
1:A:359:ASN:HA	1:A:360:GLU:HA	1.66	0.45
1:B:182:ALA:HB3	1:B:185:ASP:OD2	2.17	0.45
1:E:77:PHE:HE2	1:E:174:HIS:HA	1.80	0.45
1:E:188:ILE:CD1	1:E:189:VAL:HG23	2.47	0.45
1:C:340:SER:O	1:C:341:ASP:C	2.60	0.45
1:D:78:TYR:HB2	1:D:148:LEU:HB3	1.98	0.45
1:D:96:ARG:NH2	1:D:97:LYS:NZ	2.64	0.45
1:E:109:PRO:HG3	1:E:146:MET:HA	1.98	0.45
1:E:161:SER:HB2	1:E:163:LYS:HG3	1.98	0.45
1:D:117:GLU:HA	1:D:117:GLU:OE1	2.16	0.44
1:D:305:VAL:O	1:D:309:ALA:N	2.43	0.44
1:A:131:GLU:CD	1:A:208:LYS:HZ1	2.24	0.44
1:B:80:GLU:OE2	1:B:85:ARG:HG3	2.18	0.44
1:B:180:LEU:HB2	1:E:401:TRP:HD1	1.82	0.44
1:C:365:ILE:HB	1:C:415:VAL:HG22	1.98	0.44
1:D:87:ARG:HG3	1:D:91:GLU:HB3	1.99	0.44
1:F:359:ASN:HA	1:F:360:GLU:HA	1.57	0.44
1:A:326:LEU:HD11	1:A:442:GLU:HG3	1.99	0.44
1:B:464:PHE:HE2	1:B:472:GLY:HA2	1.82	0.44
1:C:81:HIS:O	1:C:84:VAL:HG12	2.17	0.44
1:C:313:LEU:HB3	1:C:316:PRO:HB3	1.99	0.44
1:C:381:ARG:HG3	1:C:387:ALA:HB3	2.00	0.44
1:D:407:ARG:HG2	1:D:426:VAL:HG23	1.99	0.44
1:E:192:LEU:HB2	1:E:266:LEU:HD13	1.99	0.44
1:B:93:ALA:HA	1:B:96:ARG:HG3	2.00	0.44
1:E:144:TRP:NE1	1:E:165:LEU:O	2.32	0.44
1:E:99:ASN:O	1:E:100:GLU:HG2	2.17	0.44
1:F:328:ALA:HB2	1:F:478:ILE:HG23	1.98	0.44
1:A:242:ALA:HB1	1:A:247:LEU:HB2	2.00	0.44
1:B:203:GLN:HG2	1:B:219:CYS:HB2	1.99	0.44
1:C:278:GLU:CD	1:C:282:ARG:HE	2.25	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:340:SER:HB3	1:C:344:LYS:HG2	1.99	0.44
1:C:397:ARG:HD3	1:F:238:GLU:OE2	2.16	0.44
1:C:448:ILE:O	1:C:451:THR:HG22	2.18	0.44
1:C:492:LYS:HB2	1:C:493:TYR:CE1	2.52	0.44
1:D:67:LEU:N	1:D:68:PRO:HD2	2.32	0.44
1:D:156:ILE:HD12	1:D:156:ILE:O	2.18	0.44
1:E:56:GLN:N	1:E:252:GLU:O	2.37	0.44
1:E:103:ILE:HG21	1:E:108:ILE:HG21	1.99	0.44
1:C:78:TYR:HB2	1:C:148:LEU:HD23	1.99	0.44
1:E:127:GLU:OE1	1:E:209:PHE:HA	2.18	0.44
1:E:443:ASP:O	1:E:447:ARG:N	2.47	0.44
1:F:341:ASP:OD1	1:F:342:PHE:N	2.51	0.44
1:A:205:GLU:HA	1:A:208:LYS:HD3	1.99	0.44
1:C:164:THR:HG23	2:C:2001:ADP:O1B	2.18	0.44
1:E:85:ARG:HA	1:E:110:LYS:NZ	2.33	0.44
1:E:391:HIS:NE2	1:E:394:LYS:HB2	2.33	0.44
1:F:220:VAL:HG13	1:F:229:GLN:OE1	2.18	0.44
1:A:308:LEU:O	1:A:312:TYR:HD1	2.00	0.44
1:B:85:ARG:HA	1:B:86:ASP:HA	1.67	0.44
1:B:101:MET:HE1	1:B:142:GLN:HB3	2.00	0.44
1:B:433:ILE:HG23	1:B:461:ILE:HB	1.99	0.44
1:D:164:THR:HA	1:D:167:TYR:CE2	2.53	0.44
1:D:465:THR:HG22	1:D:466:GLU:H	1.83	0.44
1:A:154:VAL:HG11	1:A:301:TRP:HZ3	1.82	0.43
1:A:186:GLY:N	1:A:257:ASN:OD1	2.50	0.43
1:B:190:LEU:O	1:B:264:LEU:HD12	2.18	0.43
1:B:308:LEU:HD13	1:B:312:TYR:HD1	1.83	0.43
1:C:300:THR:HB	1:C:302:PRO:HD3	2.00	0.43
1:D:87:ARG:N	1:D:88:SER:HB2	2.32	0.43
1:F:153:MET:HB2	1:F:317:ILE:O	2.18	0.43
1:A:403:LEU:O	1:A:407:ARG:HG3	2.18	0.43
1:C:316:PRO:O	1:C:317:ILE:HD13	2.19	0.43
1:D:156:ILE:HA	1:D:298:SER:O	2.18	0.43
1:E:235:ARG:HG2	1:E:235:ARG:HH11	1.82	0.43
1:B:353:GLU:OE2	1:B:385:TRP:HZ2	2.00	0.43
1:D:101:MET:HA	1:D:320:GLN:O	2.18	0.43
1:D:156:ILE:HD11	1:D:320:GLN:HG2	1.99	0.43
1:F:336:VAL:HG22	1:F:462:SER:OG	2.18	0.43
1:B:301:TRP:O	1:B:301:TRP:CD2	2.70	0.43
1:D:419:VAL:O	1:D:422:ARG:HB2	2.19	0.43
1:B:337:GLU:OE2	1:B:351:TYR:OH	2.29	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:84:VAL:HG22	1:C:87:ARG:NH2	2.33	0.43
1:C:87:ARG:NH1	1:C:92:ILE:HG12	2.33	0.43
1:C:484:GLN:HG3	1:C:485:ASN:N	2.33	0.43
1:E:222:GLY:HA2	1:E:246:ARG:HD3	1.99	0.43
1:E:261:VAL:HB	1:E:288:ILE:HG22	2.00	0.43
1:E:351:TYR:CE2	1:E:461:ILE:HD12	2.53	0.43
1:A:337:GLU:OE1	1:A:347:ARG:NE	2.50	0.43
1:B:362:LYS:NZ	1:B:406:PHE:O	2.39	0.43
1:C:154:VAL:HG23	1:C:296:MET:CB	2.49	0.43
1:C:182:ALA:HA	1:F:401:TRP:NE1	2.33	0.43
1:D:139:ILE:HD12	1:D:139:ILE:H	1.83	0.43
1:E:144:TRP:NE1	1:E:166:SER:HA	2.32	0.43
1:F:85:ARG:HA	1:F:86:ASP:HA	1.53	0.43
1:A:163:LYS:HB2	2:A:2001:ADP:O3B	2.18	0.43
1:B:395:ASP:HA	1:B:398:GLU:CG	2.49	0.43
1:C:92:ILE:O	1:C:96:ARG:HG2	2.19	0.43
1:C:140:GLN:NE2	1:C:162:GLY:HA3	2.33	0.43
1:D:306:LYS:HA	1:D:309:ALA:HB3	2.01	0.43
1:D:347:ARG:CZ	1:D:351:TYR:HE1	2.32	0.43
1:F:335:ILE:C	1:F:335:ILE:HD12	2.44	0.43
1:A:361:TYR:HD2	1:A:363:THR:HG23	1.83	0.43
1:B:354:THR:O	1:B:357:GLN:HG2	2.18	0.43
1:C:335:ILE:HD12	1:C:335:ILE:O	2.19	0.43
1:C:345:ARG:CZ	1:C:379:TYR:HB3	2.49	0.43
1:C:352:LEU:HD21	1:C:363:THR:HG21	2.00	0.43
1:C:434:ASN:OD1	1:C:447:ARG:HD3	2.19	0.43
1:D:97:LYS:HD2	1:D:97:LYS:N	2.34	0.43
1:D:412:PRO:HG2	1:D:413:ILE:HD12	2.00	0.43
1:E:328:ALA:HB2	1:E:478:ILE:HD12	2.01	0.43
1:F:84:VAL:O	1:F:87:ARG:HG3	2.18	0.43
1:D:441:ILE:O	1:D:445:VAL:HG22	2.18	0.43
1:A:87:ARG:N	1:A:88:SER:HB2	2.34	0.43
1:A:92:ILE:HG21	1:A:110:LYS:HE3	2.01	0.43
1:A:464:PHE:CE1	1:A:468:ASN:HB2	2.54	0.43
1:A:474:LYS:HD2	1:A:474:LYS:N	2.33	0.43
1:B:144:TRP:CZ2	1:B:169:LEU:HD13	2.54	0.43
1:D:67:LEU:HD12	1:D:67:LEU:HA	1.91	0.43
1:D:407:ARG:NE	1:D:425:ASP:O	2.48	0.43
1:D:435:TYR:HD1	1:D:435:TYR:O	2.01	0.43
1:F:86:ASP:HB3	1:F:88:SER:HB2	2.00	0.43
1:B:105:GLY:C	1:B:108:ILE:HD11	2.43	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:HIS:CE1	1:E:211:HIS:CE1	3.06	0.42
1:B:381:ARG:HB3	1:D:381:ARG:HD2	2.00	0.42
1:C:407:ARG:HG2	1:C:426:VAL:HG23	2.00	0.42
1:D:53:ASN:HD21	1:F:371:ARG:HH11	1.67	0.42
1:D:131:GLU:HG3	1:D:209:PHE:CE1	2.54	0.42
1:E:247:LEU:O	1:E:251:LEU:HD23	2.19	0.42
1:B:362:LYS:HG2	1:B:429:ILE:HG12	2.00	0.42
1:D:347:ARG:NH2	1:D:351:TYR:HE1	2.17	0.42
1:B:186:GLY:N	1:B:257:ASN:OD1	2.51	0.42
1:D:398:GLU:O	1:D:402:VAL:HG23	2.18	0.42
1:F:258:LEU:HB3	1:F:288:ILE:HG22	2.00	0.42
1:B:427:LYS:HE2	1:B:452:GLY:HA2	2.01	0.42
1:C:475:LEU:HD11	1:C:490:LEU:HD13	2.02	0.42
1:F:396:GLN:NE2	1:F:400:ASP:OD1	2.50	0.42
1:B:294:THR:OG1	1:B:313:LEU:HG	2.19	0.42
1:C:273:LEU:CD1	1:C:278:GLU:HB2	2.50	0.42
1:D:289:ARG:O	1:D:292:ARG:NE	2.53	0.42
1:A:80:GLU:OE2	1:A:85:ARG:HB2	2.19	0.42
1:B:199:ALA:O	1:B:241:ILE:HG21	2.19	0.42
1:B:258:LEU:HB3	1:B:288:ILE:CG2	2.49	0.42
1:B:359:ASN:HA	1:B:360:GLU:HA	1.52	0.42
1:B:381:ARG:HB3	1:D:381:ARG:HH11	1.84	0.42
1:C:87:ARG:HD2	1:C:92:ILE:HG13	2.01	0.42
1:C:126:ASN:O	1:F:126:ASN:HB3	2.19	0.42
1:C:181:LEU:HD12	1:C:181:LEU:HA	1.79	0.42
1:E:76:ASN:O	1:E:77:PHE:HD1	2.02	0.42
1:B:157:ALA:HB3	1:B:163:LYS:HG2	2.02	0.42
1:C:62:ASN:O	1:C:66:GLU:HG2	2.19	0.42
1:C:302:PRO:HA	1:C:303:LYS:HB3	2.01	0.42
1:F:136:PRO:HA	2:F:2001:ADP:N6	2.34	0.42
1:B:181:LEU:HA	1:B:260:ARG:HH12	1.84	0.42
1:B:278:GLU:N	1:B:279:PRO:HD2	2.35	0.42
1:E:330:HIS:CE1	1:E:482:ALA:HA	2.55	0.42
1:A:302:PRO:O	1:A:305:VAL:HG22	2.20	0.42
1:B:337:GLU:O	1:B:339:VAL:HG23	2.20	0.42
1:B:389:ALA:HA	1:B:415:VAL:O	2.20	0.42
1:B:390:ILE:O	1:B:390:ILE:HG13	2.20	0.42
1:B:450:ARG:HD3	1:B:450:ARG:N	2.34	0.42
1:D:344:LYS:HE2	1:D:435:TYR:CD1	2.55	0.42
1:B:96:ARG:O	1:B:101:MET:HG2	2.20	0.42
1:B:407:ARG:CD	1:B:426:VAL:HG23	2.47	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:372:MET:HA	1:C:375:ASP:HB2	2.01	0.42
1:D:53:ASN:HD21	1:F:371:ARG:HD2	1.84	0.41
1:E:464:PHE:HD2	1:E:490:LEU:HD12	1.85	0.41
1:F:154:VAL:O	1:F:318:GLN:HA	2.21	0.41
1:A:280:GLN:O	1:A:284:ILE:HG13	2.20	0.41
1:A:301:TRP:HA	1:A:305:VAL:HG21	2.03	0.41
1:A:370:LYS:HE2	1:A:374:ASP:OD2	2.20	0.41
1:C:105:GLY:N	1:C:108:ILE:HD11	2.35	0.41
1:C:112:ILE:HD11	1:C:144:TRP:HE3	1.85	0.41
1:C:201:GLN:O	1:C:205:GLU:HG2	2.20	0.41
1:C:296:MET:HE2	1:C:296:MET:HB3	1.92	0.41
1:C:296:MET:HG3	1:C:313:LEU:HD11	2.01	0.41
1:C:427:LYS:HE3	1:C:450:ARG:HA	2.02	0.41
1:C:479:MET:C	1:C:484:GLN:HB2	2.45	0.41
1:E:76:ASN:C	1:E:77:PHE:HD1	2.29	0.41
1:E:356:SER:HA	1:E:361:TYR:CE1	2.55	0.41
1:F:464:PHE:HZ	1:F:469:LYS:HA	1.84	0.41
1:B:282:ARG:HD3	1:B:286:ASP:OD2	2.21	0.41
1:C:376:ILE:HG12	1:C:435:TYR:CE2	2.56	0.41
1:C:476:ILE:HA	1:C:479:MET:HB3	2.02	0.41
1:C:486:ILE:O	1:C:488:PRO:HD2	2.20	0.41
1:D:96:ARG:HE	1:D:97:LYS:HZ2	1.68	0.41
1:D:154:VAL:HG13	1:D:296:MET:HB3	2.02	0.41
1:D:303:LYS:H	1:D:303:LYS:HD2	1.85	0.41
1:D:364:LEU:HD22	1:D:366:PHE:CE2	2.56	0.41
1:D:438:PRO:HD3	1:D:447:ARG:CZ	2.51	0.41
1:E:93:ALA:HA	1:E:96:ARG:NE	2.35	0.41
1:E:175:ILE:CD1	1:E:238:GLU:HB3	2.49	0.41
1:E:278:GLU:N	1:E:279:PRO:HD2	2.35	0.41
1:E:464:PHE:HD1	1:E:465:THR:H	1.66	0.41
1:A:188:ILE:HA	1:A:260:ARG:O	2.21	0.41
1:B:174:HIS:CD2	1:B:263:TYR:HB2	2.53	0.41
1:B:397:ARG:HD3	1:E:216:ARG:HD3	2.02	0.41
1:B:426:VAL:HG13	1:B:429:ILE:HD12	2.03	0.41
1:C:359:ASN:HA	1:C:360:GLU:HA	1.57	0.41
1:E:77:PHE:CE2	1:E:174:HIS:HA	2.56	0.41
1:F:222:GLY:HA2	1:F:246:ARG:HH21	1.84	0.41
1:B:481:GLU:OE1	1:B:481:GLU:HA	2.20	0.41
1:D:290:PRO:HA	1:D:292:ARG:NH2	2.36	0.41
1:E:156:ILE:HA	1:E:298:SER:O	2.21	0.41
1:F:223:GLY:N	1:F:246:ARG:HH21	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:57:GLU:HA	1:A:252:GLU:HG2	2.02	0.41
1:A:102:THR:N	1:A:320:GLN:O	2.52	0.41
1:B:304:GLU:O	1:B:308:LEU:HB2	2.20	0.41
1:C:490:LEU:HA	1:C:493:TYR:CD2	2.56	0.41
1:D:226:LYS:H	1:D:226:LYS:HG2	1.72	0.41
1:B:235:ARG:O	1:E:398:GLU:OE2	2.39	0.41
1:B:401:TRP:O	1:B:404:GLN:HG2	2.21	0.41
1:B:441:ILE:HG13	1:B:441:ILE:O	2.21	0.41
1:D:102:THR:OG1	1:D:320:GLN:HB3	2.21	0.41
1:B:260:ARG:O	1:B:262:THR:HG23	2.21	0.41
1:B:331:ASN:OD1	1:B:456:ALA:HA	2.21	0.41
1:B:397:ARG:CZ	1:E:214:ARG:HB3	2.51	0.41
1:D:94:GLN:O	1:D:98:GLU:N	2.45	0.41
1:F:81:HIS:O	1:F:84:VAL:HG22	2.21	0.41
1:A:330:HIS:ND1	1:A:482:ALA:HA	2.36	0.41
1:B:157:ALA:HB2	1:B:321:VAL:HG12	2.02	0.41
1:C:243:THR:HG23	1:C:246:ARG:H	1.85	0.41
1:C:336:VAL:HG13	1:C:462:SER:O	2.21	0.41
1:D:139:ILE:HD13	1:D:161:SER:OG	2.21	0.41
1:D:390:ILE:O	1:D:390:ILE:HG13	2.20	0.41
1:D:475:LEU:HD13	1:D:479:MET:HE2	2.02	0.41
1:F:187:PRO:HB3	1:F:240:VAL:HG23	2.02	0.41
1:F:339:VAL:HG21	1:F:463:PHE:HB3	2.03	0.41
1:A:115:PHE:CE1	1:A:136:PRO:HB3	2.57	0.40
1:A:167:TYR:CE2	1:A:265:VAL:HG11	2.56	0.40
1:A:185:ASP:HB3	1:A:260:ARG:HG3	2.02	0.40
1:B:208:LYS:O	1:B:211:HIS:HE1	2.05	0.40
1:B:397:ARG:HD3	1:E:216:ARG:CD	2.51	0.40
1:B:495:ARG:HG2	1:B:496:ARG:N	2.36	0.40
1:C:169:LEU:HD23	1:C:169:LEU:HA	1.91	0.40
1:C:284:ILE:O	1:C:288:ILE:HG13	2.21	0.40
1:D:92:ILE:O	1:D:96:ARG:HG3	2.21	0.40
1:D:231:ARG:O	1:D:234:SER:OG	2.39	0.40
1:D:444:TYR:O	1:D:448:ILE:HG13	2.21	0.40
1:E:350:LYS:HA	1:E:350:LYS:HD3	1.79	0.40
1:F:87:ARG:H	1:F:88:SER:CB	2.33	0.40
1:F:277:PHE:O	1:F:281:ILE:HG23	2.21	0.40
1:F:284:ILE:HD12	1:F:285:VAL:HG23	2.03	0.40
1:A:490:LEU:HD23	1:A:490:LEU:H	1.86	0.40
1:B:112:ILE:CG2	1:B:117:GLU:HB3	2.51	0.40
1:D:233:LEU:HD23	1:D:256:THR:HB	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:226:LYS:NZ	3:E:2004:SO4:O1	2.55	0.40
1:E:422:ARG:NH2	1:E:443:ASP:OD1	2.54	0.40
1:F:226:LYS:HG3	1:F:246:ARG:NH1	2.32	0.40
1:C:464:PHE:HZ	1:C:469:LYS:HA	1.85	0.40
1:D:110:LYS:HD3	1:D:110:LYS:N	2.35	0.40
1:D:114:THR:HG22	1:D:115:PHE:N	2.37	0.40
1:E:67:LEU:N	1:E:68:PRO:CD	2.84	0.40
1:F:257:ASN:HB2	1:F:259:LYS:HD3	2.03	0.40
1:B:126:ASN:HD22	1:E:130:ALA:HA	1.86	0.40
1:E:175:ILE:HD11	1:E:238:GLU:HB3	2.03	0.40
1:B:328:ALA:O	1:B:329:SER:C	2.64	0.40
1:B:386:PRO:O	1:B:413:ILE:HB	2.22	0.40
1:C:97:LYS:HA	1:C:100:GLU:HA	2.03	0.40
1:D:103:ILE:CG2	1:D:108:ILE:HG13	2.51	0.40
1:D:438:PRO:HG2	1:D:440:ASN:O	2.22	0.40
1:F:185:ASP:HB3	1:F:260:ARG:HD3	2.04	0.40
1:F:443:ASP:O	1:F:447:ARG:HG3	2.22	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	441/546 (81%)	437 (99%)	4 (1%)	0	100	100
1	B	442/546 (81%)	440 (100%)	1 (0%)	1 (0%)	43	70
1	C	443/546 (81%)	432 (98%)	10 (2%)	1 (0%)	43	70
1	D	442/546 (81%)	437 (99%)	4 (1%)	1 (0%)	43	70
1	E	442/546 (81%)	439 (99%)	3 (1%)	0	100	100
1	F	441/546 (81%)	437 (99%)	4 (1%)	0	100	100
All	All	2651/3276 (81%)	2622 (99%)	26 (1%)	3 (0%)	48	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	80	GLU
1	C	327	SER
1	B	324	LEU

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	383/450 (85%)	383 (100%)	0	100	100
1	B	384/450 (85%)	384 (100%)	0	100	100
1	C	385/450 (86%)	385 (100%)	0	100	100
1	D	384/450 (85%)	383 (100%)	1 (0%)	86	85
1	E	384/450 (85%)	384 (100%)	0	100	100
1	F	383/450 (85%)	383 (100%)	0	100	100
All	All	2303/2700 (85%)	2302 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	422	ARG

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

Mol	Chain	Res	Type
1	A	99	ASN
1	B	106	HIS
1	B	126	ASN
1	B	331	ASN
1	C	106	HIS
1	C	126	ASN
1	C	391	HIS
1	C	430	ASN

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Mol	Chain	Res	Type
1	D	106	HIS
1	D	176	ASN
1	D	331	ASN
1	D	483	ASN
1	E	446	HIS
1	F	391	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 3 are monoatomic - leaving 14 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	SO4	E	2002	-	4,4,4	0.24	0	6,6,6	0.09	0
3	SO4	A	2002	-	4,4,4	0.22	0	6,6,6	0.12	0
3	SO4	E	2003	-	4,4,4	0.24	0	6,6,6	0.06	0
2	ADP	D	2001	-	28,29,29	1.42	4 (14%)	43,45,45	1.86	9 (20%)
2	ADP	B	2001	-	28,29,29	1.43	4 (14%)	43,45,45	1.90	11 (25%)
2	ADP	F	2001	-	28,29,29	1.42	4 (14%)	43,45,45	1.83	11 (25%)
2	ADP	C	2001	4	28,29,29	1.39	5 (17%)	43,45,45	1.80	9 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	SO4	D	2002	-	4,4,4	0.23	0	6,6,6	0.09	0
3	SO4	C	2002	-	4,4,4	0.23	0	6,6,6	0.14	0
3	SO4	B	2002	-	4,4,4	0.24	0	6,6,6	0.09	0
3	SO4	F	2002	-	4,4,4	0.25	0	6,6,6	0.08	0
3	SO4	E	2004	-	4,4,4	0.23	0	6,6,6	0.10	0
2	ADP	E	2001	-	28,29,29	1.43	4 (14%)	43,45,45	1.86	9 (20%)
2	ADP	A	2001	4	28,29,29	1.42	4 (14%)	43,45,45	1.85	8 (18%)

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
2	ADP	D	2001	-	-	5/16/32/32	0/3/3/3
2	ADP	B	2001	-	-	4/16/32/32	0/3/3/3
2	ADP	F	2001	-	-	4/16/32/32	0/3/3/3
2	ADP	C	2001	4	-	5/16/32/32	0/3/3/3
2	ADP	E	2001	-	-	4/16/32/32	0/3/3/3
2	ADP	A	2001	4	-	4/16/32/32	0/3/3/3

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	2001	ADP	C5-C4	4.86	1.47	1.39
2	A	2001	ADP	C5-C4	4.85	1.47	1.39
2	B	2001	ADP	C5-C4	4.83	1.47	1.39
2	D	2001	ADP	C5-C4	4.82	1.47	1.39
2	F	2001	ADP	C5-C4	4.69	1.47	1.39
2	C	2001	ADP	C5-C4	4.59	1.47	1.39
2	F	2001	ADP	C5-C6	2.84	1.48	1.41
2	A	2001	ADP	C5-C6	2.82	1.48	1.41
2	C	2001	ADP	C5-C6	2.81	1.48	1.41
2	E	2001	ADP	C5-C6	2.80	1.48	1.41
2	B	2001	ADP	C5-C6	2.75	1.48	1.41
2	D	2001	ADP	C5-C6	2.75	1.48	1.41
2	C	2001	ADP	C8-N7	2.41	1.36	1.31
2	F	2001	ADP	C8-N7	2.40	1.36	1.31
2	D	2001	ADP	C5-N7	-2.37	1.34	1.39
2	B	2001	ADP	C8-N7	2.33	1.36	1.31

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	2001	ADP	C5-N7	-2.32	1.34	1.39
2	B	2001	ADP	C5-N7	-2.30	1.34	1.39
2	D	2001	ADP	C8-N7	2.28	1.36	1.31
2	E	2001	ADP	C5-N7	-2.27	1.34	1.39
2	E	2001	ADP	C8-N7	2.24	1.36	1.31
2	C	2001	ADP	C5-N7	-2.24	1.35	1.39
2	F	2001	ADP	C5-N7	-2.22	1.35	1.39
2	A	2001	ADP	C8-N7	2.22	1.35	1.31
2	C	2001	ADP	C4-N9	-2.09	1.33	1.37

All (57) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	2001	ADP	C5-C4-N3	-6.16	118.24	126.72
2	E	2001	ADP	C5-C4-N3	-5.93	118.55	126.72
2	F	2001	ADP	C5-C4-N3	-5.85	118.66	126.72
2	D	2001	ADP	C5-C4-N3	-5.82	118.71	126.72
2	B	2001	ADP	C5-C4-N3	-5.62	118.98	126.72
2	C	2001	ADP	C5-C4-N3	-5.51	119.13	126.72
2	A	2001	ADP	N3-C4-N9	4.86	135.43	127.17
2	E	2001	ADP	N3-C4-N9	4.73	135.21	127.17
2	D	2001	ADP	N3-C4-N9	4.51	134.84	127.17
2	B	2001	ADP	N3-C4-N9	4.37	134.60	127.17
2	F	2001	ADP	N3-C4-N9	4.36	134.58	127.17
2	C	2001	ADP	N3-C4-N9	4.16	134.25	127.17
2	F	2001	ADP	C4-C5-N7	-3.92	106.10	110.58
2	C	2001	ADP	C4-C5-N7	-3.86	106.17	110.58
2	A	2001	ADP	C2-N3-C4	3.68	120.83	111.83
2	F	2001	ADP	C2-N3-C4	3.66	120.77	111.83
2	D	2001	ADP	C4-C5-N7	-3.64	106.42	110.58
2	A	2001	ADP	C4-C5-N7	-3.63	106.44	110.58
2	E	2001	ADP	C2-N3-C4	3.62	120.67	111.83
2	C	2001	ADP	C2-N3-C4	3.58	120.57	111.83
2	B	2001	ADP	C4-C5-N7	-3.56	106.51	110.58
2	E	2001	ADP	C4-C5-N7	-3.52	106.55	110.58
2	B	2001	ADP	C2-N3-C4	3.50	120.38	111.83
2	D	2001	ADP	C2-N3-C4	3.48	120.32	111.83
2	C	2001	ADP	N3-C2-N1	-3.13	123.84	128.58
2	F	2001	ADP	N3-C2-N1	-3.07	123.94	128.58
2	E	2001	ADP	N3-C2-N1	-3.01	124.02	128.58
2	B	2001	ADP	N3-C2-N1	-3.01	124.03	128.58
2	A	2001	ADP	N3-C2-N1	-2.96	124.10	128.58

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2001	ADP	O3A-PA-O1A	-2.93	101.89	110.70
2	C	2001	ADP	C4-N9-C8	2.85	108.73	105.74
2	D	2001	ADP	N3-C2-N1	-2.79	124.36	128.58
2	F	2001	ADP	C5-N7-C8	2.78	107.81	103.45
2	C	2001	ADP	C5-N7-C8	2.75	107.77	103.45
2	A	2001	ADP	C5-N7-C8	2.61	107.56	103.45
2	D	2001	ADP	C5-N7-C8	2.59	107.52	103.45
2	E	2001	ADP	C5-N7-C8	2.58	107.50	103.45
2	B	2001	ADP	C5-N7-C8	2.56	107.47	103.45
2	B	2001	ADP	O2A-PA-O1A	2.55	124.31	112.44
2	E	2001	ADP	C4-N9-C8	2.50	108.37	105.74
2	B	2001	ADP	C4-N9-C8	2.48	108.34	105.74
2	F	2001	ADP	C4-N9-C8	2.46	108.32	105.74
2	D	2001	ADP	C4-N9-C8	2.43	108.28	105.74
2	C	2001	ADP	C6-C5-N7	2.40	136.71	132.09
2	A	2001	ADP	C4-N9-C8	2.37	108.23	105.74
2	D	2001	ADP	O5'-PA-O1A	-2.31	99.80	108.94
2	F	2001	ADP	C6-C5-N7	2.29	136.51	132.09
2	E	2001	ADP	O2A-PA-O1A	2.29	123.10	112.44
2	C	2001	ADP	N9-C8-N7	-2.28	110.71	113.94
2	B	2001	ADP	C3'-C2'-C1'	2.20	105.62	101.46
2	D	2001	ADP	O2A-PA-O1A	2.15	122.46	112.44
2	E	2001	ADP	C3'-C2'-C1'	2.13	105.50	101.46
2	F	2001	ADP	C5'-C4'-C3'	-2.10	107.64	115.21
2	B	2001	ADP	C6-C5-N7	2.06	136.07	132.09
2	F	2001	ADP	N9-C8-N7	-2.06	111.01	113.94
2	A	2001	ADP	O3B-PB-O2B	2.02	115.39	107.80
2	F	2001	ADP	O3B-PB-O2B	2.01	115.33	107.80

There are no chirality outliers.

All (26) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2001	ADP	C5'-O5'-PA-O1A
2	A	2001	ADP	C4'-C5'-O5'-PA
2	A	2001	ADP	O4'-C4'-C5'-O5'
2	A	2001	ADP	C3'-C4'-C5'-O5'
2	B	2001	ADP	C5'-O5'-PA-O1A
2	B	2001	ADP	C3'-C4'-C5'-O5'
2	C	2001	ADP	PA-O3A-PB-O2B
2	C	2001	ADP	PA-O3A-PB-O3B
2	D	2001	ADP	C5'-O5'-PA-O2A

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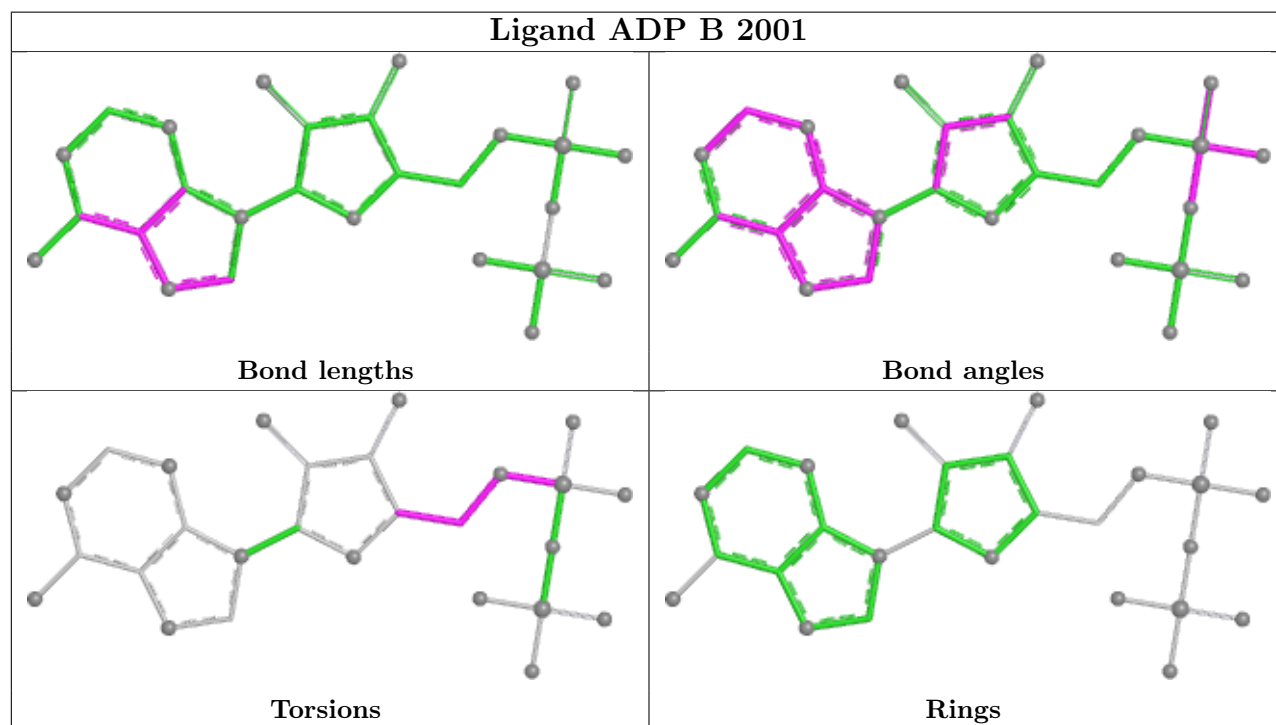
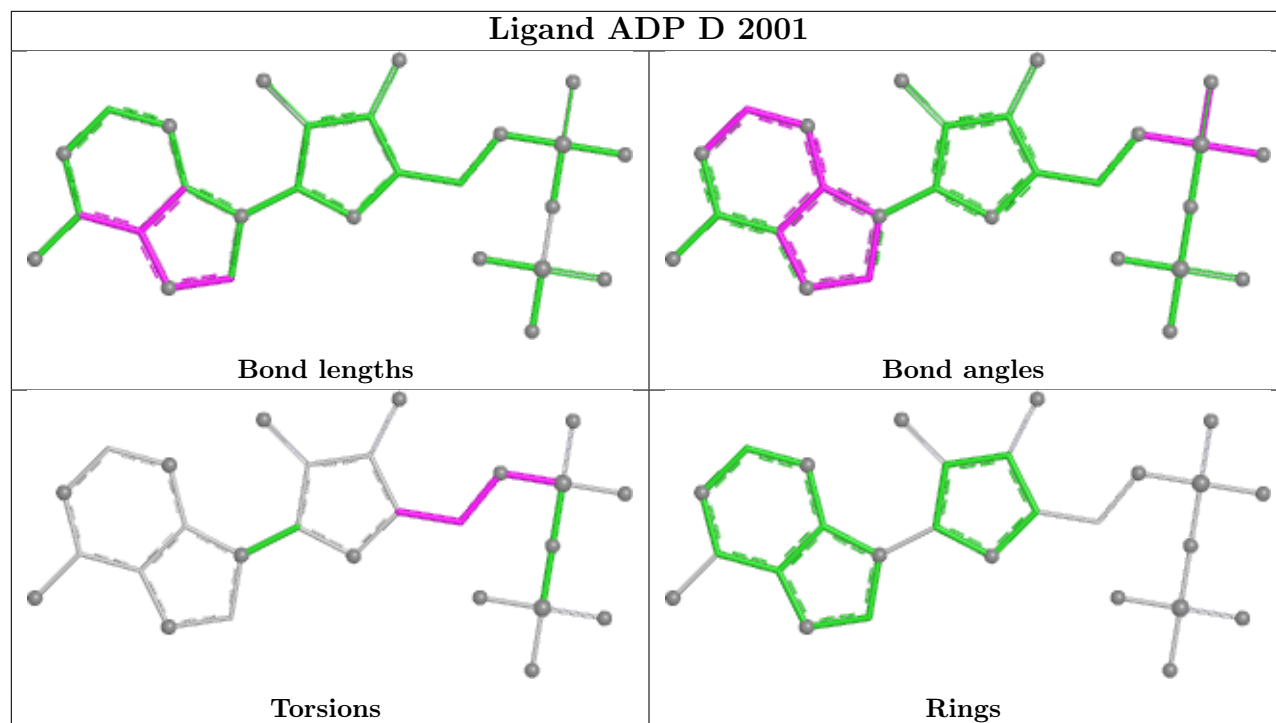
Mol	Chain	Res	Type	Atoms
2	D	2001	ADP	C5'-O5'-PA-O3A
2	D	2001	ADP	O4'-C4'-C5'-O5'
2	E	2001	ADP	C5'-O5'-PA-O1A
2	E	2001	ADP	O4'-C4'-C5'-O5'
2	F	2001	ADP	PA-O3A-PB-O2B
2	F	2001	ADP	PA-O3A-PB-O3B
2	D	2001	ADP	C3'-C4'-C5'-O5'
2	E	2001	ADP	C3'-C4'-C5'-O5'
2	F	2001	ADP	C3'-C4'-C5'-O5'
2	B	2001	ADP	O4'-C4'-C5'-O5'
2	F	2001	ADP	O4'-C4'-C5'-O5'
2	B	2001	ADP	C4'-C5'-O5'-PA
2	C	2001	ADP	C4'-C5'-O5'-PA
2	E	2001	ADP	C4'-C5'-O5'-PA
2	C	2001	ADP	O4'-C4'-C5'-O5'
2	C	2001	ADP	C3'-C4'-C5'-O5'
2	D	2001	ADP	C4'-C5'-O5'-PA

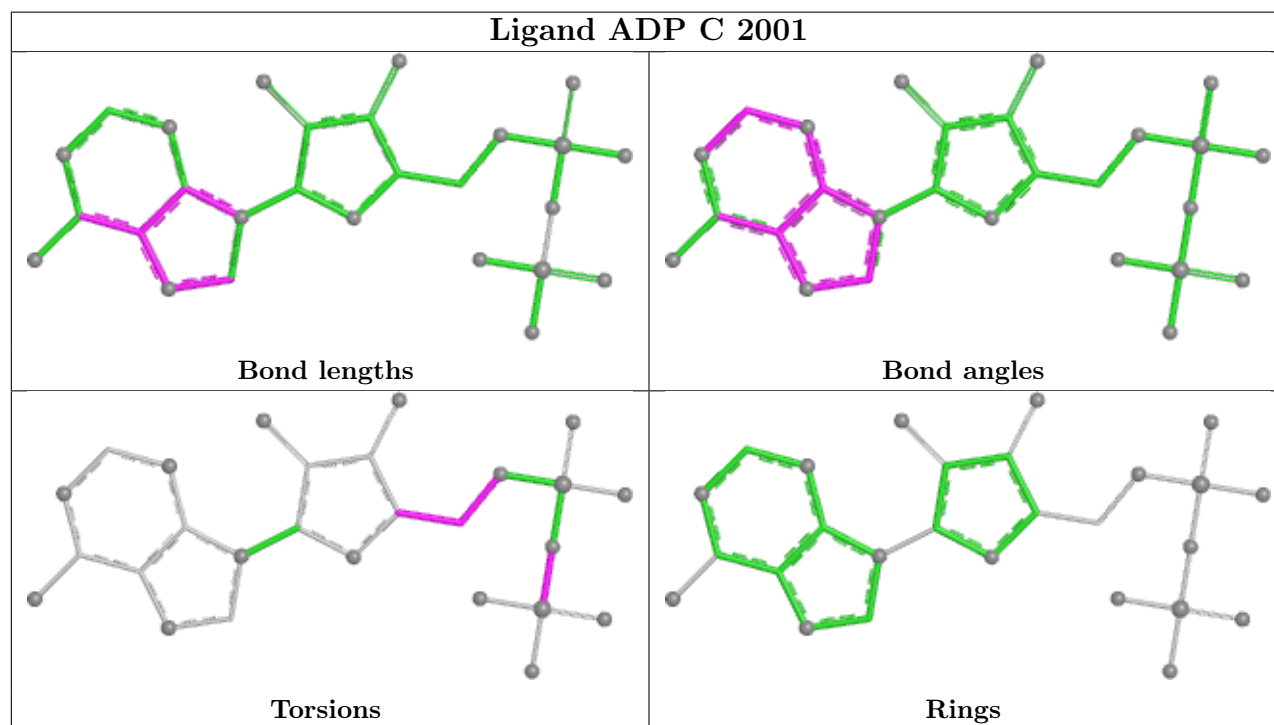
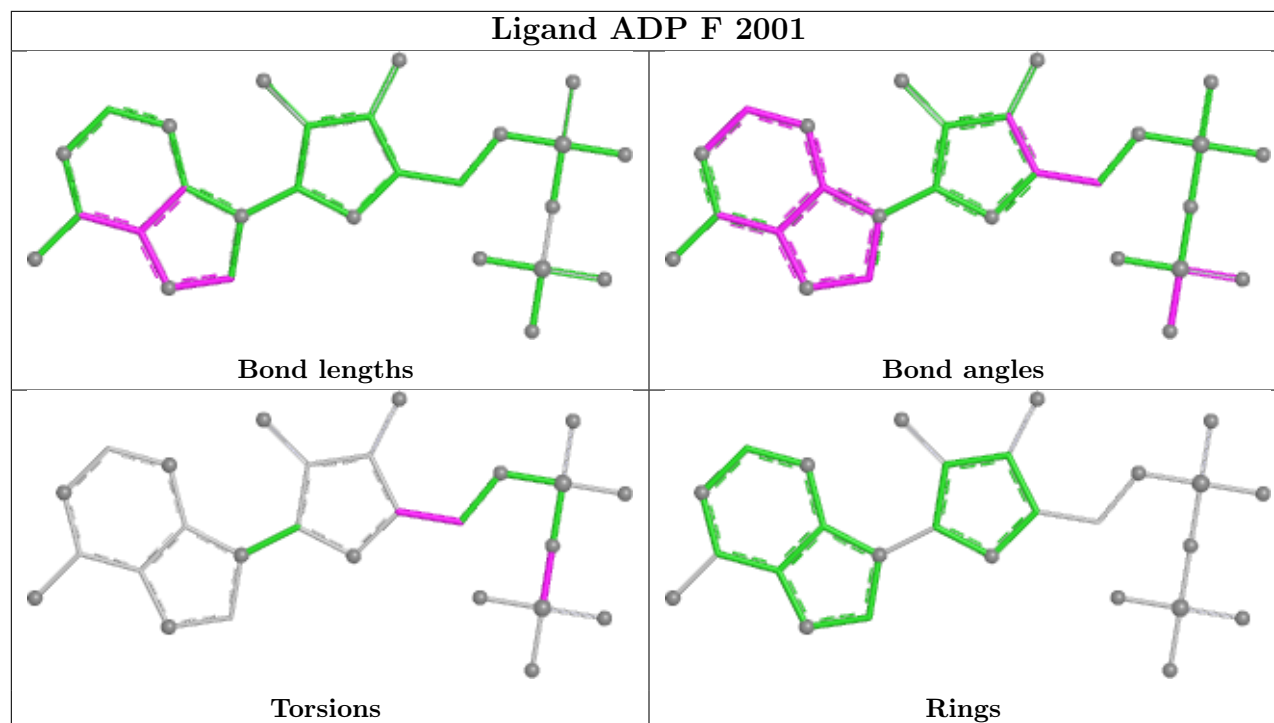
There are no ring outliers.

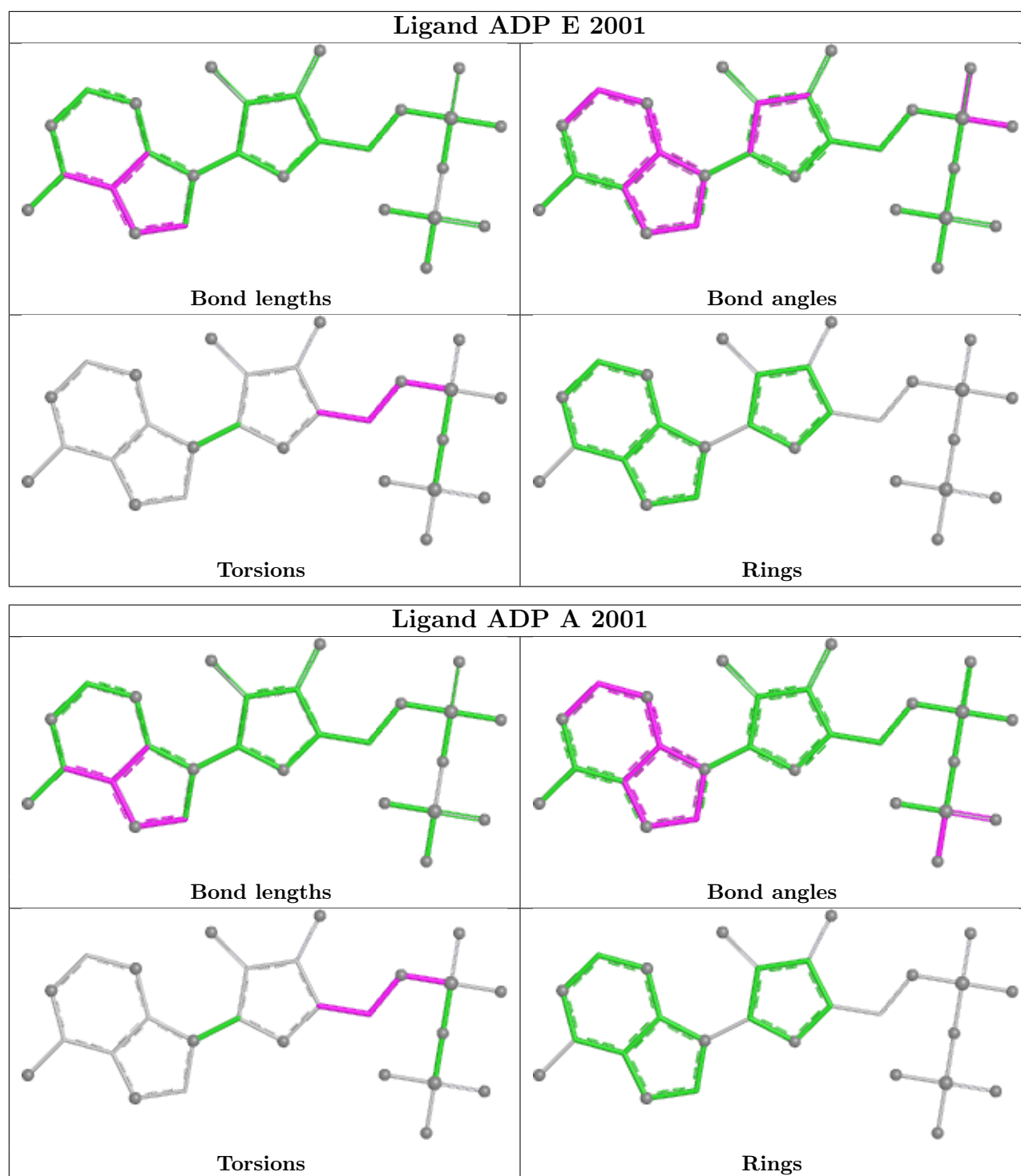
6 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	E	2002	SO4	2	0
2	D	2001	ADP	2	0
2	F	2001	ADP	1	0
2	C	2001	ADP	1	0
3	E	2004	SO4	1	0
2	A	2001	ADP	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.







5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å ²)	Q<0.9
1	A	443/546 (81%)	-0.92	0	100	100	44, 79, 135, 213	0
1	B	444/546 (81%)	-0.47	0	100	100	81, 127, 188, 295	0
1	C	445/546 (81%)	-0.61	1 (0%)	91	83	47, 104, 181, 267	0
1	D	444/546 (81%)	-0.63	1 (0%)	91	83	69, 118, 174, 280	0
1	E	444/546 (81%)	-0.66	0	100	100	53, 106, 166, 274	0
1	F	443/546 (81%)	-0.73	0	100	100	46, 93, 164, 266	0
All	All	2663/3276 (81%)	-0.67	2 (0%)	92	86	44, 106, 175, 295	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	327	SER	2.7
1	D	454	ALA	2.4

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

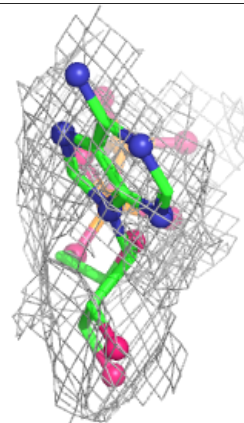
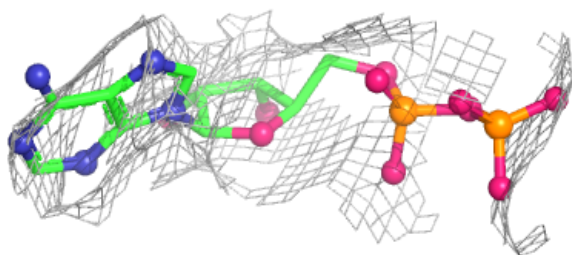
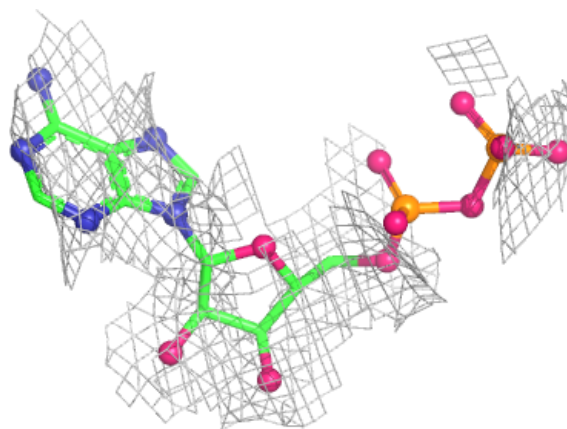
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q< 0.9’ lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	ADP	B	2001	27/27	0.98	0.05	76,105,130,146	0
3	SO4	B	2002	5/5	0.98	0.10	98,99,110,123	0
3	SO4	E	2003	5/5	0.98	0.08	116,119,133,138	0
3	SO4	E	2004	5/5	0.98	0.07	89,106,119,140	0
3	SO4	F	2002	5/5	0.98	0.09	52,63,70,72	0
4	MG	C	2003	1/1	0.98	0.08	141,141,141,141	0
3	SO4	A	2002	5/5	0.99	0.06	62,94,101,154	0
2	ADP	A	2001	27/27	0.99	0.05	56,72,87,92	0
3	SO4	C	2002	5/5	0.99	0.07	51,65,87,94	0
3	SO4	D	2002	5/5	0.99	0.06	62,74,81,84	0
3	SO4	E	2002	5/5	0.99	0.05	79,81,85,85	0
2	ADP	C	2001	27/27	0.99	0.06	71,91,108,111	0
2	ADP	D	2001	27/27	0.99	0.04	78,95,129,132	0
2	ADP	E	2001	27/27	0.99	0.05	81,94,101,103	0
4	MG	A	2003	1/1	0.99	0.04	47,47,47,47	0
2	ADP	F	2001	27/27	0.99	0.04	62,74,86,86	0
4	MG	E	2005	1/1	0.99	0.03	88,88,88,88	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.

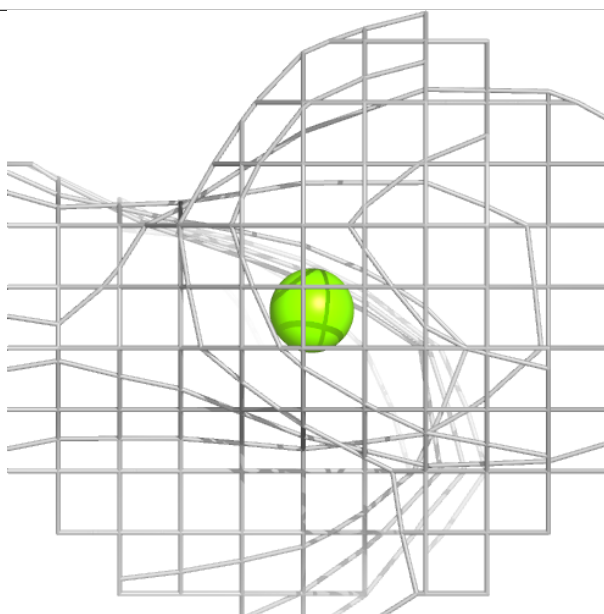
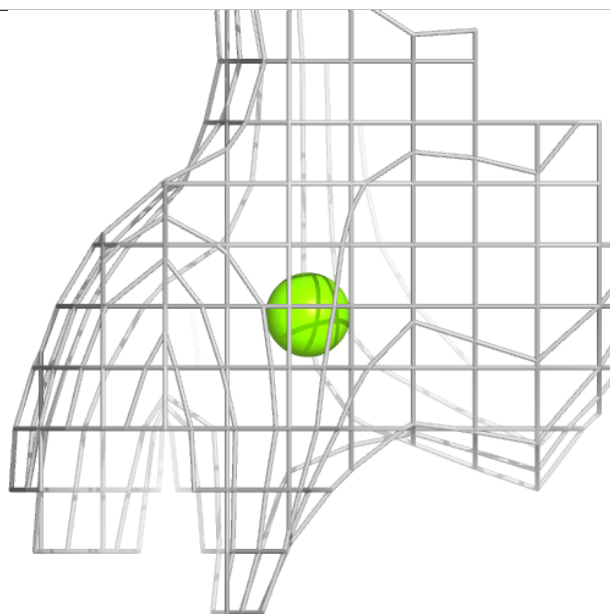
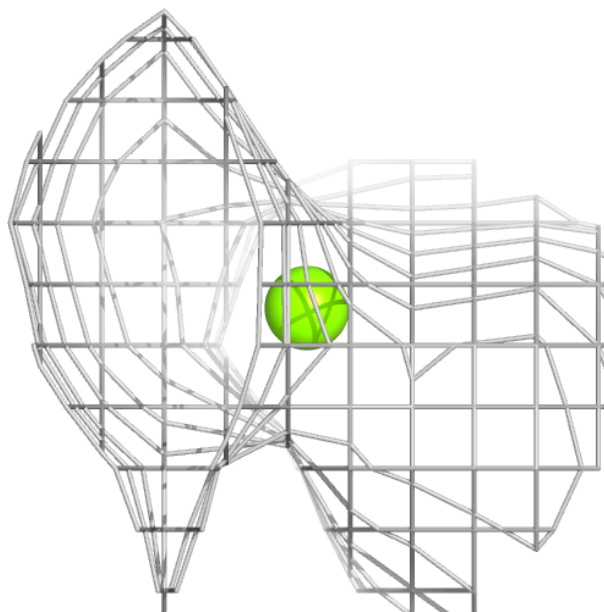
Electron density around ADP B 2001:

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



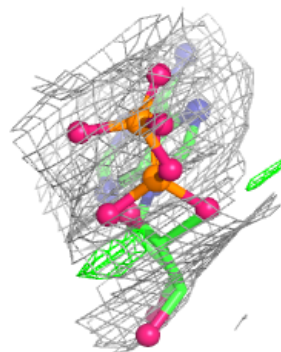
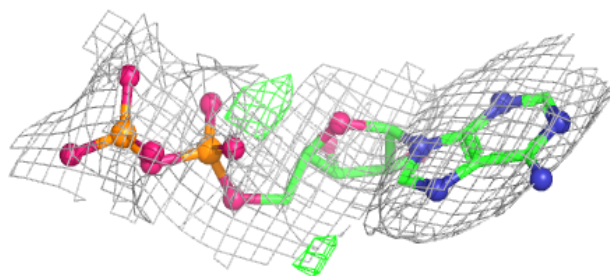
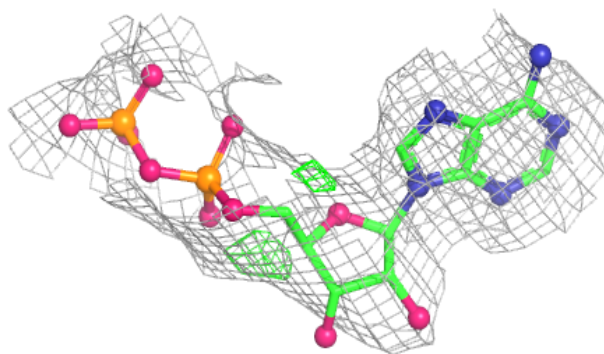
Electron density around MG C 2003:

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

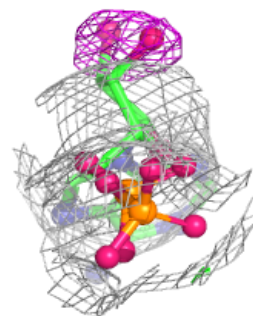
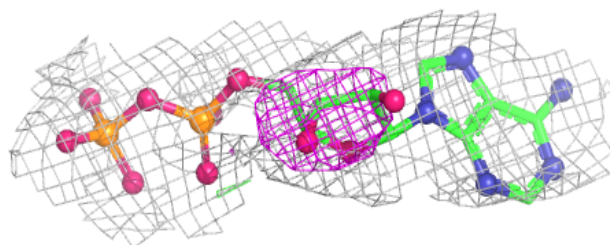
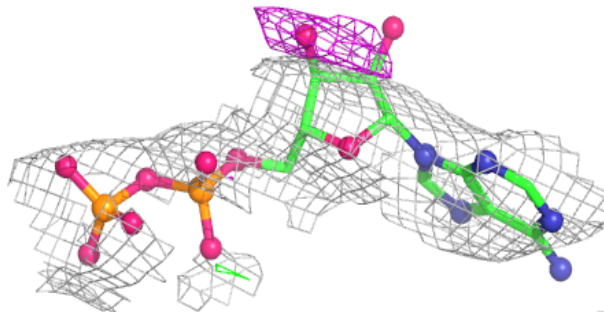


Electron density around ADP A 2001:

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

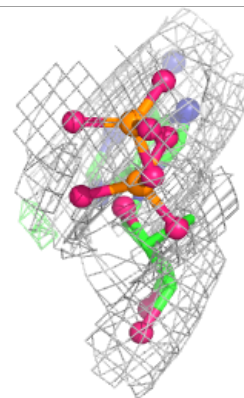
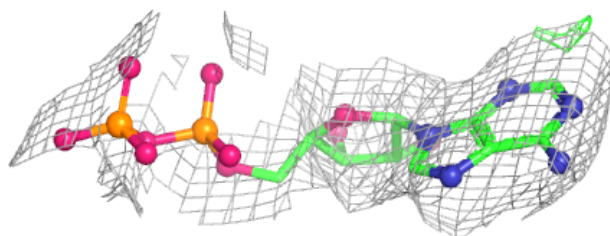
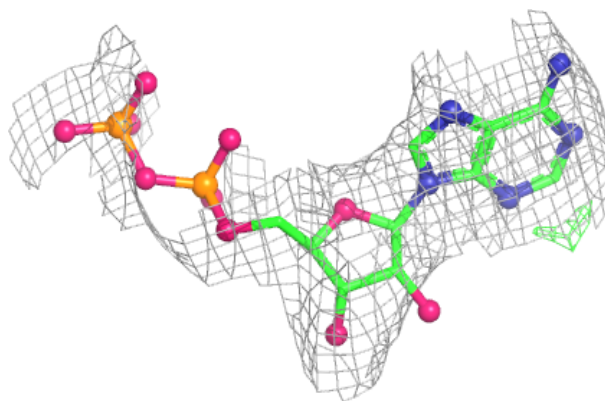
**Electron density around ADP C 2001:**

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

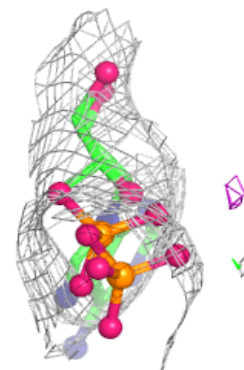
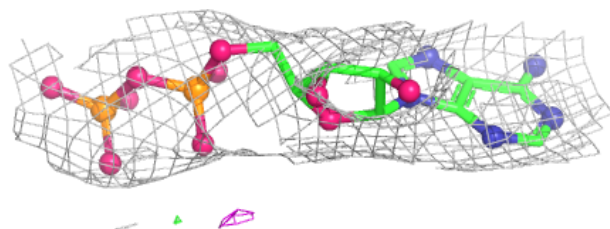


Electron density around ADP D 2001:

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

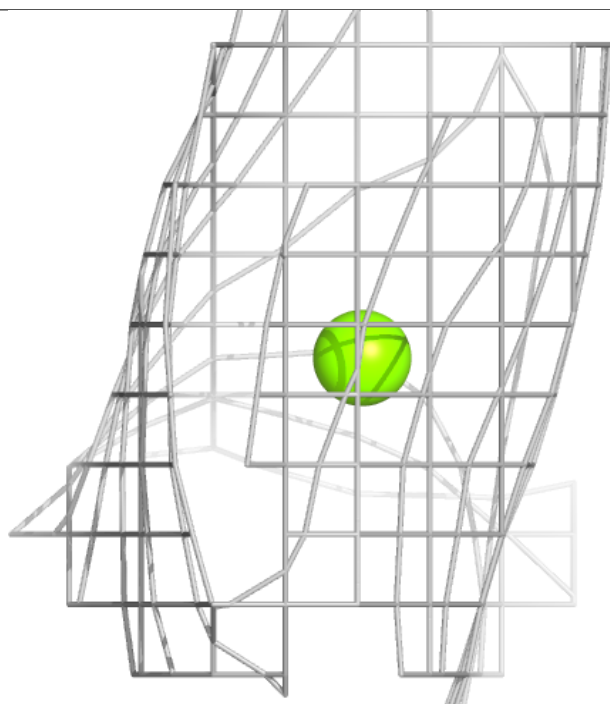
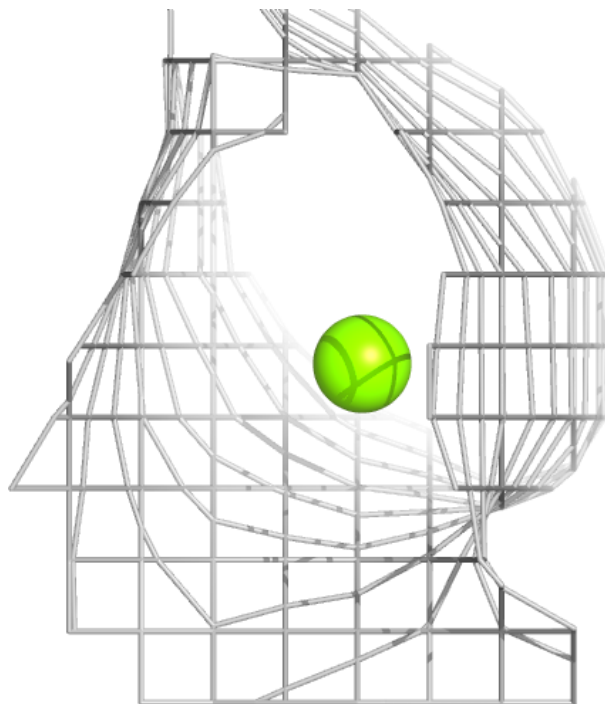
**Electron density around ADP E 2001:**

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



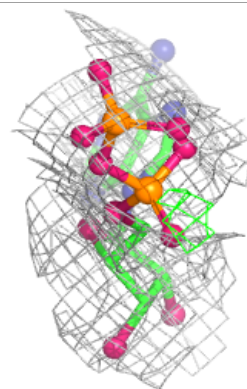
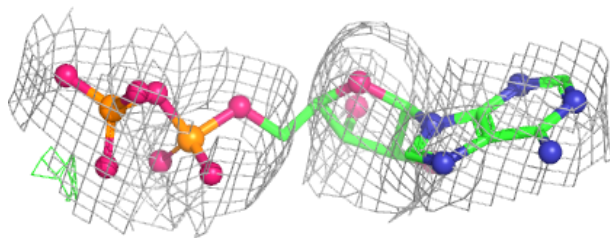
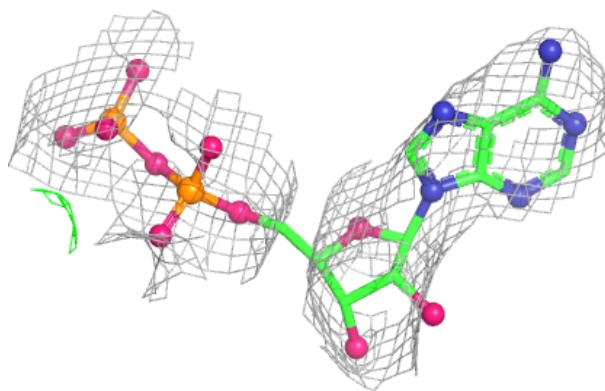
Electron density around MG A 2003:

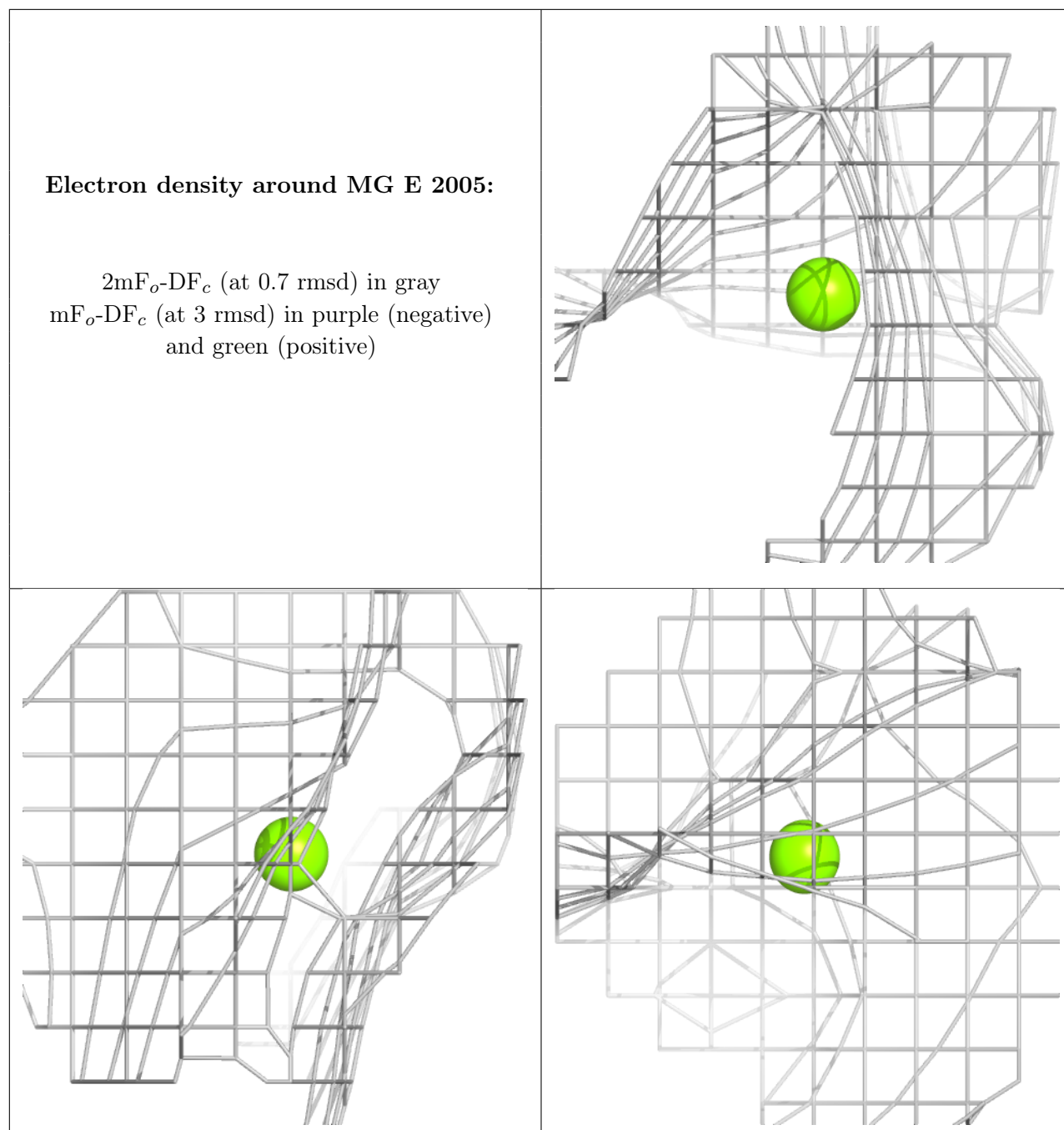
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ADP F 2001:

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





6.5 Other polymers ⓘ

There are no such residues in this entry.