



# Full wwPDB X-ray Structure Validation Report ⓘ

Aug 26, 2023 – 04:13 PM EDT

PDB ID : 3ES9  
Title : NADPH-Cytochrome P450 Reductase in an Open Conformation  
Authors : Hamdane, D.; Xia, C.; Im, S.-C.; Zhang, H.; Kim, J.-J.; Waskell, L.  
Deposited on : 2008-10-05  
Resolution : 3.40 Å(reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.35  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.35

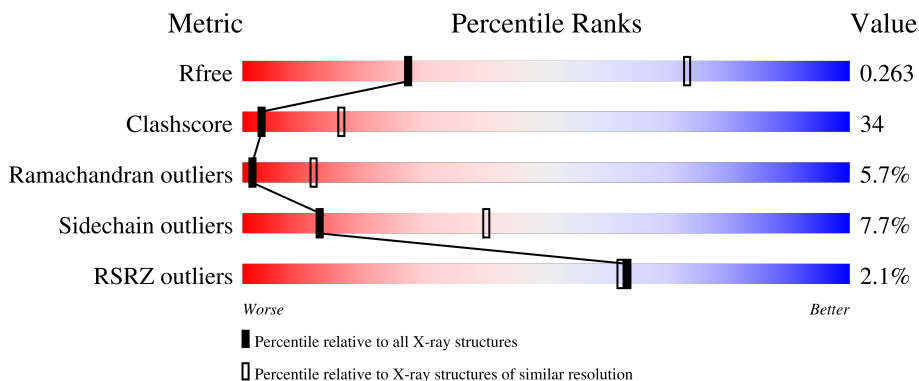
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.40 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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  $\geq 3$ , 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	618	 43% 47% 7% ..
1	B	618	 4% 39% 38% 6% 17%
1	C	618	 % 32% 33% 5% • 30%

## 2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 12762 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 NADPH–cytochrome P450 reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	603	4846	3069	834	920	23	0	0	0
1	B	515	4138	2618	726	775	19	0	0	0
1	C	435	3492	2212	617	647	16	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

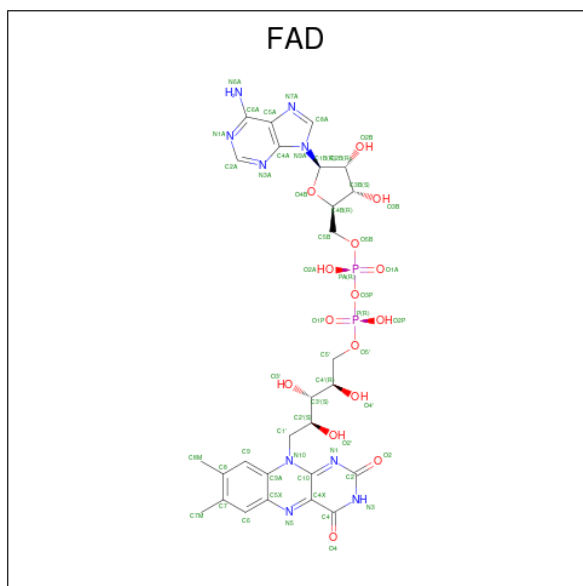
Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	THR	deletion	UNP P00388
A	?	-	GLY	deletion	UNP P00388
A	?	-	GLU	deletion	UNP P00388
A	?	-	GLU	deletion	UNP P00388
B	?	-	THR	deletion	UNP P00388
B	?	-	GLY	deletion	UNP P00388
B	?	-	GLU	deletion	UNP P00388
B	?	-	GLU	deletion	UNP P00388
C	?	-	THR	deletion	UNP P00388
C	?	-	GLY	deletion	UNP P00388
C	?	-	GLU	deletion	UNP P00388
C	?	-	GLU	deletion	UNP P00388

- Molecule 2 is FLAVIN MONONUCLEOTIDE (three-letter code: FMN) (formula: C<sub>17</sub>H<sub>21</sub>N<sub>4</sub>O<sub>9</sub>P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	31	17	4	9	1	0	0

- Molecule 3 is FLAVIN-ADENINE DINUCLEOTIDE (three-letter code: FAD) (formula:  $C_{27}H_{33}N_9O_{15}P_2$ ).



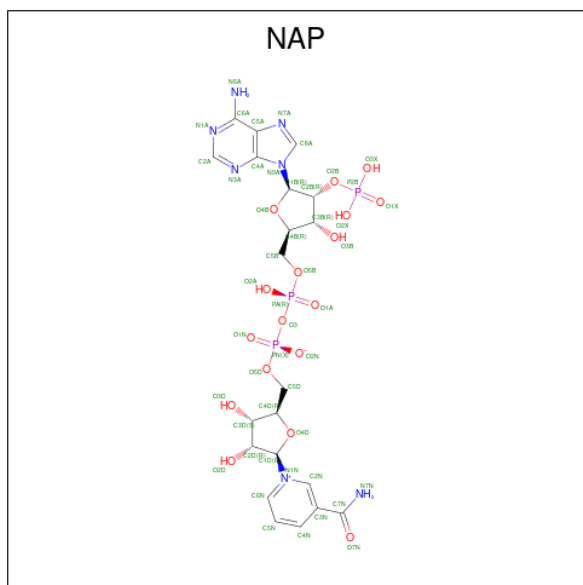
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	53	27	9	15	2	0	0
3	B	1	53	27	9	15	2	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
3	C	1	53	27	9	15	2	0	0

- Molecule 4 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula:  $C_{21}H_{28}N_7O_{17}P_3$ ).

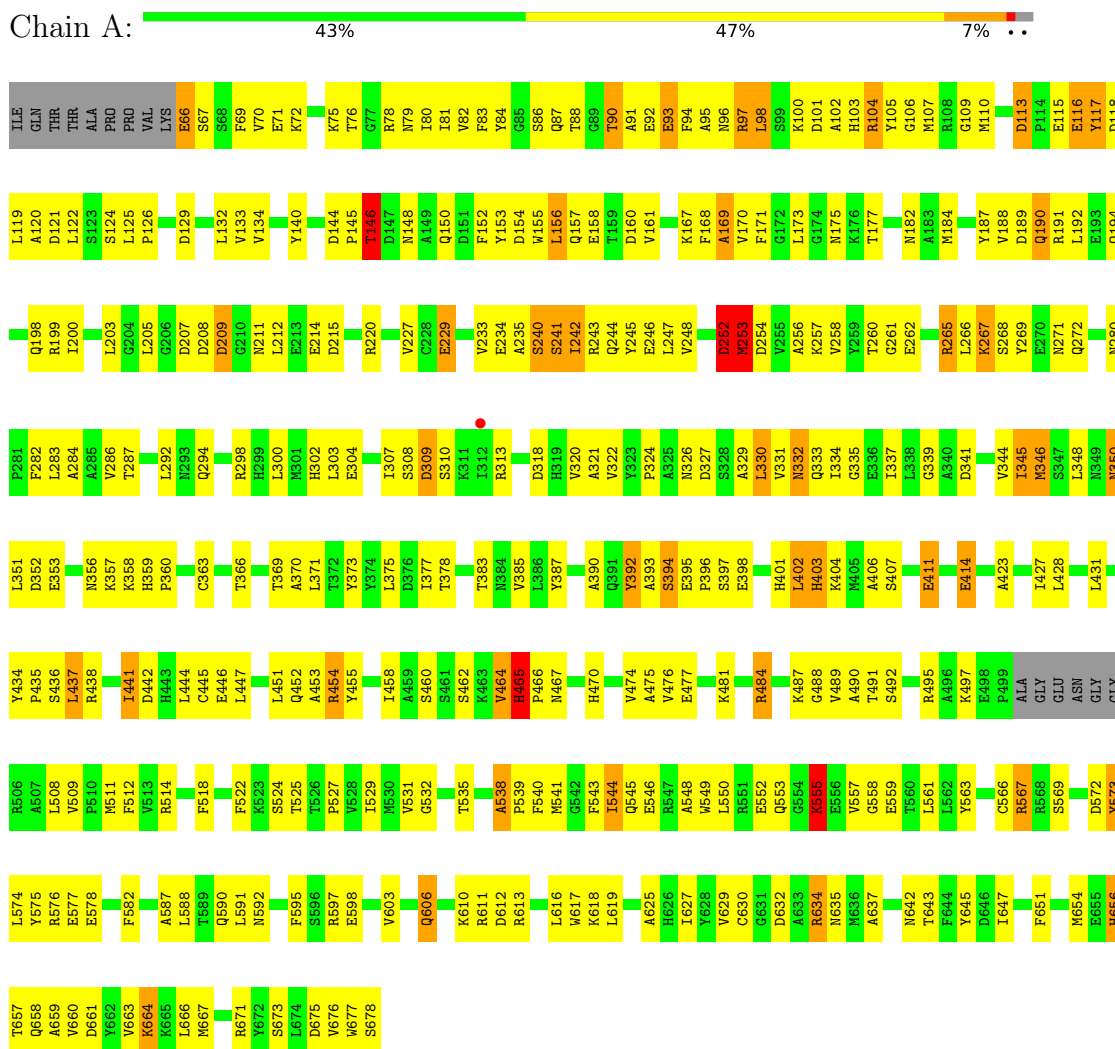


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
			Total	C	N	O			P
4	A	1	48	21	7	17	3	0	0
4	B	1	48	21	7	17	3	0	0

### 3 Residue-property plots

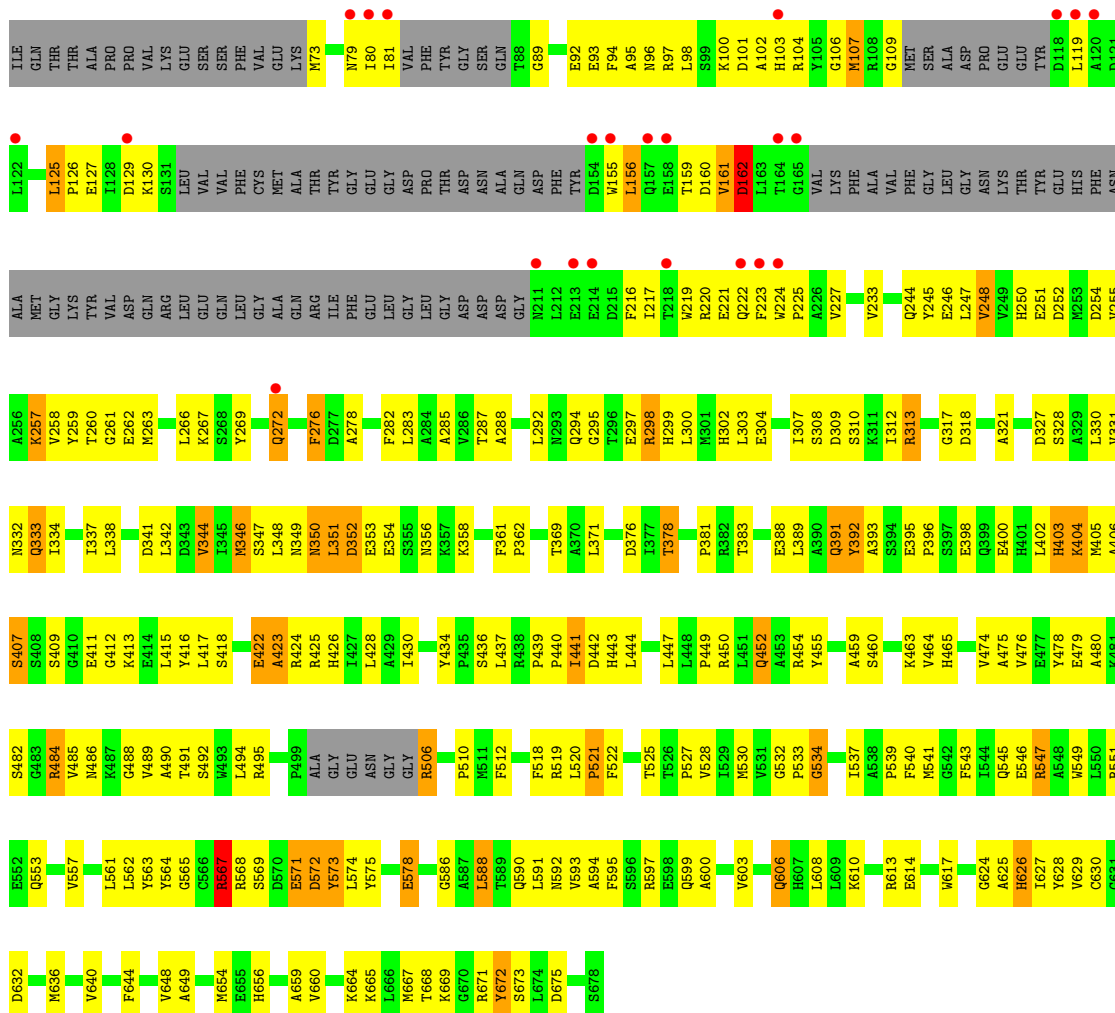
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: NADPH-cytochrome P450 reductase

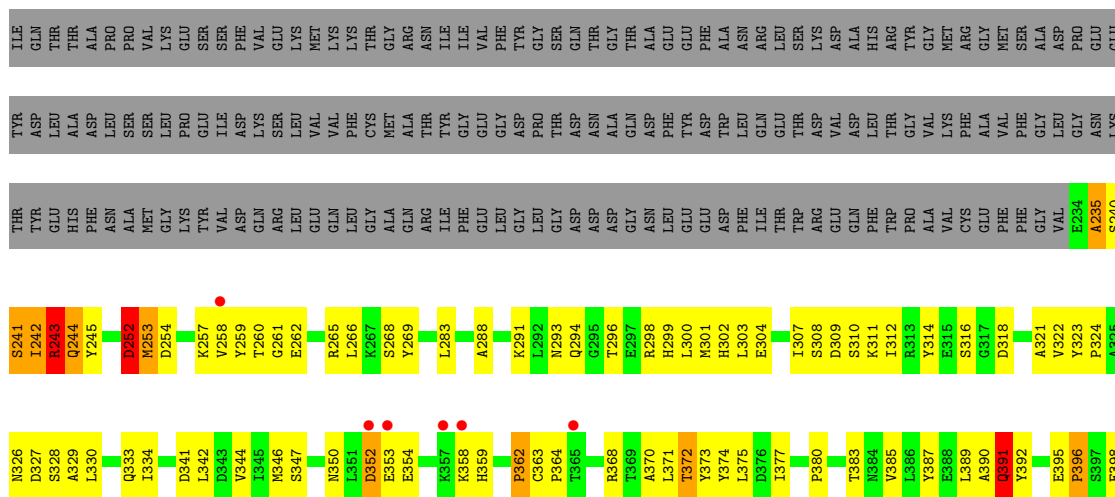


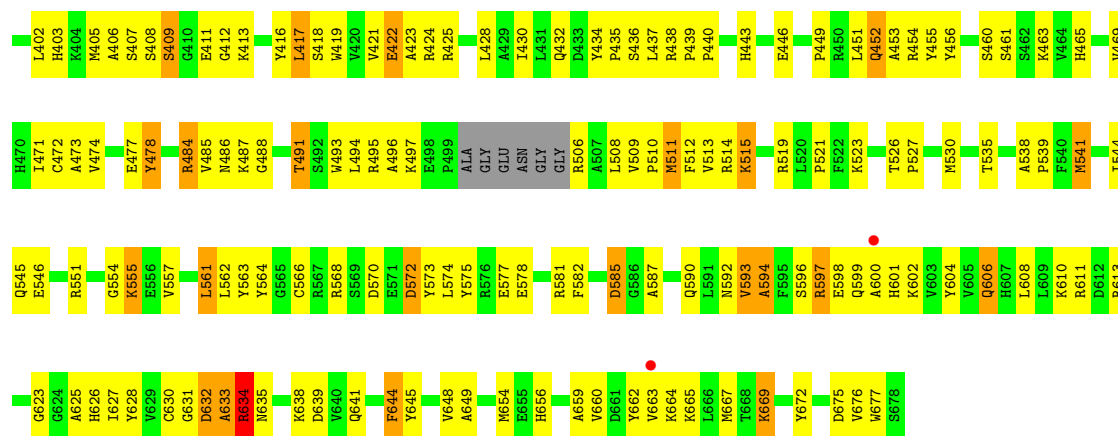
- Molecule 1: NADPH-cytochrome P450 reductase





• Molecule 1: NADPH-cytochrome P450 reductase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	109.10Å 93.00Å 125.70Å 90.00° 100.00° 90.00°	Depositor
Resolution (Å)	29.79 – 3.40 46.52 – 3.38	Depositor EDS
% Data completeness (in resolution range)	91.0 (29.79-3.40) 90.3 (46.52-3.38)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.62 (at 3.40Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, $R_{free}$	0.219 , 0.279 0.205 , 0.263	Depositor DCC
$R_{free}$ test set	1549 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	86.9	Xtrriage
Anisotropy	0.387	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 34.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	12762	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	106.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAP, FMN, FAD

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	0.41	0/4962	0.63	0/6714
1	B	0.40	0/4233	0.66	1/5725 (0.0%)
1	C	0.36	0/3576	0.60	0/4843
All	All	0.39	0/12771	0.63	1/17282 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	521	PRO	N-CA-C	5.09	125.35	112.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

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	4846	0	4692	335	0
1	B	4138	0	4026	280	0
1	C	3492	0	3425	229	0
2	A	31	0	19	0	0
3	A	53	0	31	5	0
3	B	53	0	31	7	0
3	C	53	0	31	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	48	0	25	3	0
4	B	48	0	25	2	0
All	All	12762	0	12305	841	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 34.

All (841) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:300:LEU:HD23	1:B:574:LEU:HD21	1.35	1.08
1:A:292:LEU:HD21	1:A:302:HIS:HB2	1.36	1.04
1:A:606:GLN:HE22	4:A:753:NAP:H2A	1.27	1.00
1:A:300:LEU:HD23	1:A:574:LEU:HD21	1.44	0.96
1:B:418:SER:HA	1:B:422:GLU:HB2	1.45	0.96
1:B:567:ARG:HD2	1:B:597:ARG:HD2	1.46	0.96
1:C:411:GLU:HG3	1:C:412:GLY:N	1.81	0.95
1:A:86:SER:HB2	1:A:91:ALA:HB3	1.46	0.95
1:B:590:GLN:HE21	1:B:592:ASN:HD21	1.10	0.94
1:A:82:VAL:HG11	1:A:95:ALA:HA	1.50	0.93
1:B:100:LYS:HE2	1:B:354:GLU:HG3	1.49	0.92
1:C:606:GLN:H	1:C:606:GLN:NE2	1.67	0.92
1:B:594:ALA:HB2	1:B:608:LEU:HD11	1.50	0.91
1:C:375:LEU:O	1:C:451:LEU:HB2	1.69	0.91
1:B:568:ARG:HB2	1:B:571:GLU:HB2	1.54	0.90
1:C:288:ALA:HB3	1:C:304:GLU:HG3	1.53	0.90
1:A:454:ARG:HH22	1:A:489:VAL:HB	1.36	0.90
1:C:634:ARG:HH11	1:C:634:ARG:HB3	1.35	0.89
1:C:606:GLN:H	1:C:606:GLN:HE21	1.18	0.88
1:B:272:GLN:HA	1:B:272:GLN:HE21	1.36	0.87
1:C:257:LYS:HD3	1:C:257:LYS:O	1.74	0.86
1:B:244:GLN:HE21	1:B:350:ASN:HD21	1.23	0.86
1:C:371:LEU:HD23	1:C:375:LEU:HD12	1.58	0.86
1:C:411:GLU:HG3	1:C:412:GLY:H	1.38	0.86
1:A:464:VAL:HG12	1:A:465:HIS:H	1.40	0.85
1:A:423:ALA:HA	1:A:481:LYS:HB2	1.58	0.85
1:B:590:GLN:NE2	1:B:592:ASN:HD21	1.76	0.83
1:A:395:GLU:HG3	1:A:396:PRO:HD2	1.58	0.83
1:A:402:LEU:HD11	1:A:437:LEU:HD22	1.59	0.83
1:C:596:SER:O	1:C:597:ARG:HG3	1.78	0.83
1:C:627:ILE:HG21	1:C:644:PHE:HE1	1.43	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:ASP:O	1:B:344:VAL:HG23	1.79	0.83
1:B:376:ASP:HB3	1:B:449:PRO:HG2	1.59	0.82
1:C:593:VAL:HG12	1:C:594:ALA:H	1.44	0.81
1:C:484:ARG:H	1:C:484:ARG:HD2	1.45	0.81
1:A:327:ASP:HB3	1:A:330:LEU:HB2	1.63	0.80
1:C:667:MET:HA	1:C:672:TYR:HB3	1.63	0.80
1:A:326:ASN:ND2	1:A:377:ILE:HG12	1.96	0.80
1:C:291:LYS:HE2	1:C:296:THR:HG22	1.64	0.80
1:B:79:ASN:CG	1:B:80:ILE:H	1.86	0.79
1:A:184:MET:CE	1:A:188:VAL:HG23	2.12	0.79
1:B:541:MET:O	1:B:545:GLN:HG3	1.83	0.79
1:C:460:SER:HA	1:C:545:GLN:OE1	1.82	0.78
1:C:568:ARG:NH1	1:C:598:GLU:HG2	1.99	0.78
1:C:656:HIS:O	1:C:660:VAL:HG23	1.83	0.78
1:B:338:LEU:HD21	1:B:439:PRO:HD2	1.65	0.78
1:A:546:GLU:O	1:A:550:LEU:HG	1.84	0.78
1:A:452:GLN:HE21	1:A:452:GLN:HA	1.48	0.77
1:B:269:TYR:CD2	1:B:283:LEU:HD11	2.19	0.77
1:C:293:ASN:HB3	1:C:300:LEU:HD23	1.66	0.77
1:B:452:GLN:HE21	1:B:452:GLN:HA	1.50	0.77
1:B:244:GLN:HE21	1:B:350:ASN:ND2	1.82	0.76
1:A:654:MET:HB2	1:A:658:GLN:HB3	1.67	0.76
1:B:636:MET:O	1:B:640:VAL:HG23	1.86	0.76
1:B:411:GLU:HG3	1:B:412:GLY:N	2.01	0.76
1:A:371:LEU:HD23	1:A:375:LEU:HD12	1.68	0.75
1:B:402:LEU:HD11	1:B:437:LEU:HD22	1.68	0.75
1:A:265:ARG:HB3	1:A:268:SER:HB3	1.69	0.75
1:A:488:GLY:HA2	3:A:752:FAD:O1A	1.86	0.75
1:A:582:PHE:HB3	1:A:587:ALA:HB3	1.69	0.75
1:B:378:THR:HG21	1:B:489:VAL:HG21	1.68	0.75
1:B:327:ASP:HB3	1:B:330:LEU:HB2	1.69	0.75
1:C:389:LEU:HB3	1:C:437:LEU:HD11	1.67	0.75
1:C:259:TYR:HE2	1:C:266:LEU:HA	1.53	0.74
1:C:634:ARG:HB3	1:C:634:ARG:NH1	2.02	0.74
1:B:411:GLU:HG3	1:B:412:GLY:H	1.52	0.74
1:C:321:ALA:HB2	1:C:455:TYR:CE1	2.22	0.74
1:A:272:GLN:HE22	1:A:283:LEU:N	1.86	0.74
1:B:463:LYS:HG3	1:B:546:GLU:HG3	1.67	0.74
1:B:102:ALA:HB1	1:B:107:MET:O	1.88	0.73
1:A:455:TYR:CE1	1:A:514:ARG:HD3	2.22	0.73
1:C:266:LEU:HD12	1:C:266:LEU:H	1.52	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:223:PHE:O	1:B:227:VAL:HG23	1.88	0.73
1:C:561:LEU:HD12	1:C:561:LEU:H	1.54	0.73
1:C:259:TYR:CE2	1:C:266:LEU:HG	2.23	0.72
1:A:393:ALA:HA	1:A:436:SER:O	1.88	0.72
1:B:300:LEU:CD2	1:B:574:LEU:HD21	2.17	0.72
1:B:575:TYR:HB3	1:B:578:GLU:HB2	1.71	0.72
1:A:654:MET:HB2	1:A:658:GLN:CB	2.19	0.72
1:A:666:LEU:HD22	1:A:671:ARG:HB2	1.71	0.72
1:B:106:GLY:O	1:B:107:MET:HG3	1.89	0.72
1:A:96:ASN:HB3	1:A:100:LYS:HE3	1.71	0.72
1:C:561:LEU:HD12	1:C:561:LEU:N	2.04	0.72
1:C:649:ALA:HB2	1:C:659:ALA:HB2	1.71	0.72
1:A:348:LEU:HD12	1:A:360:PRO:HG3	1.70	0.72
1:A:113:ASP:OD1	1:A:115:GLU:HB3	1.88	0.72
1:A:434:TYR:O	1:A:437:LEU:HB3	1.91	0.71
1:A:107:MET:CE	1:A:233:VAL:HG21	2.20	0.71
1:A:569:SER:HB3	1:A:595:PHE:CE1	2.26	0.71
1:A:634:ARG:HD2	1:A:678:SER:OG	1.89	0.71
1:C:253:MET:CE	1:C:254:ASP:H	2.01	0.71
1:C:523:LYS:HB2	1:C:526:THR:OG1	1.90	0.71
1:A:246:GLU:HB3	1:A:351:LEU:HD21	1.73	0.71
1:A:654:MET:HB2	1:A:658:GLN:CG	2.21	0.70
1:B:246:GLU:HB3	1:B:351:LEU:HD21	1.73	0.70
1:A:104:ARG:HD2	1:A:242:ILE:HD12	1.70	0.70
1:A:664:LYS:HE3	1:A:664:LYS:HA	1.72	0.70
1:B:476:VAL:HG21	3:B:752:FAD:H5'2	1.71	0.70
1:A:661:ASP:HA	1:A:664:LYS:HB2	1.72	0.70
1:C:259:TYR:HB2	1:C:364:PRO:O	1.92	0.69
1:C:341:ASP:HB3	1:C:344:VAL:HG23	1.74	0.69
1:A:666:LEU:HD21	1:A:671:ARG:NH1	2.07	0.69
1:A:105:TYR:O	1:A:107:MET:N	2.25	0.69
1:C:488:GLY:HA2	3:C:752:FAD:O1A	1.93	0.69
1:B:350:ASN:HD22	1:B:351:LEU:N	1.90	0.69
1:C:265:ARG:HG3	1:C:265:ARG:HH11	1.58	0.69
1:A:254:ASP:O	1:A:257:LYS:HG2	1.92	0.69
1:A:460:SER:HB3	1:A:470:HIS:HB2	1.75	0.69
1:C:478:TYR:O	1:C:485:VAL:HG13	1.93	0.69
1:A:214:GLU:HA	1:A:214:GLU:OE1	1.93	0.69
1:B:79:ASN:HD21	1:B:107:MET:HG2	1.58	0.69
1:B:518:PHE:O	1:B:519:ARG:HD3	1.93	0.69
1:A:184:MET:HE2	1:A:188:VAL:HG23	1.74	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:654:MET:HB2	1:A:658:GLN:HG2	1.75	0.68
1:B:562:LEU:HD12	1:B:563:TYR:H	1.58	0.68
1:B:479:GLU:HG2	1:B:485:VAL:HG22	1.76	0.68
1:C:418:SER:HA	1:C:422:GLU:HB2	1.74	0.68
1:C:435:PRO:HA	1:C:438:ARG:NH2	2.06	0.68
1:B:254:ASP:HB3	1:B:257:LYS:HD2	1.75	0.68
1:C:645:TYR:HA	1:C:663:VAL:HG21	1.75	0.68
1:A:265:ARG:CB	1:A:268:SER:HB3	2.23	0.68
1:C:326:ASN:ND2	1:C:377:ILE:HG12	2.08	0.68
1:A:292:LEU:CD2	1:A:302:HIS:HB2	2.18	0.68
1:A:441:ILE:HG23	1:A:442:ASP:H	1.59	0.68
1:C:253:MET:HE2	1:C:254:ASP:H	1.58	0.68
1:C:324:PRO:HG2	1:C:451:LEU:HD21	1.76	0.68
1:B:409:SER:HA	1:B:413:LYS:HB2	1.75	0.67
1:B:527:PRO:HB2	1:B:625:ALA:HB2	1.75	0.67
1:A:329:ALA:O	1:A:333:GLN:HB2	1.94	0.67
1:C:302:HIS:HD2	1:C:575:TYR:OH	1.77	0.67
1:A:487:LYS:HB3	1:A:492:SER:OG	1.94	0.67
1:A:266:LEU:O	1:A:267:LYS:HB2	1.95	0.67
1:B:244:GLN:NE2	1:B:350:ASN:HD21	1.90	0.67
1:B:518:PHE:CD2	1:B:675:ASP:HB2	2.29	0.67
1:C:627:ILE:HG21	1:C:644:PHE:CE1	2.29	0.67
1:B:338:LEU:CD2	1:B:439:PRO:HD2	2.25	0.66
1:A:477:GLU:HG3	1:A:487:LYS:HG2	1.76	0.66
1:A:527:PRO:HB2	1:A:625:ALA:HB2	1.75	0.66
1:C:477:GLU:HG3	1:C:487:LYS:HD2	1.76	0.66
1:C:606:GLN:HE21	1:C:606:GLN:N	1.92	0.66
1:A:282:PHE:CE2	1:A:310:SER:HB3	2.31	0.66
1:B:395:GLU:HG2	1:B:398:GLU:HG3	1.78	0.66
1:A:484:ARG:H	1:A:484:ARG:HD2	1.60	0.66
1:A:78:ARG:NH1	1:A:110:MET:HB3	2.11	0.66
1:C:454:ARG:HG2	3:C:752:FAD:O1P	1.96	0.66
1:A:155:TRP:CZ2	1:A:161:VAL:HG11	2.31	0.66
1:A:154:ASP:O	1:A:158:GLU:HG2	1.97	0.65
1:A:566:CYS:HB2	1:A:572:ASP:OD1	1.96	0.65
1:A:452:GLN:HA	1:A:452:GLN:NE2	2.11	0.65
1:C:411:GLU:CG	1:C:412:GLY:H	2.10	0.65
1:A:272:GLN:HE22	1:A:283:LEU:H	1.43	0.65
1:B:521:PRO:O	1:B:522:PHE:HB3	1.96	0.65
1:B:100:LYS:HE2	1:B:354:GLU:CG	2.24	0.65
1:B:254:ASP:HB3	1:B:257:LYS:CD	2.26	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:555:LYS:H	1:A:555:LYS:HD2	1.61	0.65
1:A:253:MET:HE2	1:A:257:LYS:HD3	1.77	0.64
1:A:441:ILE:HG23	1:A:442:ASP:N	2.12	0.64
1:B:92:GLU:O	1:B:95:ALA:HB3	1.97	0.64
1:C:240:SER:CB	1:C:387:TYR:HE1	2.10	0.64
1:A:184:MET:HE1	1:A:188:VAL:HG23	1.78	0.64
1:A:82:VAL:HG22	1:A:134:VAL:HB	1.79	0.64
1:B:562:LEU:HD12	1:B:563:TYR:N	2.13	0.64
1:B:664:LYS:O	1:B:668:THR:HG23	1.98	0.64
1:A:66:GLU:HG2	1:A:67:SER:N	2.13	0.64
1:A:548:ALA:HB2	1:A:587:ALA:HB2	1.80	0.64
1:C:342:LEU:HD12	1:C:342:LEU:H	1.63	0.64
1:A:86:SER:CB	1:A:91:ALA:HB3	2.25	0.63
1:A:93:GLU:OE2	1:A:97:ARG:HD3	1.98	0.63
1:B:376:ASP:OD2	1:B:378:THR:HG23	1.97	0.63
1:B:216:PHE:HE2	1:B:220:ARG:HD2	1.62	0.63
1:C:590:GLN:HE21	1:C:592:ASN:HD21	1.45	0.63
1:B:310:SER:OG	1:B:312:ILE:HG13	1.99	0.63
1:C:645:TYR:HD2	1:C:663:VAL:HG21	1.62	0.63
1:A:595:PHE:O	1:A:603:VAL:HB	1.98	0.63
1:C:568:ARG:HH12	1:C:598:GLU:HG2	1.63	0.62
1:B:79:ASN:CG	1:B:80:ILE:N	2.52	0.62
1:C:308:SER:O	1:C:309:ASP:HB2	1.98	0.62
1:C:551:ARG:CG	1:C:557:VAL:HG21	2.29	0.62
1:C:352:ASP:O	1:C:354:GLU:N	2.28	0.62
1:A:175:ASN:OD1	1:A:177:THR:HG23	2.00	0.62
1:A:455:TYR:HE1	1:A:514:ARG:HD3	1.62	0.62
1:B:567:ARG:HB2	1:B:572:ASP:OD1	2.00	0.62
1:C:599:GLN:O	1:C:601:HIS:N	2.33	0.62
1:B:627:ILE:O	1:B:628:TYR:HD2	1.82	0.61
1:A:87:GLN:HB3	1:A:140:TYR:CE1	2.35	0.61
1:A:395:GLU:HB2	1:A:436:SER:OG	2.00	0.61
1:A:632:ASP:HA	1:A:677:TRP:O	2.00	0.61
1:B:330:LEU:O	1:B:334:ILE:HG13	2.00	0.61
1:B:606:GLN:HE22	4:B:753:NAP:H2A	1.66	0.61
1:B:416:TYR:C	1:B:418:SER:H	2.04	0.61
1:B:610:LYS:O	1:B:613:ARG:HB3	2.01	0.60
1:A:107:MET:HE2	1:A:233:VAL:HG21	1.82	0.60
1:B:79:ASN:ND2	1:B:107:MET:HG2	2.17	0.60
1:B:262:GLU:HA	1:B:269:TYR:CE1	2.35	0.60
1:C:461:SER:HB2	1:C:546:GLU:OE1	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:ILE:O	1:A:242:ILE:HG22	2.01	0.60
1:A:529:ILE:HD13	1:A:616:LEU:HD22	1.84	0.60
1:C:265:ARG:HB2	1:C:268:SER:HB3	1.84	0.60
1:A:247:LEU:HD11	1:A:346:MET:HB2	1.83	0.60
1:C:633:ALA:HB2	1:C:676:VAL:HB	1.83	0.60
1:B:328:SER:O	1:B:331:VAL:HG12	2.02	0.60
1:B:259:TYR:CD2	1:B:362:PRO:HB3	2.36	0.59
1:C:544:ILE:HD11	1:C:562:LEU:HD22	1.84	0.59
1:B:302:HIS:HE1	1:B:304:GLU:HG2	1.66	0.59
1:A:145:PRO:HB3	1:A:184:MET:SD	2.42	0.59
1:A:337:ILE:HB	1:A:438:ARG:NH1	2.17	0.59
1:B:246:GLU:HB3	1:B:351:LEU:CD2	2.33	0.59
1:B:269:TYR:HD2	1:B:283:LEU:HD21	1.67	0.59
1:A:229:GLU:OE1	1:A:387:TYR:HE2	1.86	0.59
1:B:269:TYR:HE2	1:B:510:PRO:CG	2.16	0.59
1:C:425:ARG:HB3	1:C:430:ILE:CD1	2.33	0.59
1:C:634:ARG:O	1:C:638:LYS:HG2	2.02	0.59
1:B:418:SER:HA	1:B:422:GLU:CB	2.27	0.59
1:B:488:GLY:HA2	3:B:752:FAD:O1A	2.03	0.59
1:C:301:MET:CE	1:C:495:ARG:HA	2.32	0.59
1:A:118:ASP:OD2	1:A:120:ALA:HB3	2.02	0.59
1:B:528:VAL:HG23	1:B:547:ARG:NH2	2.18	0.59
1:A:324:PRO:HG2	1:A:451:LEU:HD21	1.85	0.59
1:C:575:TYR:HB3	1:C:578:GLU:HB2	1.84	0.59
1:A:378:THR:HG21	1:A:489:VAL:CG2	2.33	0.58
1:C:321:ALA:HA	1:C:454:ARG:O	2.03	0.58
1:A:454:ARG:HD2	1:A:454:ARG:N	2.17	0.58
1:C:590:GLN:HG3	1:C:592:ASN:HD21	1.68	0.58
1:C:541:MET:CE	1:C:541:MET:HA	2.33	0.58
1:A:398:GLU:OE2	1:A:434:TYR:HA	2.03	0.58
1:B:104:ARG:HH11	1:B:104:ARG:HB2	1.69	0.58
1:C:604:TYR:HB3	1:C:606:GLN:HE22	1.67	0.58
1:A:145:PRO:HG2	1:A:153:TYR:CG	2.38	0.58
1:B:423:ALA:O	1:B:480:ALA:HB1	2.03	0.58
1:A:104:ARG:HD2	1:A:242:ILE:CD1	2.34	0.58
1:B:262:GLU:HA	1:B:269:TYR:CD1	2.39	0.58
1:C:561:LEU:H	1:C:561:LEU:CD1	2.16	0.58
1:C:593:VAL:O	1:C:594:ALA:HB2	2.03	0.58
1:A:544:ILE:HD13	1:A:588:LEU:HD21	1.84	0.58
1:A:606:GLN:NE2	4:A:753:NAP:H2A	2.09	0.58
1:C:630:CYS:SG	1:C:631:GLY:N	2.76	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:TYR:HB3	1:A:92:GLU:HA	1.85	0.58
1:A:524:SER:HB2	1:A:557:VAL:HG22	1.85	0.58
1:B:303:LEU:HD21	1:B:494:LEU:HB3	1.84	0.58
1:B:478:TYR:HE2	1:B:480:ALA:HB2	1.69	0.58
1:C:347:SER:HA	1:C:363:CYS:SG	2.44	0.58
1:A:87:GLN:HB2	1:A:146:THR:HG22	1.86	0.57
1:A:272:GLN:HE22	1:A:282:PHE:HA	1.69	0.57
1:A:71:GLU:O	1:A:75:LYS:HG2	2.04	0.57
1:A:282:PHE:HE1	1:A:284:ALA:HA	1.69	0.57
1:A:158:GLU:HB2	1:B:278:ALA:CB	2.34	0.57
1:A:298:ARG:HD2	1:A:567:ARG:NH2	2.19	0.57
1:A:327:ASP:HB3	1:A:330:LEU:CB	2.33	0.57
1:C:266:LEU:HD12	1:C:266:LEU:N	2.18	0.57
1:C:667:MET:HG2	1:C:672:TYR:CD2	2.39	0.57
1:A:252:ASP:OD1	1:A:253:MET:N	2.37	0.57
1:A:233:VAL:HG12	1:A:234:GLU:N	2.18	0.57
1:C:539:PRO:HG3	1:C:630:CYS:SG	2.45	0.57
1:A:283:LEU:HD23	1:A:508:LEU:CD1	2.34	0.57
1:A:304:GLU:HG2	1:A:470:HIS:CD2	2.40	0.57
1:C:259:TYR:CE2	1:C:266:LEU:HA	2.37	0.57
1:A:173:LEU:HD23	1:A:212:LEU:HD21	1.85	0.57
1:C:383:THR:O	1:C:406:ALA:HB1	2.05	0.57
1:C:474:VAL:O	1:C:491:THR:HG21	2.05	0.57
1:C:608:LEU:CD2	1:C:611:ARG:HD3	2.35	0.57
1:B:216:PHE:CE2	1:B:220:ARG:HD2	2.40	0.57
1:B:257:LYS:HA	1:B:266:LEU:HD21	1.87	0.57
1:C:515:LYS:HD3	1:C:519:ARG:NH2	2.20	0.57
1:A:103:HIS:O	1:A:105:TYR:N	2.38	0.57
1:A:119:LEU:HG	1:A:152:PHE:CD1	2.40	0.57
1:A:189:ASP:OD2	1:A:203:LEU:HB2	2.05	0.56
1:B:222:GLN:HA	1:B:225:PRO:HD2	1.87	0.56
1:C:307:ILE:HD13	1:C:469:VAL:CG2	2.34	0.56
1:A:158:GLU:HB2	1:B:278:ALA:HB2	1.87	0.56
1:A:190:GLN:O	1:A:194:GLN:HG3	2.04	0.56
1:B:248:VAL:HG21	1:B:349:ASN:HD21	1.70	0.56
1:B:376:ASP:CB	1:B:449:PRO:HG2	2.34	0.56
1:B:482:SER:O	1:B:484:ARG:HD2	2.04	0.56
1:B:331:VAL:HG13	1:B:332:ASN:HD22	1.71	0.56
1:A:462:SER:O	1:A:466:PRO:HB3	2.06	0.56
1:B:530:MET:HB3	1:B:540:PHE:CD1	2.40	0.56
1:B:388:GLU:O	1:B:391:GLN:HG3	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:395:GLU:HG2	1:C:398:GLU:HG3	1.87	0.56
1:A:359:HIS:CD2	1:A:363:CYS:HB2	2.40	0.56
1:B:568:ARG:HG2	1:B:568:ARG:HH11	1.71	0.56
1:B:263:MET:H	1:B:269:TYR:HE1	1.52	0.56
1:A:283:LEU:HD23	1:A:508:LEU:HD13	1.87	0.56
1:B:298:ARG:NH1	1:B:567:ARG:NH1	2.54	0.56
1:B:567:ARG:HG3	1:B:572:ASP:OD2	2.05	0.56
1:B:125:LEU:HB3	1:B:126:PRO:HD3	1.87	0.55
1:B:303:LEU:HD22	1:B:494:LEU:HD13	1.87	0.55
1:C:592:ASN:HB3	1:C:608:LEU:HD13	1.88	0.55
1:B:125:LEU:H	1:B:126:PRO:CD	2.19	0.55
1:C:551:ARG:HG2	1:C:557:VAL:HG21	1.88	0.55
1:B:482:SER:OG	1:B:484:ARG:HG2	2.06	0.55
1:B:624:GLY:HA2	1:B:671:ARG:NH2	2.22	0.55
1:C:301:MET:HE1	1:C:495:ARG:HA	1.87	0.55
1:C:428:LEU:O	1:C:432:GLN:HG3	2.07	0.55
1:A:318:ASP:O	1:A:458:ILE:HG13	2.06	0.55
1:B:321:ALA:HB2	1:B:455:TYR:CE1	2.42	0.55
1:B:272:GLN:HE21	1:B:272:GLN:CA	2.13	0.55
1:B:313:ARG:HG2	1:B:313:ARG:HH11	1.72	0.55
1:C:358:LYS:HB3	1:C:359:HIS:CE1	2.42	0.55
1:C:551:ARG:HG3	1:C:557:VAL:HG21	1.89	0.55
1:B:392:TYR:CE1	1:B:440:PRO:HD3	2.42	0.55
1:C:602:LYS:HB3	1:C:604:TYR:HE1	1.71	0.55
1:A:569:SER:HB2	1:A:576:ARG:HH21	1.72	0.55
1:B:219:TRP:C	1:B:221:GLU:H	2.10	0.55
1:C:354:GLU:OE2	1:C:354:GLU:HA	2.06	0.55
1:B:561:LEU:CD1	1:B:561:LEU:N	2.70	0.54
1:A:70:VAL:HG21	1:A:124:SER:HB2	1.88	0.54
1:A:241:SER:O	1:A:242:ILE:HB	2.06	0.54
1:B:561:LEU:N	1:B:561:LEU:HD12	2.21	0.54
1:B:266:LEU:O	1:B:267:LYS:HB2	2.07	0.54
1:A:262:GLU:HA	1:A:269:TYR:CE1	2.42	0.54
1:B:292:LEU:CD1	1:B:302:HIS:HB2	2.37	0.54
1:A:152:PHE:CZ	1:A:156:LEU:HD11	2.42	0.54
1:B:422:GLU:O	1:B:424:ARG:HG2	2.07	0.54
1:B:426:HIS:CD2	1:B:428:LEU:HB3	2.42	0.54
1:B:594:ALA:HB2	1:B:608:LEU:CD1	2.33	0.54
1:C:590:GLN:HG3	1:C:592:ASN:ND2	2.23	0.54
1:A:540:PHE:O	1:A:544:ILE:HG13	2.08	0.54
1:A:244:GLN:NE2	1:A:350:ASN:HD21	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:248:VAL:HG21	1:B:349:ASN:ND2	2.23	0.54
1:B:627:ILE:O	1:B:628:TYR:CD2	2.61	0.54
1:C:334:ILE:HG12	1:C:428:LEU:HD13	1.88	0.54
1:B:533:PRO:HG3	1:B:636:MET:HG3	1.90	0.53
1:B:251:GLU:O	1:B:252:ASP:HB3	2.06	0.53
1:B:356:ASN:O	1:B:358:LYS:N	2.41	0.53
1:A:79:ASN:HD21	1:A:107:MET:CG	2.21	0.53
1:B:155:TRP:O	1:B:159:THR:HB	2.08	0.53
1:A:378:THR:HG21	1:A:489:VAL:HG23	1.89	0.53
1:B:217:ILE:HG22	1:B:217:ILE:O	2.08	0.53
1:B:292:LEU:HD11	1:B:302:HIS:HB2	1.90	0.53
1:A:86:SER:OG	1:A:87:GLN:N	2.40	0.53
1:A:235:ALA:O	1:A:240:SER:HB3	2.08	0.53
1:A:324:PRO:HB2	1:A:489:VAL:HG12	1.91	0.53
1:B:295:GLY:HA3	1:B:571:GLU:OE1	2.09	0.53
1:C:664:LYS:HA	1:C:667:MET:HG3	1.91	0.53
1:A:78:ARG:HH11	1:A:110:MET:HB3	1.72	0.53
1:A:561:LEU:HD23	1:A:563:TYR:OH	2.08	0.53
1:C:389:LEU:O	1:C:392:TYR:HB2	2.09	0.53
1:A:140:TYR:O	1:A:144:ASP:HB2	2.09	0.52
1:A:308:SER:O	1:A:309:ASP:HB2	2.10	0.52
1:B:530:MET:HB3	1:B:540:PHE:CE1	2.44	0.52
1:B:613:ARG:HG3	1:B:614:GLU:N	2.25	0.52
1:C:307:ILE:HD13	1:C:469:VAL:HG23	1.91	0.52
1:B:125:LEU:C	1:B:127:GLU:H	2.11	0.52
1:B:255:VAL:HA	1:B:258:VAL:CG2	2.40	0.52
1:C:478:TYR:CE1	1:C:486:ASN:HB2	2.44	0.52
1:A:635:ASN:HB3	4:A:753:NAP:N6A	2.24	0.52
1:A:272:GLN:NE2	1:A:283:LEU:H	2.07	0.52
1:B:403:HIS:C	1:B:405:MET:H	2.13	0.52
1:B:490:ALA:N	3:B:752:FAD:O2P	2.42	0.52
1:C:245:TYR:CD2	1:C:446:GLU:HG3	2.45	0.52
1:A:294:GLN:O	1:A:294:GLN:HG2	2.09	0.52
1:C:440:PRO:HG2	1:C:443:HIS:CB	2.40	0.52
1:A:356:ASN:O	1:A:358:LYS:N	2.43	0.52
1:B:161:VAL:O	1:B:161:VAL:HG13	2.10	0.52
1:B:217:ILE:O	1:B:221:GLU:HB2	2.10	0.52
1:C:648:VAL:HG11	1:C:662:TYR:HB3	1.91	0.52
1:A:105:TYR:HB3	1:A:233:VAL:HG11	1.90	0.52
1:A:133:VAL:HG12	1:A:167:LYS:O	2.09	0.52
1:C:371:LEU:HD23	1:C:375:LEU:CD1	2.36	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:84:TYR:CB	1:A:92:GLU:HA	2.40	0.51
1:A:452:GLN:HE21	1:A:452:GLN:CA	2.12	0.51
1:A:466:PRO:HG2	1:A:467:ASN:OD1	2.10	0.51
1:A:214:GLU:O	1:A:215:ASP:C	2.47	0.51
1:A:254:ASP:HB2	1:A:257:LYS:HD2	1.91	0.51
1:A:337:ILE:HB	1:A:438:ARG:HH12	1.76	0.51
1:A:337:ILE:HD11	1:A:431:LEU:HD13	1.90	0.51
1:A:371:LEU:CD2	1:A:375:LEU:HD12	2.40	0.51
1:A:656:HIS:O	1:A:659:ALA:N	2.43	0.51
1:B:411:GLU:CG	1:B:412:GLY:H	2.21	0.51
1:B:478:TYR:CE2	1:B:486:ASN:HB2	2.45	0.51
1:C:606:GLN:HG3	1:C:639:ASP:HB3	1.92	0.51
1:A:525:THR:O	1:A:558:GLY:HA3	2.10	0.51
1:B:416:TYR:C	1:B:418:SER:N	2.64	0.51
1:C:417:LEU:O	1:C:421:VAL:HB	2.10	0.51
1:A:245:TYR:HD2	1:A:446:GLU:HG3	1.74	0.51
1:A:464:VAL:HG12	1:A:465:HIS:N	2.17	0.51
1:B:351:LEU:O	1:B:352:ASP:HB2	2.10	0.51
1:B:527:PRO:HB2	1:B:625:ALA:CB	2.40	0.51
3:B:752:FAD:O1P	3:B:752:FAD:H3'	2.11	0.51
1:C:630:CYS:HA	1:C:675:ASP:O	2.10	0.51
1:A:96:ASN:O	1:A:98:LEU:N	2.43	0.51
1:A:300:LEU:CD2	1:A:574:LEU:HD21	2.29	0.51
1:C:334:ILE:HD12	1:C:377:ILE:HD12	1.91	0.51
1:C:574:LEU:O	1:C:575:TYR:C	2.49	0.51
1:B:250:HIS:CE1	1:B:347:SER:HB2	2.46	0.51
1:C:389:LEU:HD22	1:C:439:PRO:HG3	1.93	0.51
1:B:474:VAL:O	1:B:491:THR:HG21	2.11	0.51
1:B:480:ALA:C	1:B:482:SER:H	2.15	0.51
1:C:314:TYR:OH	1:C:465:HIS:O	2.24	0.51
1:A:464:VAL:O	1:A:466:PRO:HD3	2.11	0.51
1:C:318:ASP:OD1	1:C:519:ARG:NH2	2.44	0.51
1:C:515:LYS:HD3	1:C:519:ARG:HH21	1.75	0.51
1:C:521:PRO:HD3	1:C:628:TYR:OH	2.11	0.51
1:A:84:TYR:CE2	1:A:113:ASP:HB2	2.46	0.51
1:A:541:MET:HG3	1:A:575:TYR:CE2	2.46	0.51
1:C:243:ARG:O	1:C:245:TYR:N	2.43	0.51
1:C:506:ARG:HG3	1:C:506:ARG:HH11	1.76	0.51
1:C:561:LEU:N	1:C:561:LEU:CD1	2.73	0.51
1:A:394:SER:N	1:A:436:SER:O	2.44	0.50
1:B:308:SER:O	1:B:309:ASP:HB2	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:82:VAL:HG12	1:A:83:PHE:N	2.26	0.50
1:B:269:TYR:CE2	1:B:283:LEU:HD11	2.46	0.50
1:B:331:VAL:HG13	1:B:332:ASN:N	2.26	0.50
1:B:606:GLN:HE22	4:B:753:NAP:C2A	2.23	0.50
1:A:544:ILE:O	1:A:544:ILE:HG22	2.11	0.50
1:B:129:ASP:O	1:B:130:LYS:HB2	2.11	0.50
1:B:629:VAL:HG12	1:B:630:CYS:N	2.25	0.50
1:C:301:MET:HG2	1:C:473:ALA:O	2.10	0.50
1:C:493:TRP:CH2	1:C:509:VAL:HG13	2.46	0.50
1:A:120:ALA:HA	1:A:155:TRP:CZ2	2.46	0.50
1:A:132:LEU:HD12	1:A:133:VAL:H	1.77	0.50
1:A:488:GLY:O	1:A:492:SER:HB2	2.12	0.50
1:B:224:TRP:HB2	1:B:225:PRO:HD3	1.94	0.50
1:B:491:THR:HG23	3:B:752:FAD:O4'	2.11	0.50
1:C:419:TRP:O	1:C:425:ARG:HD2	2.12	0.50
1:A:258:VAL:HG21	1:A:345:ILE:HD13	1.92	0.50
1:B:278:ALA:HB2	1:B:512:PHE:CE2	2.47	0.50
1:B:292:LEU:HG	1:B:302:HIS:HB2	1.94	0.50
1:B:321:ALA:HB2	1:B:455:TYR:CD1	2.47	0.50
1:B:418:SER:O	1:B:422:GLU:HB3	2.11	0.50
1:A:94:PHE:O	1:A:95:ALA:C	2.50	0.50
1:A:150:GLN:O	1:A:153:TYR:HB3	2.12	0.50
1:A:538:ALA:HB3	1:A:539:PRO:CD	2.42	0.50
1:B:285:ALA:O	1:B:287:THR:HG23	2.12	0.50
1:B:452:GLN:HA	1:B:452:GLN:NE2	2.23	0.50
1:A:245:TYR:CD2	1:A:446:GLU:HG3	2.46	0.50
1:A:266:LEU:O	1:A:267:LYS:CB	2.59	0.50
1:B:586:GLY:C	1:B:588:LEU:H	2.13	0.50
1:A:153:TYR:CE2	1:A:157:GLN:NE2	2.80	0.50
1:A:257:LYS:HA	1:A:266:LEU:HD21	1.93	0.50
3:C:752:FAD:O1P	3:C:752:FAD:H3'	2.11	0.50
1:A:322:VAL:HG12	1:A:511:MET:HB3	1.93	0.50
1:B:442:ASP:C	1:B:444:LEU:H	2.14	0.50
1:B:644:PHE:O	1:B:648:VAL:HG23	2.12	0.50
1:C:596:SER:O	1:C:597:ARG:CG	2.56	0.50
1:A:78:ARG:HH11	1:A:78:ARG:HG3	1.76	0.49
1:A:80:ILE:HG23	1:A:109:GLY:HA3	1.93	0.49
1:A:80:ILE:HG23	1:A:109:GLY:CA	2.41	0.49
1:A:518:PHE:CE2	1:A:675:ASP:HB2	2.47	0.49
1:A:286:VAL:HG21	1:A:497:LYS:HB3	1.94	0.49
1:B:259:TYR:CE2	1:B:362:PRO:HB3	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:452:GLN:HE21	1:B:452:GLN:CA	2.17	0.49
1:A:67:SER:HB2	1:B:356:ASN:HD21	1.76	0.49
1:B:104:ARG:HB2	1:B:104:ARG:NH1	2.27	0.49
1:A:69:PHE:HZ	1:A:122:LEU:HD23	1.77	0.49
1:A:455:TYR:HE1	1:A:514:ARG:CD	2.25	0.49
1:A:642:ASN:HB2	1:B:656:HIS:CD2	2.48	0.49
1:C:409:SER:HB3	1:C:413:LYS:HD2	1.94	0.49
1:A:617:TRP:CD1	1:A:651:PHE:HB3	2.47	0.49
1:C:463:LYS:HG3	1:C:546:GLU:HG3	1.95	0.49
1:A:637:ALA:HB2	1:A:676:VAL:HG11	1.93	0.49
1:B:262:GLU:HG2	1:B:267:LYS:H	1.78	0.49
1:A:101:ASP:O	1:A:103:HIS:N	2.45	0.49
1:A:271:ASN:OD1	1:A:271:ASN:O	2.29	0.49
1:B:606:GLN:H	1:B:606:GLN:NE2	2.09	0.49
1:C:409:SER:CB	1:C:413:LYS:HD2	2.43	0.49
1:C:659:ALA:O	1:C:663:VAL:HG23	2.13	0.49
1:A:272:GLN:NE2	1:A:282:PHE:HA	2.27	0.49
1:C:593:VAL:HG12	1:C:594:ALA:N	2.19	0.49
1:A:411:GLU:HA	1:A:414:GLU:HB2	1.94	0.49
1:B:549:TRP:CE2	1:B:553:GLN:HG3	2.48	0.49
1:C:241:SER:O	1:C:242:ILE:CB	2.61	0.49
1:C:301:MET:HE2	1:C:303:LEU:HD11	1.94	0.49
1:C:334:ILE:CG1	1:C:428:LEU:HD13	2.42	0.49
1:C:372:THR:HG22	1:C:373:TYR:CD2	2.47	0.49
1:C:581:ARG:O	1:C:585:ASP:HB2	2.13	0.49
1:A:427:ILE:HG23	1:A:428:LEU:N	2.28	0.48
1:A:474:VAL:HG12	1:A:535:THR:HG21	1.95	0.48
1:A:612:ASP:O	1:A:613:ARG:C	2.51	0.48
1:B:404:LYS:O	1:B:412:GLY:HA3	2.12	0.48
1:C:665:LYS:O	1:C:669:LYS:HB2	2.12	0.48
1:A:341:ASP:O	1:A:344:VAL:HG23	2.12	0.48
1:A:539:PRO:HG3	1:A:630:CYS:SG	2.53	0.48
1:C:261:GLY:HA2	1:C:374:TYR:CZ	2.47	0.48
1:B:665:LYS:O	1:B:669:LYS:HG2	2.14	0.48
1:C:424:ARG:HG3	1:C:478:TYR:HE2	1.79	0.48
1:B:361:PHE:HB2	1:B:362:PRO:HD2	1.95	0.48
1:C:318:ASP:OD1	1:C:515:LYS:HA	2.14	0.48
1:C:402:LEU:HD21	1:C:434:TYR:CE2	2.48	0.48
1:C:648:VAL:HG13	1:C:662:TYR:CD1	2.47	0.48
1:B:260:THR:O	1:B:369:THR:HG23	2.14	0.48
1:B:331:VAL:HG23	1:B:371:LEU:HB3	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:599:GLN:NE2	1:B:603:VAL:HG23	2.29	0.48
1:B:282:PHE:HE1	1:B:307:ILE:HA	1.78	0.48
1:B:454:ARG:HG2	3:B:752:FAD:O1P	2.14	0.48
1:B:537:ILE:HB	1:B:564:TYR:CD1	2.48	0.48
1:C:265:ARG:HG3	1:C:265:ARG:NH1	2.27	0.48
1:C:269:TYR:CD2	1:C:283:LEU:HD21	2.48	0.48
1:C:391:GLN:HE21	1:C:391:GLN:C	2.17	0.48
1:C:493:TRP:HH2	1:C:509:VAL:HG13	1.79	0.48
1:C:577:GLU:O	1:C:578:GLU:C	2.51	0.48
1:A:169:ALA:HB2	1:A:200:ILE:HG22	1.95	0.48
1:A:656:HIS:O	1:A:657:THR:C	2.50	0.48
1:C:253:MET:HG2	1:C:258:VAL:HG22	1.96	0.48
1:C:409:SER:HA	1:C:413:LYS:HB2	1.95	0.48
1:A:187:TYR:CE1	1:A:191:ARG:HD3	2.48	0.48
1:C:568:ARG:NH1	1:C:598:GLU:HA	2.29	0.48
1:A:307:ILE:HG13	1:A:467:ASN:HA	1.95	0.48
1:A:435:PRO:C	1:A:437:LEU:H	2.17	0.48
1:B:255:VAL:HA	1:B:258:VAL:HG21	1.96	0.48
1:A:253:MET:HA	1:A:253:MET:CE	2.44	0.47
1:A:262:GLU:HG2	1:A:267:LYS:H	1.78	0.47
1:C:626:HIS:HB3	1:C:628:TYR:CE1	2.48	0.47
1:A:358:LYS:HB3	1:A:359:HIS:CE1	2.49	0.47
1:C:440:PRO:HG2	1:C:443:HIS:HB2	1.95	0.47
1:A:569:SER:HA	1:A:573:TYR:HB2	1.96	0.47
1:C:370:ALA:HA	1:C:374:TYR:CD2	2.49	0.47
1:A:543:PHE:C	1:A:545:GLN:H	2.17	0.47
1:B:96:ASN:C	1:B:98:LEU:H	2.18	0.47
1:A:76:THR:OG1	1:A:78:ARG:HG2	2.15	0.47
1:A:227:VAL:HG12	1:A:227:VAL:O	2.14	0.47
1:A:244:GLN:HE21	1:A:350:ASN:ND2	2.13	0.47
1:B:352:ASP:C	1:B:354:GLU:H	2.18	0.47
1:C:456:TYR:HB3	1:C:471:ILE:HG23	1.96	0.47
1:A:577:GLU:CD	1:A:577:GLU:H	2.17	0.47
1:A:627:ILE:N	1:A:671:ARG:O	2.39	0.47
1:B:276:PHE:N	1:B:276:PHE:CD1	2.82	0.47
1:B:352:ASP:O	1:B:354:GLU:N	2.48	0.47
1:B:406:ALA:O	1:B:407:SER:O	2.33	0.47
1:B:533:PRO:O	1:B:534:GLY:C	2.53	0.47
1:C:253:MET:HE3	1:C:254:ASP:H	1.76	0.47
1:A:455:TYR:CE1	1:A:514:ARG:NH1	2.83	0.47
1:B:416:TYR:O	1:B:418:SER:N	2.47	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:442:ASP:C	1:B:444:LEU:N	2.66	0.47
1:B:518:PHE:CE2	1:B:675:ASP:HB2	2.49	0.47
1:C:294:GLN:NE2	1:C:570:ASP:HB2	2.29	0.47
1:C:327:ASP:OD1	1:C:329:ALA:HB3	2.14	0.47
1:C:599:GLN:CG	1:C:601:HIS:CE1	2.98	0.47
1:A:260:THR:HA	1:A:369:THR:HG21	1.97	0.47
1:B:351:LEU:N	1:B:351:LEU:HD23	2.30	0.47
1:C:310:SER:C	1:C:312:ILE:H	2.18	0.47
1:A:332:ASN:HD22	1:A:332:ASN:C	2.13	0.47
1:C:494:LEU:C	1:C:494:LEU:HD23	2.35	0.47
1:A:84:TYR:HB3	1:A:95:ALA:HB2	1.97	0.47
1:A:243:ARG:NH1	1:A:442:ASP:OD2	2.41	0.47
1:A:390:ALA:HB1	1:A:403:HIS:CE1	2.50	0.47
1:A:595:PHE:HB3	1:A:598:GLU:HG2	1.97	0.47
1:B:222:GLN:CA	1:B:225:PRO:HD2	2.46	0.47
1:B:563:TYR:CD1	1:B:592:ASN:HB2	2.50	0.47
1:B:533:PRO:HD2	1:B:636:MET:CE	2.45	0.46
1:B:96:ASN:HB3	1:B:100:LYS:HE3	1.97	0.46
1:C:235:ALA:HB3	1:C:391:GLN:HG2	1.97	0.46
1:C:253:MET:HE2	1:C:254:ASP:N	2.28	0.46
1:C:307:ILE:HG13	1:C:307:ILE:O	2.15	0.46
1:A:272:GLN:HE22	1:A:282:PHE:CA	2.28	0.46
1:A:348:LEU:CD1	1:A:360:PRO:HG3	2.43	0.46
1:A:549:TRP:HE3	1:A:550:LEU:HD23	1.80	0.46
1:B:255:VAL:HG12	1:B:255:VAL:O	2.15	0.46
1:B:594:ALA:CB	1:B:608:LEU:HD11	2.32	0.46
1:C:342:LEU:HD12	1:C:342:LEU:N	2.28	0.46
1:A:101:ASP:C	1:A:103:HIS:N	2.69	0.46
1:A:116:GLU:O	1:A:117:TYR:C	2.54	0.46
1:A:119:LEU:C	1:A:121:ASP:H	2.19	0.46
1:A:458:ILE:HG22	1:A:460:SER:H	1.80	0.46
1:A:557:VAL:HG12	1:A:558:GLY:O	2.16	0.46
1:B:668:THR:O	1:B:669:LYS:HD3	2.16	0.46
1:C:568:ARG:HG2	1:C:568:ARG:HH11	1.80	0.46
1:C:648:VAL:HG21	1:C:663:VAL:HG22	1.98	0.46
1:A:155:TRP:HZ2	1:A:161:VAL:HG11	1.81	0.46
1:A:187:TYR:C	1:A:189:ASP:N	2.69	0.46
1:A:211:ASN:ND2	1:A:214:GLU:HG2	2.31	0.46
1:A:645:TYR:CE2	1:A:660:VAL:HA	2.50	0.46
1:B:288:ALA:O	1:B:303:LEU:HA	2.16	0.46
1:C:321:ALA:HB2	1:C:455:TYR:CD1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:513:VAL:HG12	1:C:514:ARG:N	2.30	0.46
1:A:475:ALA:HA	1:A:491:THR:HB	1.97	0.46
1:C:390:ALA:C	1:C:392:TYR:H	2.19	0.46
1:C:418:SER:O	1:C:422:GLU:HB2	2.15	0.46
1:A:145:PRO:HG2	1:A:153:TYR:CD1	2.51	0.46
1:A:157:GLN:HG2	1:A:187:TYR:OH	2.16	0.46
1:A:308:SER:O	1:A:309:ASP:CB	2.64	0.45
1:C:310:SER:HB2	1:C:312:ILE:HG13	1.99	0.45
1:C:530:MET:O	1:C:563:TYR:N	2.46	0.45
1:A:170:VAL:HG12	1:A:171:PHE:N	2.31	0.45
1:A:262:GLU:HA	1:A:269:TYR:CD1	2.51	0.45
1:A:455:TYR:N	1:A:455:TYR:CD2	2.84	0.45
1:B:422:GLU:O	1:B:424:ARG:N	2.49	0.45
1:C:242:ILE:O	1:C:243:ARG:HG2	2.15	0.45
1:B:254:ASP:HB3	1:B:257:LYS:HD3	1.98	0.45
1:B:300:LEU:HD12	1:B:300:LEU:N	2.31	0.45
1:B:302:HIS:CE1	1:B:304:GLU:HG2	2.50	0.45
1:B:567:ARG:HD2	1:B:597:ARG:CD	2.32	0.45
1:A:244:GLN:NE2	1:A:350:ASN:ND2	2.65	0.45
1:A:337:ILE:HD12	1:A:438:ARG:HH12	1.82	0.45
1:A:567:ARG:HG3	1:A:572:ASP:OD2	2.16	0.45
1:A:358:LYS:HB3	1:A:359:HIS:ND1	2.32	0.45
1:B:244:GLN:O	1:B:244:GLN:HG3	2.17	0.45
1:B:573:TYR:HE1	1:B:595:PHE:HZ	1.64	0.45
1:B:627:ILE:HG21	1:B:644:PHE:CZ	2.51	0.45
1:C:245:TYR:HD2	1:C:446:GLU:HG3	1.81	0.45
1:C:266:LEU:H	1:C:266:LEU:CD1	2.25	0.45
1:C:283:LEU:HD23	1:C:508:LEU:HD13	1.98	0.45
1:A:331:VAL:O	1:A:334:ILE:HB	2.17	0.45
1:C:299:HIS:CE1	1:C:495:ARG:HH21	2.34	0.45
1:C:405:MET:HG2	1:C:416:TYR:HB2	1.99	0.45
1:A:446:GLU:O	1:A:446:GLU:HG2	2.15	0.45
1:A:509:VAL:O	1:A:511:MET:HG3	2.16	0.45
1:A:455:TYR:N	1:A:455:TYR:HD2	2.15	0.45
1:B:220:ARG:HG2	1:B:220:ARG:O	2.16	0.45
1:B:393:ALA:HA	1:B:436:SER:O	2.16	0.45
1:C:590:GLN:NE2	1:C:592:ASN:HD21	2.13	0.45
1:A:107:MET:HE1	1:A:233:VAL:HG21	1.96	0.45
1:A:390:ALA:HB1	1:A:403:HIS:ND1	2.32	0.45
1:B:567:ARG:HE	1:B:597:ARG:NH1	2.15	0.45
1:C:554:GLY:O	1:C:555:LYS:O	2.35	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:GLU:O	1:B:97:ARG:HG3	2.18	0.44
1:B:459:ALA:O	1:B:460:SER:HB3	2.15	0.44
1:C:403:HIS:O	1:C:407:SER:HB3	2.17	0.44
1:B:156:LEU:HD23	1:B:159:THR:CG2	2.47	0.44
1:B:632:ASP:O	1:B:636:MET:HB3	2.17	0.44
1:C:316:SER:OG	1:C:461:SER:HA	2.16	0.44
1:C:358:LYS:HB3	1:C:359:HIS:ND1	2.32	0.44
1:A:200:ILE:HD12	1:A:200:ILE:HA	1.73	0.44
1:A:385:VAL:HG13	1:A:447:LEU:HB3	1.99	0.44
1:C:301:MET:HE3	1:C:495:ARG:HA	1.99	0.44
1:A:272:GLN:NE2	1:A:283:LEU:N	2.60	0.44
1:C:261:GLY:HA2	1:C:374:TYR:OH	2.16	0.44
1:A:79:ASN:HD21	1:A:107:MET:HG2	1.82	0.44
1:A:175:ASN:OD1	1:A:209:ASP:HB2	2.17	0.44
1:A:643:THR:O	1:A:647:ILE:HG13	2.18	0.44
1:B:81:ILE:HG23	1:B:81:ILE:O	2.18	0.44
1:B:119:LEU:N	1:B:119:LEU:HD22	2.33	0.44
1:B:159:THR:O	1:B:159:THR:HG23	2.18	0.44
1:B:403:HIS:O	1:B:405:MET:N	2.51	0.44
1:C:259:TYR:HE2	1:C:266:LEU:CA	2.26	0.44
1:C:262:GLU:HA	1:C:269:TYR:CE1	2.51	0.44
1:A:119:LEU:C	1:A:121:ASP:N	2.70	0.44
1:A:265:ARG:HB2	1:A:268:SER:HB3	1.97	0.44
1:A:282:PHE:CD2	1:A:310:SER:HB3	2.53	0.44
1:A:664:LYS:O	1:A:667:MET:HB2	2.17	0.44
1:B:494:LEU:O	1:B:495:ARG:C	2.55	0.44
1:C:627:ILE:HD13	1:C:644:PHE:CE1	2.52	0.44
1:A:90:THR:O	1:A:93:GLU:HB3	2.18	0.44
1:A:208:ASP:O	1:A:209:ASP:C	2.56	0.44
1:A:313:ARG:HG3	1:A:313:ARG:HH11	1.83	0.44
1:A:444:LEU:C	1:A:446:GLU:H	2.21	0.44
1:A:610:LYS:O	1:A:613:ARG:HG2	2.17	0.44
1:B:591:LEU:O	1:B:591:LEU:HG	2.18	0.44
1:A:199:ARG:HB2	1:A:199:ARG:NH1	2.32	0.44
1:B:302:HIS:ND1	1:B:302:HIS:C	2.70	0.44
1:B:331:VAL:CG1	1:B:332:ASN:N	2.81	0.44
1:B:402:LEU:HG	1:B:434:TYR:CE2	2.53	0.44
1:B:573:TYR:OH	1:B:593:VAL:HG21	2.18	0.44
1:C:411:GLU:CG	1:C:412:GLY:N	2.59	0.44
1:C:633:ALA:O	1:C:635:ASN:N	2.50	0.44
1:A:337:ILE:HD12	1:A:431:LEU:HB3	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:752:FAD:O1P	3:A:752:FAD:H3'	2.17	0.43
1:B:299:HIS:CD2	1:B:495:ARG:HE	2.36	0.43
1:B:327:ASP:HB3	1:B:330:LEU:CB	2.44	0.43
1:B:478:TYR:CE2	1:B:480:ALA:HB2	2.51	0.43
1:B:480:ALA:C	1:B:482:SER:N	2.72	0.43
1:B:488:GLY:O	1:B:492:SER:HB3	2.18	0.43
1:C:649:ALA:HB1	1:C:654:MET:O	2.18	0.43
1:A:72:LYS:O	1:A:72:LYS:HG2	2.19	0.43
1:A:559:GLU:OE2	1:A:619:LEU:HD21	2.18	0.43
1:A:611:ARG:HG2	1:A:612:ASP:OD2	2.17	0.43
1:B:73:MET:O	1:B:73:MET:HG2	2.17	0.43
1:B:222:GLN:C	1:B:225:PRO:HD2	2.38	0.43
1:B:617:TRP:O	1:B:617:TRP:CG	2.72	0.43
1:C:314:TYR:HB3	1:C:513:VAL:HG21	1.99	0.43
1:C:413:LYS:O	1:C:417:LEU:HB2	2.17	0.43
1:C:439:PRO:HB2	1:C:440:PRO:HD2	2.00	0.43
1:C:632:ASP:HA	1:C:677:TRP:O	2.17	0.43
1:A:454:ARG:HG2	1:A:490:ALA:HB2	1.99	0.43
1:B:125:LEU:N	1:B:126:PRO:CD	2.80	0.43
1:B:263:MET:N	1:B:269:TYR:HE1	2.16	0.43
1:B:506:ARG:N	1:B:506:ARG:HD3	2.33	0.43
1:B:664:LYS:HE3	1:B:664:LYS:HB2	1.81	0.43
1:A:370:ALA:O	1:A:375:LEU:N	2.47	0.43
1:A:453:ALA:C	1:A:454:ARG:HD2	2.39	0.43
1:A:464:VAL:O	1:A:466:PRO:N	2.51	0.43
1:A:590:GLN:NE2	1:A:592:ASN:HD21	2.17	0.43
1:A:664:LYS:HE3	1:A:667:MET:HE3	2.00	0.43
1:A:549:TRP:CE3	1:A:550:LEU:HD23	2.53	0.43
1:B:283:LEU:N	1:B:283:LEU:CD1	2.82	0.43
1:C:260:THR:HG22	1:C:260:THR:O	2.18	0.43
1:C:262:GLU:O	1:C:374:TYR:HE1	2.02	0.43
1:C:390:ALA:HB1	1:C:403:HIS:CE1	2.53	0.43
1:A:261:GLY:HA2	1:A:373:TYR:CD2	2.53	0.43
1:B:396:PRO:O	1:B:400:GLU:HB2	2.18	0.43
1:C:425:ARG:HB3	1:C:430:ILE:HD11	1.99	0.43
1:C:527:PRO:HB2	1:C:625:ALA:HB2	2.00	0.43
1:A:93:GLU:OE1	1:A:93:GLU:O	2.37	0.43
1:A:125:LEU:HD12	1:A:125:LEU:HA	1.77	0.43
1:A:404:LYS:O	1:A:407:SER:N	2.47	0.43
1:B:79:ASN:ND2	1:B:80:ILE:H	2.16	0.43
1:B:247:LEU:HD12	1:B:248:VAL:H	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:330:LEU:HD23	1:B:334:ILE:HD11	2.00	0.43
1:C:484:ARG:H	1:C:484:ARG:CD	2.22	0.43
1:A:575:TYR:HA	1:A:578:GLU:OE1	2.18	0.43
1:B:425:ARG:HG3	1:B:425:ARG:HH11	1.83	0.43
1:C:310:SER:O	1:C:311:LYS:HB2	2.19	0.43
1:C:538:ALA:N	1:C:539:PRO:HD2	2.34	0.43
1:B:160:ASP:O	1:B:162:ASP:N	2.52	0.43
1:B:346:MET:SD	1:B:346:MET:C	2.97	0.43
1:B:381:PRO:HG2	1:B:430:ILE:HD12	2.01	0.43
1:B:551:ARG:HD3	1:B:557:VAL:HB	2.00	0.43
1:C:638:LYS:O	1:C:641:GLN:N	2.52	0.43
1:A:271:ASN:O	1:A:271:ASN:CG	2.57	0.43
1:A:393:ALA:HA	1:A:437:LEU:HA	2.01	0.43
1:A:454:ARG:HH22	1:A:489:VAL:CB	2.19	0.43
1:A:569:SER:HB3	1:A:595:PHE:CZ	2.54	0.43
1:B:292:LEU:CG	1:B:302:HIS:HB2	2.48	0.43
1:B:537:ILE:O	1:B:537:ILE:HG13	2.19	0.43
1:C:566:CYS:HB2	1:C:572:ASP:OD1	2.19	0.43
1:C:649:ALA:HB2	1:C:659:ALA:CB	2.46	0.43
1:B:440:PRO:O	1:B:442:ASP:N	2.51	0.42
1:C:610:LYS:O	1:C:613:ARG:HD3	2.19	0.42
1:A:383:THR:HB	1:A:406:ALA:HA	2.01	0.42
1:A:511:MET:SD	1:A:511:MET:C	2.98	0.42
1:A:67:SER:HB2	1:B:356:ASN:ND2	2.35	0.42
1:A:438:ARG:NE	1:C:311:LYS:HZ3	2.16	0.42
1:B:156:LEU:HA	1:B:159:THR:HG22	2.01	0.42
1:B:283:LEU:N	1:B:283:LEU:HD12	2.32	0.42
1:B:434:TYR:HB3	1:B:437:LEU:HB2	2.00	0.42
1:B:588:LEU:HD22	1:B:590:GLN:O	2.20	0.42
1:C:314:TYR:O	1:C:314:TYR:CG	2.72	0.42
1:C:519:ARG:O	1:C:628:TYR:CE2	2.72	0.42
1:C:667:MET:CA	1:C:672:TYR:HB3	2.42	0.42
1:B:333:GLN:O	1:B:337:ILE:HG22	2.20	0.42
1:B:672:TYR:C	1:B:672:TYR:CD2	2.92	0.42
1:C:368:ARG:O	1:C:372:THR:HB	2.19	0.42
1:C:452:GLN:CD	1:C:452:GLN:H	2.22	0.42
1:C:627:ILE:O	1:C:672:TYR:HA	2.20	0.42
1:B:317:GLY:HA3	1:B:518:PHE:O	2.20	0.42
1:C:608:LEU:HD22	1:C:611:ARG:CZ	2.49	0.42
1:A:476:VAL:CG2	3:A:752:FAD:H5'2	2.49	0.42
1:A:567:ARG:HD2	1:A:597:ARG:CZ	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:593:VAL:O	1:C:608:LEU:HD12	2.20	0.42
1:A:168:PHE:CE1	1:A:199:ARG:HA	2.55	0.42
1:B:422:GLU:HB3	1:B:423:ALA:H	1.75	0.42
1:B:475:ALA:HA	1:B:491:THR:HB	2.01	0.42
1:A:187:TYR:C	1:A:189:ASP:H	2.23	0.42
1:A:203:LEU:HD21	1:A:205:LEU:HD21	2.01	0.42
1:A:220:ARG:HH11	1:A:220:ARG:HB3	1.84	0.42
1:A:350:ASN:C	1:A:352:ASP:H	2.22	0.42
1:B:443:HIS:O	1:B:447:LEU:HG	2.20	0.42
1:B:488:GLY:CA	3:B:752:FAD:O1A	2.68	0.42
1:C:385:VAL:O	1:C:385:VAL:HG12	2.19	0.42
1:A:393:ALA:CA	1:A:436:SER:O	2.62	0.42
1:B:129:ASP:O	1:B:130:LYS:CB	2.67	0.42
1:B:649:ALA:HA	1:B:654:MET:HG3	2.00	0.42
1:C:298:ARG:HH21	1:C:300:LEU:HD11	1.84	0.42
1:C:599:GLN:HG3	1:C:601:HIS:CE1	2.55	0.42
1:A:320:VAL:HG13	1:A:320:VAL:O	2.20	0.42
1:A:333:GLN:HB3	1:A:428:LEU:HD21	2.01	0.42
1:A:401:HIS:O	1:A:404:LYS:N	2.53	0.42
1:A:464:VAL:O	1:A:465:HIS:C	2.58	0.42
1:C:252:ASP:OD1	1:C:253:MET:N	2.37	0.42
1:C:513:VAL:CG1	1:C:514:ARG:N	2.82	0.42
1:A:125:LEU:N	1:A:126:PRO:CD	2.83	0.41
1:A:335:GLY:O	1:A:339:GLY:N	2.52	0.41
1:B:539:PRO:HG3	1:B:630:CYS:SG	2.60	0.41
1:C:408:SER:O	1:C:409:SER:CB	2.68	0.41
1:A:155:TRP:CH2	1:A:161:VAL:HG11	2.56	0.41
1:A:254:ASP:C	1:A:256:ALA:N	2.73	0.41
1:A:392:TYR:O	1:A:437:LEU:HA	2.20	0.41
1:A:548:ALA:O	1:A:552:GLU:HG3	2.20	0.41
1:A:455:TYR:CE1	1:A:514:ARG:CD	3.00	0.41
1:A:490:ALA:HB3	3:A:752:FAD:O1P	2.20	0.41
1:A:573:TYR:C	1:A:573:TYR:CD2	2.93	0.41
1:A:645:TYR:HE2	1:A:663:VAL:HB	1.85	0.41
1:B:276:PHE:CE1	1:B:310:SER:HB2	2.55	0.41
1:A:454:ARG:HG2	1:A:490:ALA:CB	2.51	0.41
1:A:464:VAL:O	1:A:466:PRO:CD	2.68	0.41
1:A:664:LYS:HA	1:A:664:LYS:CE	2.44	0.41
1:B:217:ILE:O	1:B:217:ILE:CG2	2.68	0.41
1:B:350:ASN:HD22	1:B:351:LEU:H	1.66	0.41
1:B:626:HIS:HB3	1:B:628:TYR:CE2	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:654:MET:SD	1:B:659:ALA:HA	2.60	0.41
1:C:423:ALA:O	1:C:424:ARG:HB2	2.20	0.41
1:A:105:TYR:C	1:A:233:VAL:HG11	2.40	0.41
1:A:666:LEU:HD23	1:A:666:LEU:HA	1.94	0.41
1:B:569:SER:HA	1:B:595:PHE:CE1	2.55	0.41
1:C:551:ARG:HG2	1:C:557:VAL:CG2	2.51	0.41
1:A:115:GLU:HB2	1:A:148:ASN:HB2	2.02	0.41
1:A:531:VAL:O	1:A:629:VAL:HA	2.20	0.41
1:B:564:TYR:CG	1:B:565:GLY:N	2.88	0.41
1:C:329:ALA:O	1:C:333:GLN:HG3	2.20	0.41
1:C:645:TYR:O	1:C:659:ALA:HB1	2.19	0.41
1:A:567:ARG:HD2	1:A:597:ARG:NE	2.35	0.41
1:B:441:ILE:HG23	1:B:442:ASP:N	2.36	0.41
1:B:563:TYR:CE1	1:B:592:ASN:ND2	2.89	0.41
1:B:672:TYR:C	1:B:672:TYR:HD2	2.23	0.41
1:C:322:VAL:HG12	1:C:511:MET:HB3	2.02	0.41
1:B:94:PHE:HB3	1:B:216:PHE:CZ	2.55	0.41
1:B:350:ASN:ND2	1:B:351:LEU:N	2.64	0.41
1:B:464:VAL:HG12	1:B:465:HIS:CE1	2.55	0.41
1:B:528:VAL:HG12	1:B:530:MET:CG	2.51	0.41
1:C:322:VAL:O	1:C:453:ALA:HB1	2.21	0.41
1:A:82:VAL:HG11	1:A:95:ALA:CA	2.34	0.41
1:A:254:ASP:O	1:A:256:ALA:N	2.54	0.41
1:A:321:ALA:HB3	1:A:512:PHE:CE1	2.56	0.41
1:A:569:SER:HB3	1:A:595:PHE:HE1	1.83	0.41
1:B:80:ILE:HG23	1:B:109:GLY:HA3	2.02	0.41
1:B:104:ARG:NH1	1:B:104:ARG:CB	2.83	0.41
1:B:520:LEU:HG	1:B:543:PHE:CE2	2.55	0.41
1:B:521:PRO:O	1:B:522:PHE:CB	2.66	0.41
1:C:511:MET:O	1:C:512:PHE:HB3	2.21	0.41
1:C:564:TYR:O	1:C:593:VAL:HA	2.21	0.41
1:C:631:GLY:O	1:C:632:ASP:O	2.38	0.41
1:A:175:ASN:HA	1:A:207:ASP:OD1	2.21	0.41
1:A:233:VAL:CG1	1:A:234:GLU:N	2.83	0.41
1:B:101:ASP:HB2	1:B:224:TRP:CZ2	2.56	0.41
1:B:321:ALA:HB3	1:B:512:PHE:CE1	2.56	0.41
1:B:567:ARG:NE	1:B:597:ARG:NH1	2.69	0.41
1:B:573:TYR:CE1	1:B:595:PHE:HZ	2.39	0.41
1:C:323:TYR:HB2	1:C:510:PRO:HB2	2.04	0.41
1:C:648:VAL:CG1	1:C:662:TYR:HD1	2.34	0.41
1:A:88:THR:HG23	1:A:140:TYR:OH	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:282:PHE:CD1	1:A:283:LEU:N	2.89	0.40
1:A:341:ASP:OD2	1:A:341:ASP:C	2.60	0.40
1:A:573:TYR:C	1:A:573:TYR:HD2	2.24	0.40
1:A:606:GLN:HE21	1:A:606:GLN:HB3	1.65	0.40
1:C:514:ARG:O	1:C:515:LYS:C	2.59	0.40
1:A:96:ASN:O	1:A:100:LYS:HG3	2.21	0.40
1:A:156:LEU:CD1	1:A:188:VAL:HG22	2.51	0.40
1:A:187:TYR:O	1:A:189:ASP:N	2.54	0.40
1:A:247:LEU:HD12	1:A:248:VAL:H	1.86	0.40
1:A:330:LEU:HD12	1:A:377:ILE:HD12	2.03	0.40
1:A:441:ILE:CG2	1:A:442:ASP:N	2.82	0.40
1:A:591:LEU:HG	1:A:591:LEU:O	2.21	0.40
1:B:318:ASP:OD1	1:B:519:ARG:NH2	2.50	0.40
1:B:450:ARG:HA	1:B:450:ARG:HD2	1.84	0.40
1:A:192:LEU:HA	1:A:192:LEU:HD23	1.83	0.40
1:A:657:THR:O	1:A:658:GLN:C	2.60	0.40
1:B:245:TYR:HB3	1:B:348:LEU:HD22	2.03	0.40
1:B:300:LEU:N	1:B:300:LEU:CD1	2.84	0.40
1:B:389:LEU:O	1:B:437:LEU:HD11	2.22	0.40
1:B:411:GLU:CG	1:B:412:GLY:N	2.73	0.40
1:C:596:SER:C	1:C:597:ARG:HG3	2.40	0.40
1:A:544:ILE:HG21	1:A:588:LEU:HG	2.04	0.40
1:A:618:LYS:HE2	1:A:618:LYS:HB3	1.93	0.40
1:B:464:VAL:HG21	1:B:545:GLN:HB3	2.03	0.40
1:C:496:ALA:O	1:C:497:LYS:C	2.60	0.40
1:A:243:ARG:HE	1:A:243:ARG:HB3	1.75	0.40
1:A:253:MET:HE2	1:A:253:MET:HA	2.03	0.40
1:A:476:VAL:HG21	3:A:752:FAD:H5'2	2.03	0.40
1:A:548:ALA:HB2	1:A:587:ALA:CB	2.50	0.40
1:C:391:GLN:H	1:C:391:GLN:HG3	1.60	0.40
1:C:395:GLU:HA	1:C:396:PRO:HD3	1.93	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	599/618 (97%)	481 (80%)	85 (14%)	33 (6%)	2	12
1	B	503/618 (81%)	374 (74%)	102 (20%)	27 (5%)	2	13
1	C	431/618 (70%)	320 (74%)	84 (20%)	27 (6%)	1	9
All	All	1533/1854 (83%)	1175 (77%)	271 (18%)	87 (6%)	1	12

All (87) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	90	THR
1	A	106	GLY
1	A	240	SER
1	A	253	MET
1	A	267	LYS
1	A	357	LYS
1	A	538	ALA
1	B	161	VAL
1	B	352	ASP
1	B	353	GLU
1	B	407	SER
1	B	422	GLU
1	B	441	ILE
1	B	600	ALA
1	C	242	ILE
1	C	244	GLN
1	C	252	ASP
1	C	253	MET
1	C	353	GLU
1	C	409	SER
1	C	555	LYS
1	C	594	ALA
1	C	600	ALA
1	C	632	ASP
1	A	97	ARG
1	A	104	ARG
1	A	116	GLU
1	A	252	ASP
1	A	309	ASP
1	A	353	GLU
1	A	544	ILE

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	555	LYS
1	A	634	ARG
1	B	404	LYS
1	B	423	ALA
1	B	534	GLY
1	C	391	GLN
1	A	102	ALA
1	A	160	ASP
1	A	209	ASP
1	B	107	MET
1	B	162	ASP
1	B	233	VAL
1	B	297	GLU
1	B	333	GLN
1	B	344	VAL
1	B	392	TYR
1	B	417	LEU
1	B	588	LEU
1	C	235	ALA
1	C	241	SER
1	C	243	ARG
1	C	515	LYS
1	C	587	ALA
1	C	633	ALA
1	C	634	ARG
1	A	146	THR
1	A	169	ALA
1	A	345	ILE
1	A	392	TYR
1	A	656	HIS
1	B	89	GLY
1	B	342	LEU
1	B	383	THR
1	B	567	ARG
1	C	362	PRO
1	C	597	ARG
1	A	156	LEU
1	A	402	LEU
1	A	445	CYS
1	C	436	SER
1	C	449	PRO
1	A	241	SER

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Mol	Chain	Res	Type
1	A	242	ILE
1	C	352	ASP
1	C	623	GLY
1	A	441	ILE
1	A	465	HIS
1	C	396	PRO
1	C	593	VAL
1	B	125	LEU
1	B	248	VAL
1	B	261	GLY
1	B	532	GLY
1	C	380	PRO
1	A	464	VAL
1	A	532	GLY

### 5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	518/528 (98%)	477 (92%)	41 (8%)	12 39
1	B	441/528 (84%)	409 (93%)	32 (7%)	14 43
1	C	373/528 (71%)	344 (92%)	29 (8%)	12 39
All	All	1332/1584 (84%)	1230 (92%)	102 (8%)	13 40

All (102) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	66	GLU
1	A	81	ILE
1	A	93	GLU
1	A	98	LEU
1	A	113	ASP
1	A	117	TYR
1	A	129	ASP
1	A	146	THR

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	182	ASN
1	A	190	GLN
1	A	198	GLN
1	A	229	GLU
1	A	252	ASP
1	A	253	MET
1	A	265	ARG
1	A	280	ASN
1	A	287	THR
1	A	303	LEU
1	A	330	LEU
1	A	332	ASN
1	A	346	MET
1	A	350	ASN
1	A	366	THR
1	A	394	SER
1	A	397	SER
1	A	403	HIS
1	A	411	GLU
1	A	414	GLU
1	A	437	LEU
1	A	454	ARG
1	A	465	HIS
1	A	484	ARG
1	A	495	ARG
1	A	522	PHE
1	A	553	GLN
1	A	555	LYS
1	A	567	ARG
1	A	573	TYR
1	A	606	GLN
1	A	664	LYS
1	A	673	SER
1	B	103	HIS
1	B	156	LEU
1	B	162	ASP
1	B	257	LYS
1	B	272	GLN
1	B	276	PHE
1	B	294	GLN
1	B	298	ARG
1	B	313	ARG

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	B	346	MET
1	B	350	ASN
1	B	351	LEU
1	B	378	THR
1	B	391	GLN
1	B	403	HIS
1	B	415	LEU
1	B	452	GLN
1	B	484	ARG
1	B	506	ARG
1	B	525	THR
1	B	547	ARG
1	B	567	ARG
1	B	571	GLU
1	B	572	ASP
1	B	573	TYR
1	B	578	GLU
1	B	606	GLN
1	B	626	HIS
1	B	660	VAL
1	B	667	MET
1	B	672	TYR
1	B	673	SER
1	C	243	ARG
1	C	244	GLN
1	C	252	ASP
1	C	328	SER
1	C	330	LEU
1	C	346	MET
1	C	350	ASN
1	C	362	PRO
1	C	372	THR
1	C	391	GLN
1	C	417	LEU
1	C	422	GLU
1	C	452	GLN
1	C	472	CYS
1	C	478	TYR
1	C	484	ARG
1	C	491	THR
1	C	511	MET
1	C	535	THR

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Mol	Chain	Res	Type
1	C	541	MET
1	C	561	LEU
1	C	572	ASP
1	C	573	TYR
1	C	582	PHE
1	C	585	ASP
1	C	606	GLN
1	C	634	ARG
1	C	644	PHE
1	C	669	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (43) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	157	GLN
1	A	182	ASN
1	A	244	GLN
1	A	272	GLN
1	A	280	ASN
1	A	294	GLN
1	A	319	HIS
1	A	350	ASN
1	A	399	GLN
1	A	426	HIS
1	A	452	GLN
1	A	486	ASN
1	A	590	GLN
1	A	606	GLN
1	A	641	GLN
1	B	272	GLN
1	B	280	ASN
1	B	294	GLN
1	B	302	HIS
1	B	332	ASN
1	B	349	ASN
1	B	350	ASN
1	B	391	GLN
1	B	399	GLN
1	B	452	GLN
1	B	486	ASN
1	B	517	GLN
1	B	590	GLN

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Mol	Chain	Res	Type
1	B	606	GLN
1	B	626	HIS
1	B	656	HIS
1	B	658	GLN
1	C	280	ASN
1	C	302	HIS
1	C	350	ASN
1	C	359	HIS
1	C	391	GLN
1	C	403	HIS
1	C	486	ASN
1	C	583	HIS
1	C	590	GLN
1	C	606	GLN
1	C	626	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 monosaccharides in this entry.

### 5.6 Ligand geometry [i](#)

6 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	FAD	B	752	-	53,58,58	2.77	21 (39%)	68,89,89	2.02	15 (22%)
3	FAD	C	752	-	53,58,58	2.79	20 (37%)	68,89,89	1.94	17 (25%)
3	FAD	A	752	-	53,58,58	2.91	21 (39%)	68,89,89	1.97	13 (19%)
4	NAP	A	753	-	45,52,52	2.49	15 (33%)	56,80,80	1.45	9 (16%)
4	NAP	B	753	-	45,52,52	2.57	15 (33%)	56,80,80	1.44	7 (12%)
2	FMN	A	751	-	33,33,33	2.54	11 (33%)	48,50,50	1.58	9 (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
3	FAD	B	752	-	-	7/30/50/50	0/6/6/6
3	FAD	C	752	-	-	8/30/50/50	0/6/6/6
3	FAD	A	752	-	-	10/30/50/50	0/6/6/6
4	NAP	A	753	-	-	8/31/67/67	0/5/5/5
4	NAP	B	753	-	-	9/31/67/67	0/5/5/5
2	FMN	A	751	-	-	0/18/18/18	0/3/3/3

All (103) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	753	NAP	C4A-N3A	11.23	1.51	1.35
4	A	753	NAP	C4A-N3A	11.16	1.51	1.35
3	C	752	FAD	C4A-N3A	8.90	1.47	1.35
3	A	752	FAD	C4A-N3A	8.38	1.47	1.35
3	B	752	FAD	C2A-N1A	7.98	1.48	1.33
3	A	752	FAD	C2A-N1A	7.85	1.48	1.33
3	C	752	FAD	C2A-N1A	7.63	1.48	1.33
3	B	752	FAD	C4A-N3A	7.44	1.45	1.35
2	A	751	FMN	C10-N10	6.41	1.51	1.37
3	A	752	FAD	C9A-N10	6.36	1.52	1.41
3	A	752	FAD	C9A-C5X	6.13	1.51	1.41
3	C	752	FAD	C9A-C5X	5.93	1.51	1.41
3	B	752	FAD	C9A-N10	5.87	1.51	1.41
3	C	752	FAD	C9A-N10	5.51	1.50	1.41
2	A	751	FMN	C4A-N5	5.45	1.41	1.30
3	B	752	FAD	C9A-C5X	5.26	1.50	1.41
2	A	751	FMN	C9A-N10	5.20	1.50	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	751	FMN	C9-C9A	5.19	1.48	1.39
3	A	752	FAD	C4X-N5	5.12	1.40	1.30
3	B	752	FAD	C4X-N5	4.92	1.40	1.30
3	C	752	FAD	C4X-N5	4.79	1.40	1.30
3	C	752	FAD	C8-C7	4.69	1.52	1.40
3	A	752	FAD	C1'-C2'	4.60	1.59	1.52
3	B	752	FAD	C10-N1	4.56	1.42	1.33
4	B	753	NAP	C7N-N7N	4.47	1.41	1.33
3	B	752	FAD	C6-C5X	4.32	1.46	1.40
4	A	753	NAP	C7N-N7N	4.20	1.41	1.33
3	A	752	FAD	C6-C5X	4.11	1.46	1.40
4	B	753	NAP	C2A-N1A	4.10	1.41	1.33
4	B	753	NAP	C2N-N1N	4.07	1.39	1.35
3	C	752	FAD	C6-C5X	4.02	1.46	1.40
3	B	752	FAD	C8-C7	3.93	1.50	1.40
3	A	752	FAD	C9-C9A	3.90	1.46	1.39
4	A	753	NAP	C6N-N1N	3.90	1.44	1.35
4	B	753	NAP	C6N-N1N	3.86	1.44	1.35
4	A	753	NAP	C2A-N1A	3.84	1.41	1.33
3	A	752	FAD	C10-N1	3.80	1.41	1.33
3	B	752	FAD	C5'-C4'	3.75	1.57	1.51
3	C	752	FAD	C9-C9A	3.70	1.45	1.39
3	A	752	FAD	C8-C7	3.68	1.50	1.40
2	A	751	FMN	C9A-C5A	3.68	1.47	1.41
2	A	751	FMN	C8-C7	3.68	1.50	1.40
4	B	753	NAP	C4N-C3N	3.62	1.45	1.39
3	B	752	FAD	C9-C9A	3.56	1.45	1.39
3	B	752	FAD	C1'-C2'	3.56	1.57	1.52
3	A	752	FAD	C5'-C4'	3.55	1.56	1.51
3	A	752	FAD	O2'-C2'	3.50	1.50	1.43
3	C	752	FAD	C1'-C2'	3.45	1.57	1.52
4	B	753	NAP	O4D-C1D	3.42	1.45	1.41
3	C	752	FAD	C10-N1	3.28	1.39	1.33
3	C	752	FAD	C8A-N7A	3.27	1.40	1.34
4	A	753	NAP	C2N-N1N	3.24	1.38	1.35
3	C	752	FAD	C2A-N3A	3.22	1.37	1.32
4	A	753	NAP	P2B-O1X	3.22	1.60	1.50
4	A	753	NAP	O2D-C2D	3.21	1.50	1.43
4	B	753	NAP	P2B-O1X	3.19	1.60	1.50
4	A	753	NAP	C4N-C3N	3.18	1.44	1.39
4	B	753	NAP	O2D-C2D	3.16	1.50	1.43
4	A	753	NAP	O4D-C1D	3.10	1.45	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	752	FAD	C2A-N3A	3.10	1.37	1.32
4	A	753	NAP	P2B-O2B	3.05	1.65	1.59
3	A	752	FAD	C4'-C3'	3.02	1.59	1.53
2	A	751	FMN	C1'-C2'	3.02	1.56	1.52
3	B	752	FAD	C2A-N3A	3.01	1.36	1.32
2	A	751	FMN	C10-N1	3.00	1.39	1.33
3	A	752	FAD	PA-O5B	-2.99	1.47	1.59
3	B	752	FAD	C4-N3	2.97	1.44	1.38
3	B	752	FAD	PA-O5B	-2.94	1.47	1.59
3	B	752	FAD	C8A-N7A	2.92	1.39	1.34
4	B	753	NAP	P2B-O2B	2.90	1.64	1.59
2	A	751	FMN	C6-C5A	2.89	1.44	1.40
3	B	752	FAD	C10-N10	2.77	1.43	1.37
3	C	752	FAD	C6-C7	2.76	1.43	1.39
3	A	752	FAD	C6-C7	2.75	1.43	1.39
3	C	752	FAD	O2'-C2'	2.70	1.49	1.43
2	A	751	FMN	C8M-C8	2.70	1.56	1.51
3	A	752	FAD	C8A-N7A	2.69	1.39	1.34
3	A	752	FAD	C4-N3	2.62	1.43	1.38
3	A	752	FAD	C1'-N10	2.58	1.54	1.48
4	B	753	NAP	PA-O5B	-2.56	1.48	1.59
3	C	752	FAD	PA-O5B	-2.55	1.49	1.59
3	C	752	FAD	C4'-C3'	2.55	1.58	1.53
3	B	752	FAD	O2'-C2'	2.54	1.48	1.43
4	B	753	NAP	C2D-C1D	2.46	1.57	1.53
3	C	752	FAD	C4-N3	2.45	1.43	1.38
4	B	753	NAP	C5A-C4A	2.43	1.47	1.40
4	A	753	NAP	C5A-C4A	2.42	1.47	1.40
3	B	752	FAD	C4'-C3'	2.39	1.58	1.53
4	A	753	NAP	PA-O5B	-2.37	1.49	1.59
3	B	752	FAD	C5A-C4A	2.34	1.47	1.40
4	A	753	NAP	C8A-N7A	2.31	1.38	1.34
3	C	752	FAD	C5'-C4'	2.30	1.55	1.51
3	A	752	FAD	C10-N10	2.29	1.42	1.37
3	B	752	FAD	C6-C7	2.26	1.42	1.39
4	A	753	NAP	C2A-N3A	2.25	1.35	1.32
3	C	752	FAD	C2B-C1B	2.20	1.57	1.53
3	C	752	FAD	C5A-C4A	2.20	1.46	1.40
4	A	753	NAP	C2D-C1D	2.16	1.57	1.53
3	A	752	FAD	C2'-C3'	2.15	1.57	1.53
4	B	753	NAP	C2A-N3A	2.12	1.35	1.32
3	B	752	FAD	C2B-C1B	2.10	1.57	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	753	NAP	C8A-N7A	2.09	1.38	1.34
2	A	751	FMN	O4'-C4'	2.02	1.47	1.43

All (70) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	752	FAD	O5'-P-O1P	-6.51	83.62	109.07
3	A	752	FAD	O5'-P-O1P	-6.41	84.03	109.07
3	C	752	FAD	O5'-P-O1P	-6.13	85.12	109.07
3	B	752	FAD	O5'-C5'-C4'	6.09	125.62	109.36
4	B	753	NAP	C2D-C3D-C4D	5.51	113.35	102.64
4	A	753	NAP	C2D-C3D-C4D	5.50	113.33	102.64
3	A	752	FAD	N3A-C2A-N1A	-5.18	120.58	128.68
3	A	752	FAD	O5'-C5'-C4'	5.15	123.10	109.36
3	C	752	FAD	N3A-C2A-N1A	-5.15	120.63	128.68
3	C	752	FAD	O5'-C5'-C4'	5.11	123.00	109.36
3	B	752	FAD	N3A-C2A-N1A	-4.91	121.00	128.68
3	C	752	FAD	C2A-N1A-C6A	4.58	126.59	118.75
3	B	752	FAD	C2A-N1A-C6A	4.54	126.52	118.75
3	A	752	FAD	C2A-N1A-C6A	4.47	126.41	118.75
2	A	751	FMN	C9A-C5A-N5	4.26	127.06	122.43
3	A	752	FAD	C1B-N9A-C4A	-3.99	119.63	126.64
3	A	752	FAD	O2-C2-N3	3.61	125.66	118.65
2	A	751	FMN	O4-C4-N3	-3.51	113.39	120.12
3	C	752	FAD	C1B-N9A-C4A	-3.38	120.69	126.64
4	B	753	NAP	N3A-C2A-N1A	-3.37	123.41	128.68
3	B	752	FAD	C1B-N9A-C4A	-3.33	120.79	126.64
4	B	753	NAP	C6N-N1N-C2N	-3.30	118.97	121.97
3	C	752	FAD	O2-C2-N3	3.29	125.03	118.65
4	A	753	NAP	C6N-N1N-C2N	-3.28	118.98	121.97
4	B	753	NAP	C4A-C5A-N7A	3.28	112.81	109.40
3	C	752	FAD	O2P-P-O5'	-3.23	92.73	107.75
4	A	753	NAP	N3A-C2A-N1A	-3.23	123.63	128.68
4	A	753	NAP	C4A-C5A-N7A	3.17	112.70	109.40
3	B	752	FAD	O2-C2-N3	3.15	124.78	118.65
3	A	752	FAD	C9-C9A-N10	3.13	126.07	121.84
2	A	751	FMN	C9-C9A-N10	3.12	126.06	121.84
2	A	751	FMN	P-O5'-C5'	3.08	126.79	118.30
3	A	752	FAD	C10-N1-C2	3.03	122.96	116.90
3	A	752	FAD	C1'-N10-C9A	2.97	125.46	120.51
3	B	752	FAD	C9-C9A-N10	2.95	125.82	121.84
3	B	752	FAD	C10-N1-C2	2.91	122.72	116.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	751	FMN	C5A-C9A-N10	-2.79	115.07	117.95
3	C	752	FAD	C10-N1-C2	2.77	122.43	116.90
3	A	752	FAD	C9A-C5X-N5	2.75	125.42	122.43
3	B	752	FAD	C9A-C5X-N5	2.70	125.37	122.43
3	C	752	FAD	C5A-C6A-N6A	2.62	124.34	120.35
3	C	752	FAD	C9A-C5X-N5	2.60	125.25	122.43
3	B	752	FAD	O2P-P-O5'	-2.59	95.72	107.75
4	A	753	NAP	O4D-C1D-C2D	2.51	110.60	106.93
3	B	752	FAD	C5A-C6A-N6A	2.47	124.11	120.35
3	C	752	FAD	C9-C9A-N10	2.42	125.11	121.84
3	A	752	FAD	C5X-C9A-N10	-2.37	115.51	117.95
3	A	752	FAD	C5A-C6A-N6A	2.35	123.92	120.35
3	B	752	FAD	C5'-C4'-C3'	2.34	116.73	112.20
2	A	751	FMN	O3P-P-O5'	-2.34	100.51	106.73
3	C	752	FAD	P-O3P-PA	-2.32	124.87	132.83
4	B	753	NAP	O3D-C3D-C4D	-2.28	104.46	111.05
3	A	752	FAD	O2-C2-N1	-2.28	118.06	121.83
4	A	753	NAP	O4B-C1B-C2B	-2.27	102.66	106.59
3	B	752	FAD	C5X-C9A-N10	-2.26	115.62	117.95
3	C	752	FAD	C8M-C8-C9	-2.25	115.32	119.49
3	B	752	FAD	C3B-C2B-C1B	2.24	104.35	100.98
2	A	751	FMN	C6-C5A-N5	-2.20	114.67	118.51
3	C	752	FAD	C4'-C3'-C2'	2.20	117.94	113.36
2	A	751	FMN	C7M-C7-C6	-2.14	115.53	119.49
4	A	753	NAP	O5D-C5D-C4D	2.12	116.27	108.99
4	B	753	NAP	O5D-C5D-C4D	2.11	116.25	108.99
3	C	752	FAD	C5X-C9A-N10	-2.09	115.79	117.95
3	C	752	FAD	O2-C2-N1	-2.08	118.39	121.83
4	A	753	NAP	C3B-C2B-C1B	-2.05	99.04	102.89
2	A	751	FMN	O4'-C4'-C3'	-2.02	104.18	109.10
4	B	753	NAP	C3B-C2B-C1B	-2.02	99.09	102.89
3	C	752	FAD	C5'-C4'-C3'	2.02	116.10	112.20
3	B	752	FAD	O4B-C1B-C2B	2.01	109.86	106.93
4	A	753	NAP	O3D-C3D-C4D	-2.00	105.26	111.05

There are no chirality outliers.

All (42) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	752	FAD	C1'-C2'-C3'-O3'
3	A	752	FAD	C1'-C2'-C3'-C4'
3	A	752	FAD	O4'-C4'-C5'-O5'

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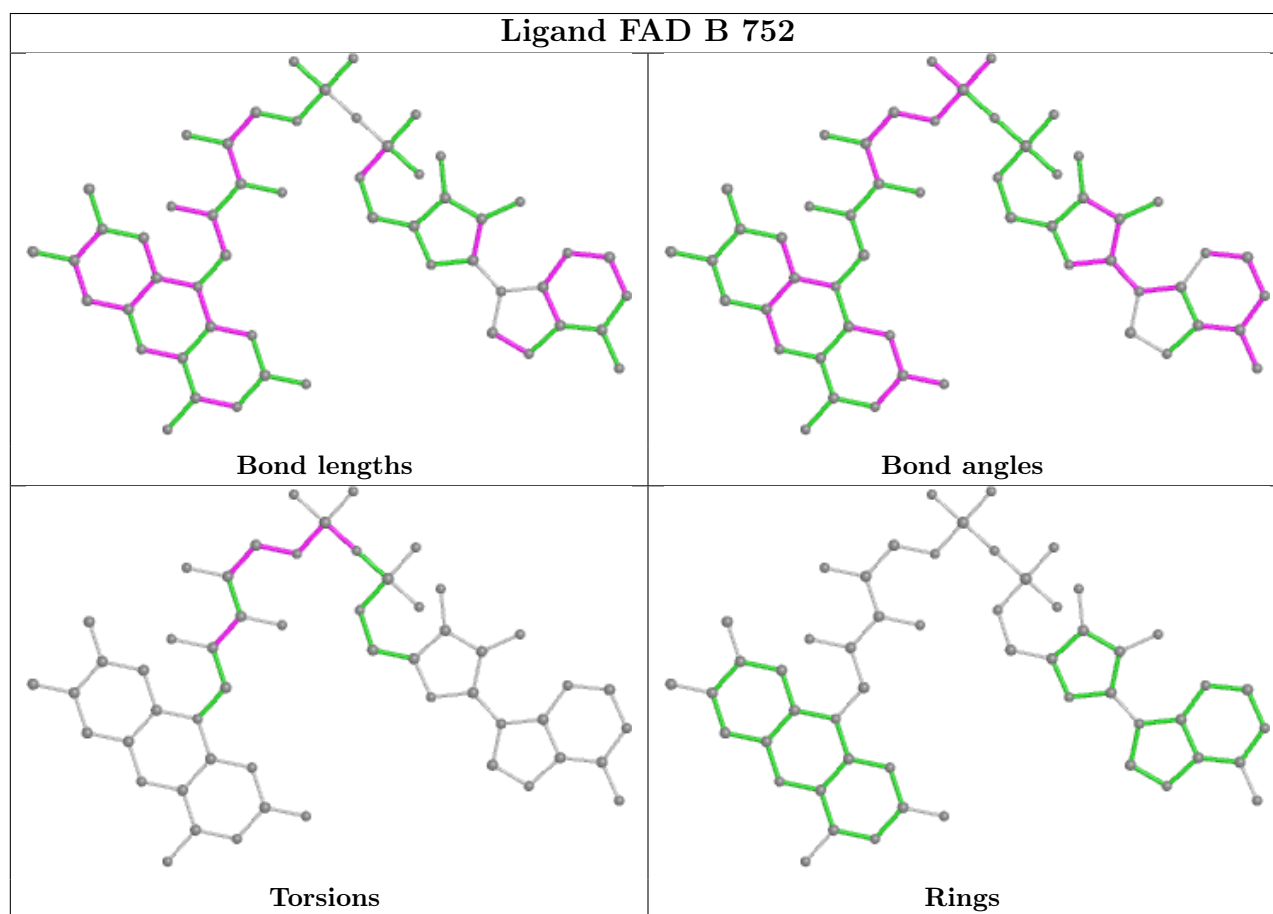
Mol	Chain	Res	Type	Atoms
3	B	752	FAD	C1'-C2'-C3'-C4'
3	C	752	FAD	C1'-C2'-C3'-O3'
3	C	752	FAD	C1'-C2'-C3'-C4'
3	C	752	FAD	O4'-C4'-C5'-O5'
4	A	753	NAP	C3D-C4D-C5D-O5D
4	A	753	NAP	C2N-C3N-C7N-O7N
4	A	753	NAP	C2N-C3N-C7N-N7N
4	A	753	NAP	C4N-C3N-C7N-N7N
4	B	753	NAP	C3D-C4D-C5D-O5D
4	A	753	NAP	C4N-C3N-C7N-O7N
3	C	752	FAD	O2'-C2'-C3'-O3'
4	A	753	NAP	O4D-C4D-C5D-O5D
3	A	752	FAD	C4'-C5'-O5'-P
3	B	752	FAD	C4'-C5'-O5'-P
3	C	752	FAD	C4'-C5'-O5'-P
4	B	753	NAP	C2N-C3N-C7N-O7N
4	B	753	NAP	C2N-C3N-C7N-N7N
4	B	753	NAP	O4D-C4D-C5D-O5D
3	A	752	FAD	O2'-C2'-C3'-C4'
3	C	752	FAD	O2'-C2'-C3'-C4'
3	A	752	FAD	O2'-C2'-C3'-O3'
4	B	753	NAP	C4N-C3N-C7N-N7N
4	B	753	NAP	C4N-C3N-C7N-O7N
4	A	753	NAP	O4B-C4B-C5B-O5B
3	B	752	FAD	O2'-C2'-C3'-C4'
3	A	752	FAD	C3'-C4'-C5'-O5'
3	C	752	FAD	C3'-C4'-C5'-O5'
4	A	753	NAP	C3B-C4B-C5B-O5B
4	B	753	NAP	C2B-O2B-P2B-O1X
3	A	752	FAD	C5B-O5B-PA-O3P
4	B	753	NAP	C2B-O2B-P2B-O3X
4	B	753	NAP	PA-O3-PN-O1N
3	C	752	FAD	PA-O3P-P-O2P
3	B	752	FAD	O2'-C2'-C3'-O3'
3	A	752	FAD	PA-O3P-P-O2P
3	B	752	FAD	PA-O3P-P-O2P
3	A	752	FAD	C5'-O5'-P-O1P
3	B	752	FAD	C5'-O5'-P-O1P
3	B	752	FAD	O4'-C4'-C5'-O5'

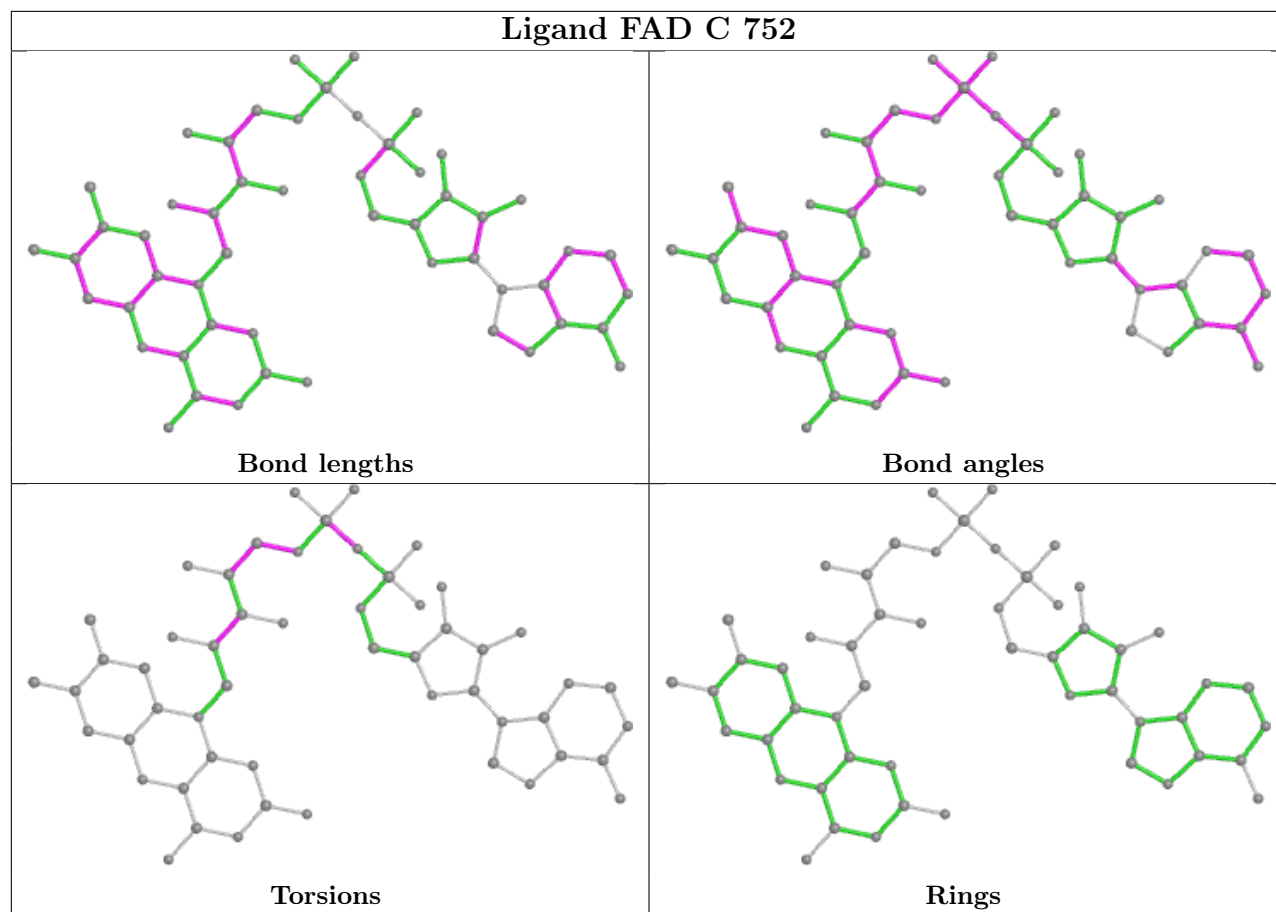
There are no ring outliers.

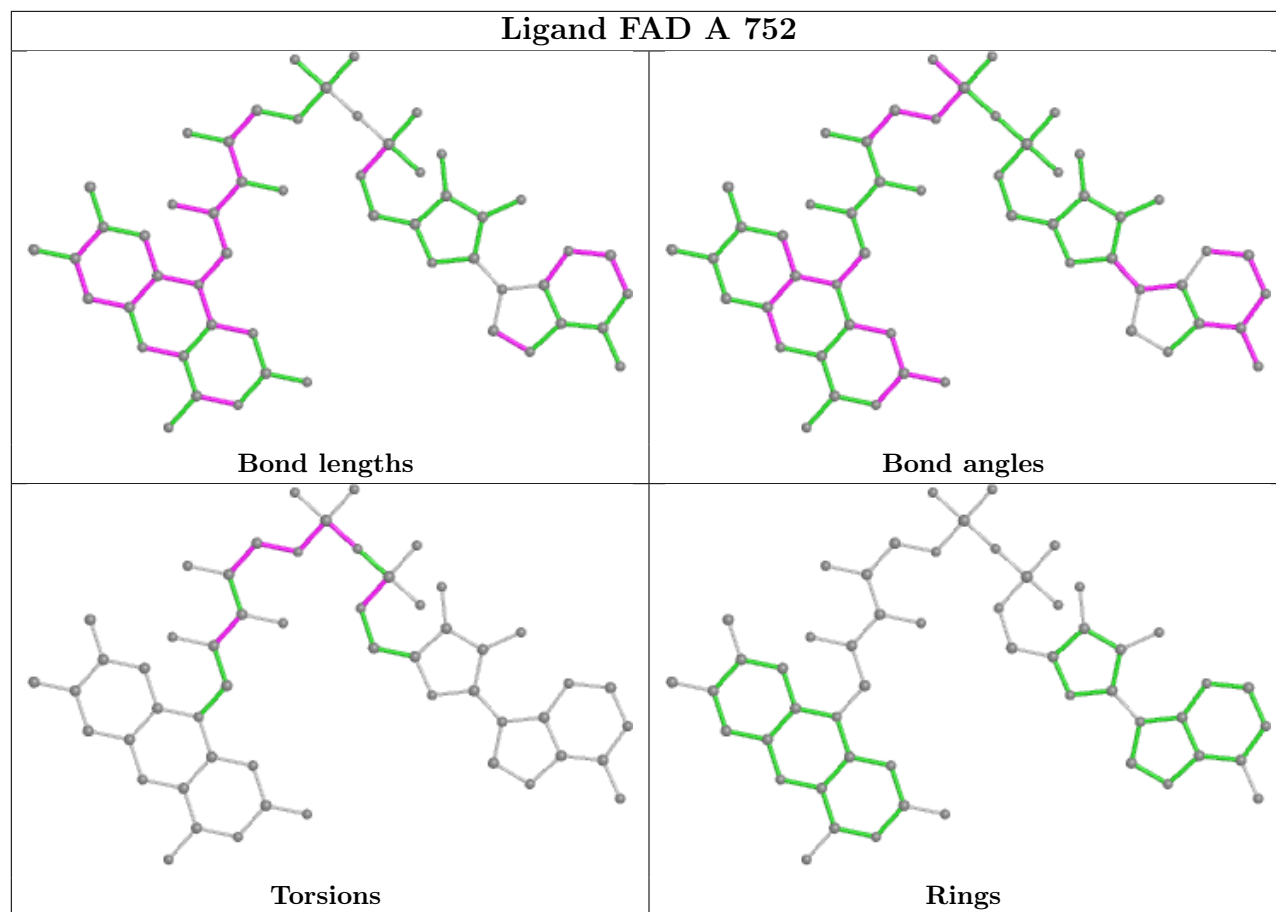
5 monomers are involved in 20 short contacts:

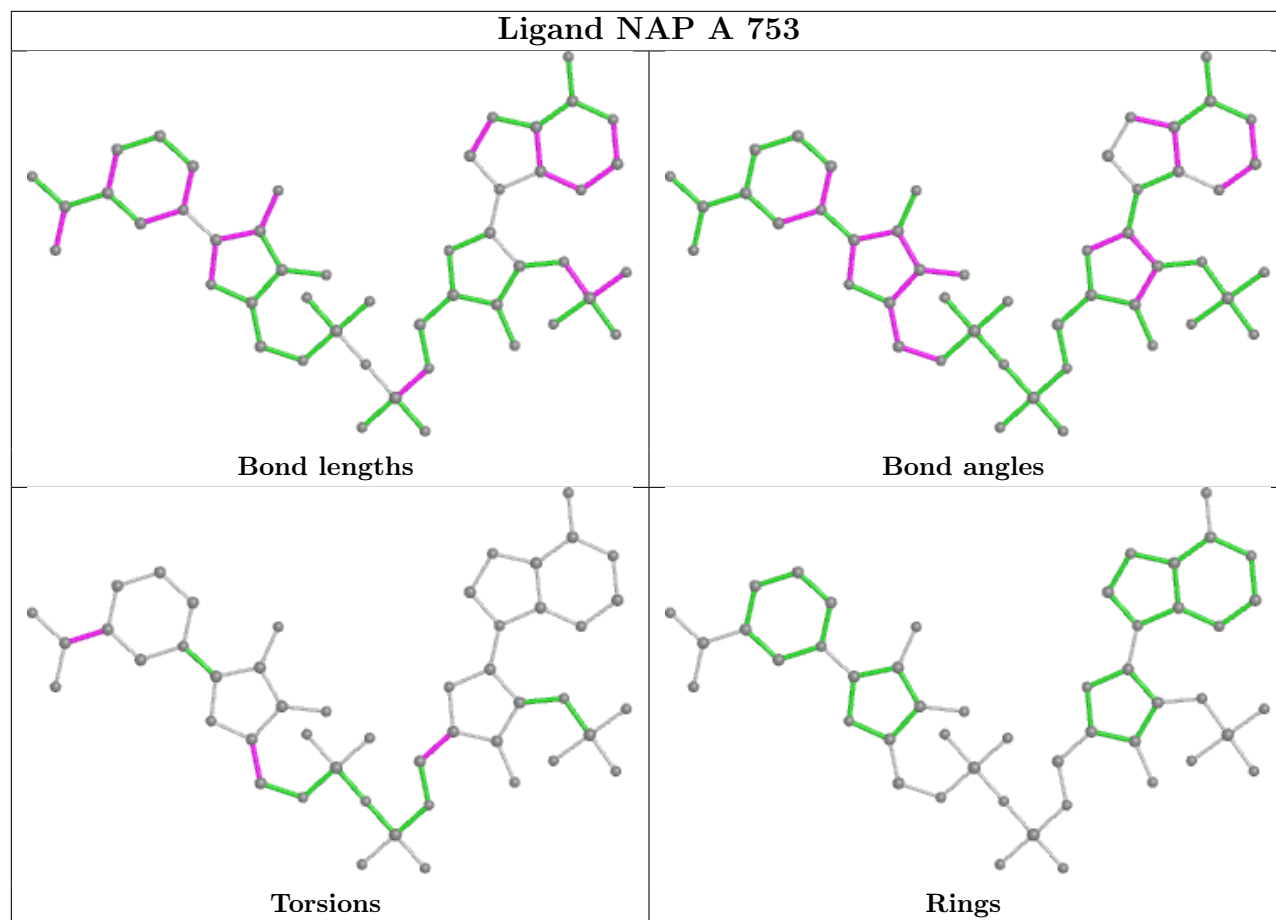
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	752	FAD	7	0
3	C	752	FAD	3	0
3	A	752	FAD	5	0
4	A	753	NAP	3	0
4	B	753	NAP	2	0

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

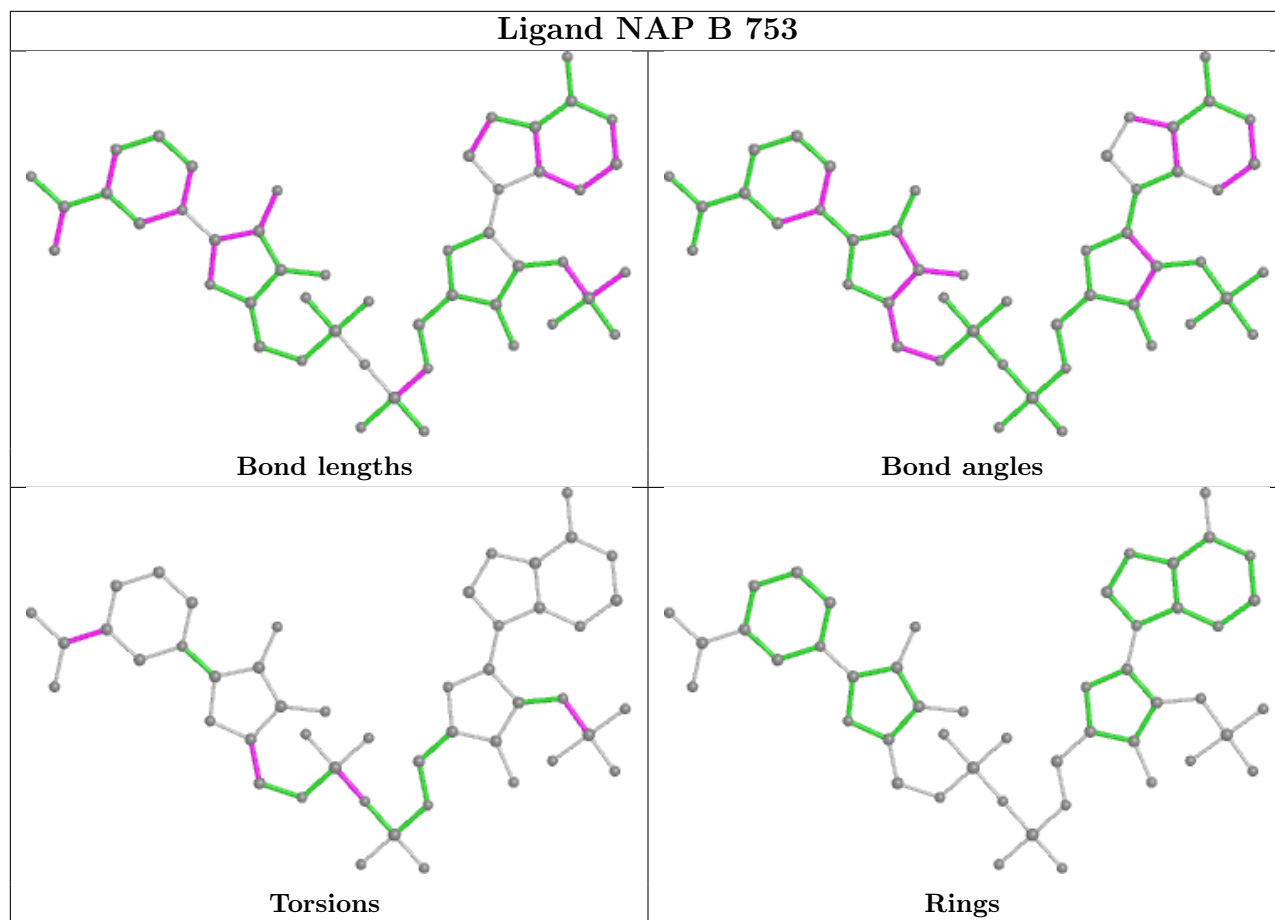


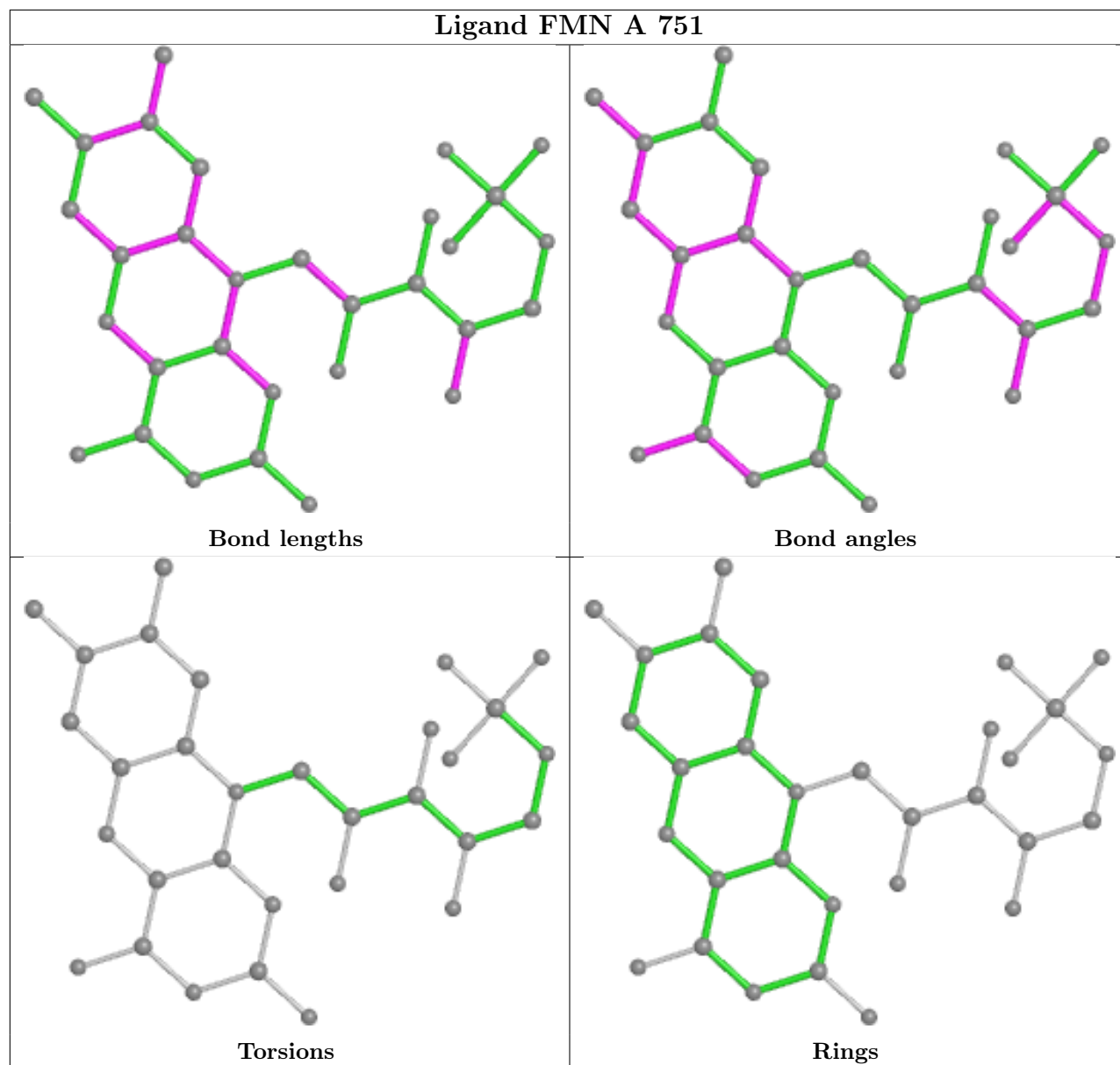












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	603/618 (97%)	-0.18	1 (0%) 95 95	72, 95, 116, 136	0
1	B	515/618 (83%)	0.11	23 (4%) 33 33	65, 96, 175, 202	0
1	C	435/618 (70%)	0.03	8 (1%) 68 67	84, 116, 149, 161	0
All	All	1553/1854 (83%)	-0.02	32 (2%) 63 62	65, 101, 155, 202	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	119	LEU	4.6
1	B	155	TRP	4.6
1	B	164	THR	4.6
1	B	80	ILE	4.2
1	B	154	ASP	4.0
1	B	211	ASN	3.9
1	C	663	VAL	3.7
1	B	213	GLU	3.6
1	B	118	ASP	3.6
1	B	103	HIS	3.4
1	B	81	ILE	3.3
1	B	122	LEU	3.2
1	B	165	GLY	3.2
1	B	158	GLU	3.1
1	B	157	GLN	3.1
1	C	258	VAL	2.8
1	B	223	PHE	2.7
1	B	214	GLU	2.6
1	C	353	GLU	2.6
1	B	224	TRP	2.5
1	B	120	ALA	2.5
1	B	272	GLN	2.5
1	C	600	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	357	LYS	2.3
1	B	218	THR	2.3
1	B	129	ASP	2.3
1	C	358	LYS	2.3
1	C	352	ASP	2.2
1	C	365	THR	2.2
1	A	312	ILE	2.1
1	B	79	ASN	2.1
1	B	222	GLN	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 6.4 Ligands [i](#)

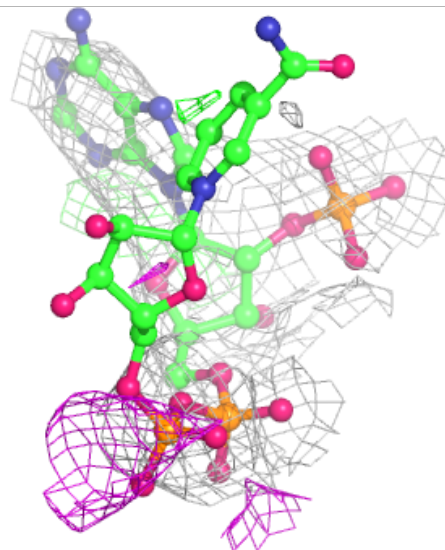
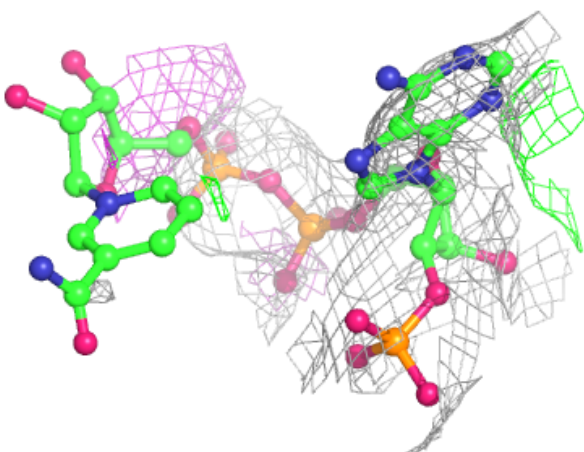
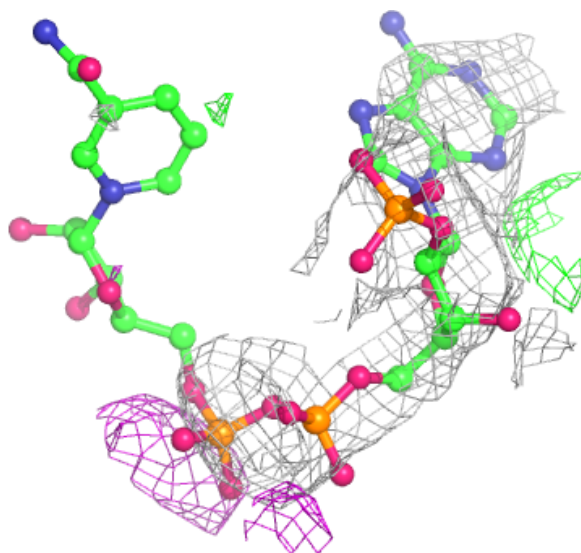
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
4	NAP	A	753	48/48	0.77	0.40	201,219,224,224	0
4	NAP	B	753	48/48	0.78	0.34	173,198,214,215	0
3	FAD	B	752	53/53	0.93	0.26	78,87,105,107	0
3	FAD	C	752	53/53	0.93	0.24	98,102,114,114	0
2	FMN	A	751	31/31	0.96	0.17	102,108,109,110	0
3	FAD	A	752	53/53	0.96	0.21	73,79,87,88	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.

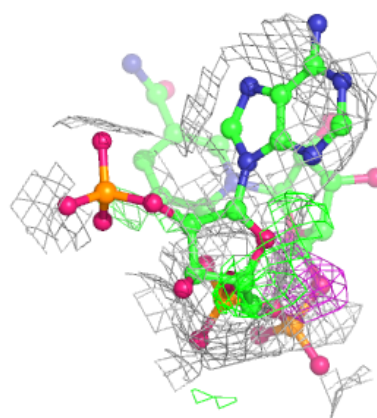
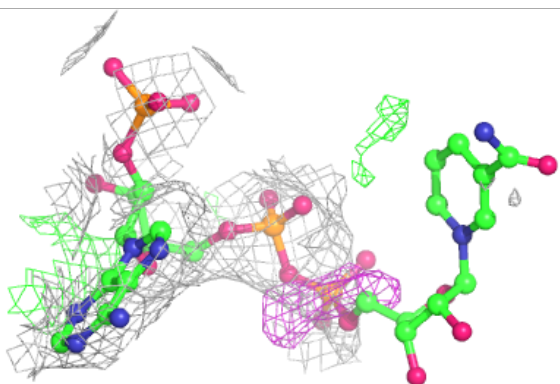
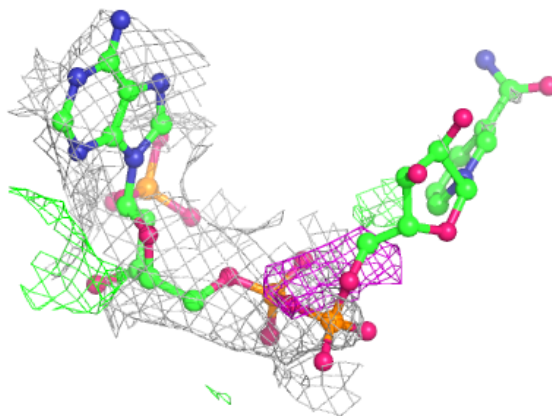
**Electron density around NAP A 753:**

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



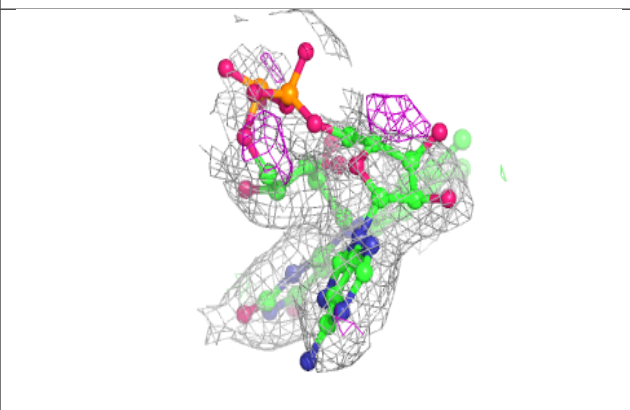
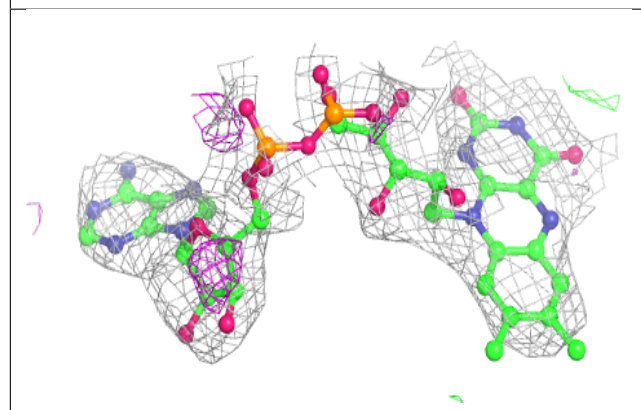
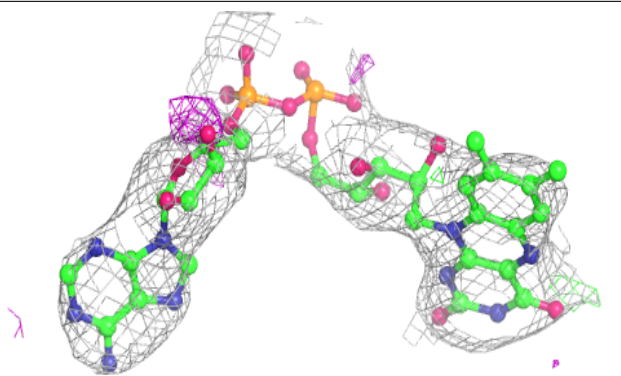
**Electron density around NAP B 753:**

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

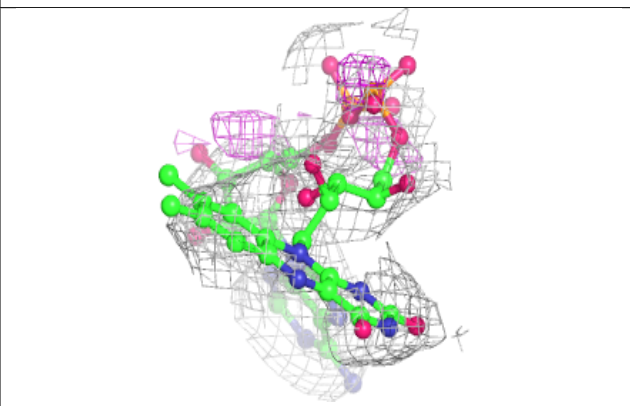
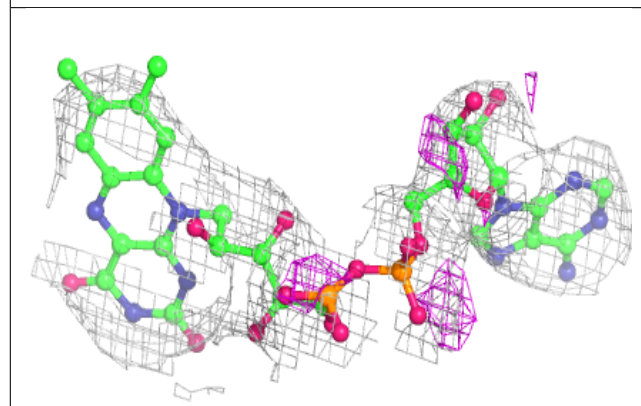
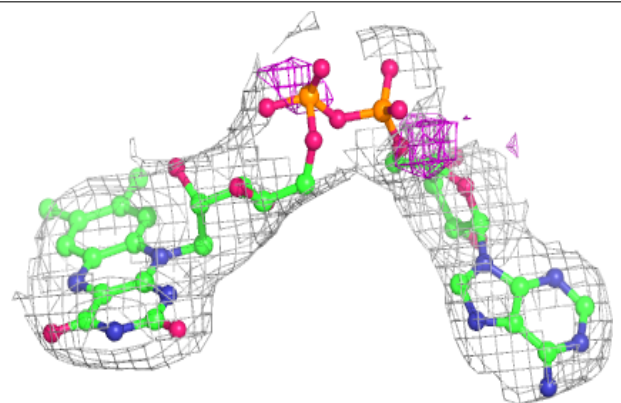


**Electron density around FAD B 752:**

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

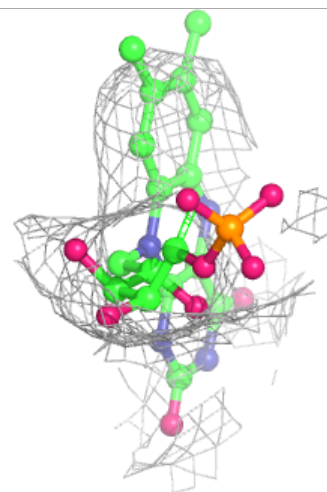
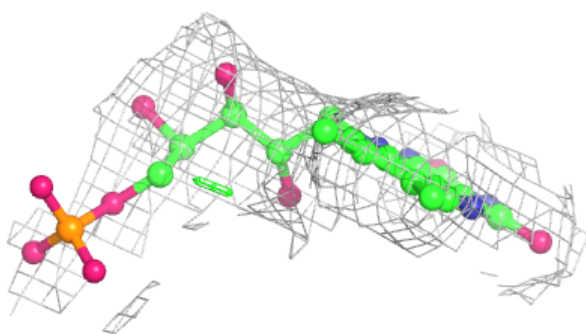
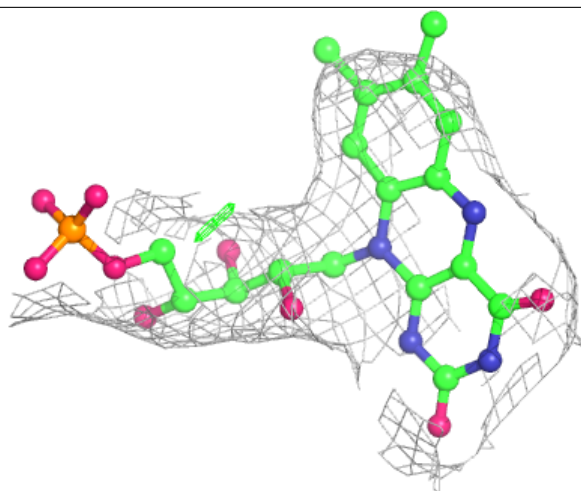
**Electron density around FAD C 752:**

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

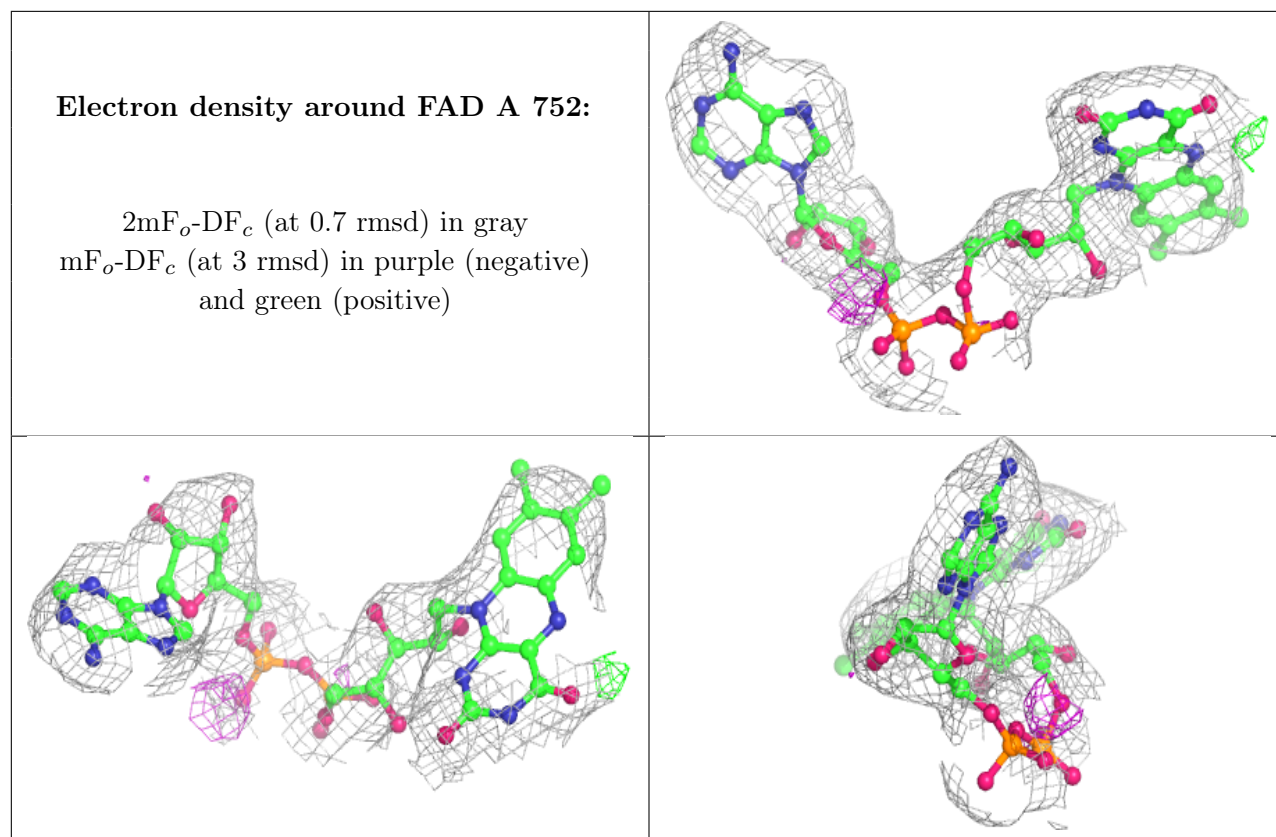


**Electron density around FMN A 751:**

$2mF_o-DF_c$  (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.