



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:28 AM GMT

PDB ID : 3AYF
Title : Crystal structure of nitric oxide reductase
Authors : Matsumoto, Y.; Tosha, T.; Pisiakov, A.V.; Hino, T.; Sugimoti, H.; Nagano, S.; Sugita, Y.; Shiro, Y.
Deposited on : 2011-05-06
Resolution : 2.50 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

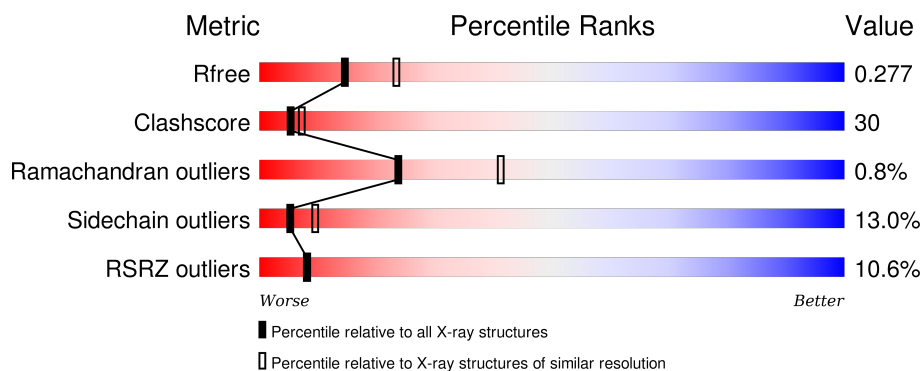
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	91344	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	800	<div> <div>10%</div> <div>49%</div> <div>37%</div> <div>8%</div> <div>6%</div> </div>

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
5	BOG	A	806	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	EPE	A	808	-	-	-	X
7	LOP	A	809	-	-	-	X
7	LOP	A	810	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 6455 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.

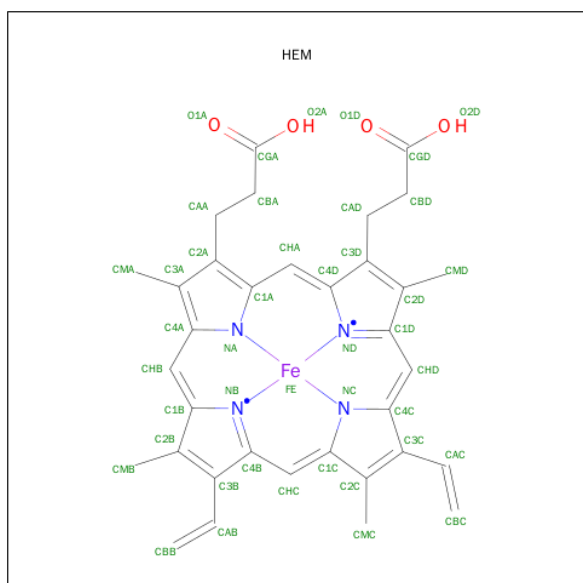
- Molecule 1 is a protein called Nitric oxide reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	754	6078	4055	966	1034	23	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	793	LEU	-	EXPRESSION TAG	UNP B3Y963
A	794	GLU	-	EXPRESSION TAG	UNP B3Y963
A	795	HIS	-	EXPRESSION TAG	UNP B3Y963
A	796	HIS	-	EXPRESSION TAG	UNP B3Y963
A	797	HIS	-	EXPRESSION TAG	UNP B3Y963
A	798	HIS	-	EXPRESSION TAG	UNP B3Y963
A	799	HIS	-	EXPRESSION TAG	UNP B3Y963
A	800	HIS	-	EXPRESSION TAG	UNP B3Y963

- Molecule 2 is PROTOPORPHYRIN IX CONTAINING FE (three-letter code: HEM) (formula: $C_{34}H_{32}FeN_4O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	
2	A	1	Total	C	Fe	N	O	
			43	34	1	4	4	

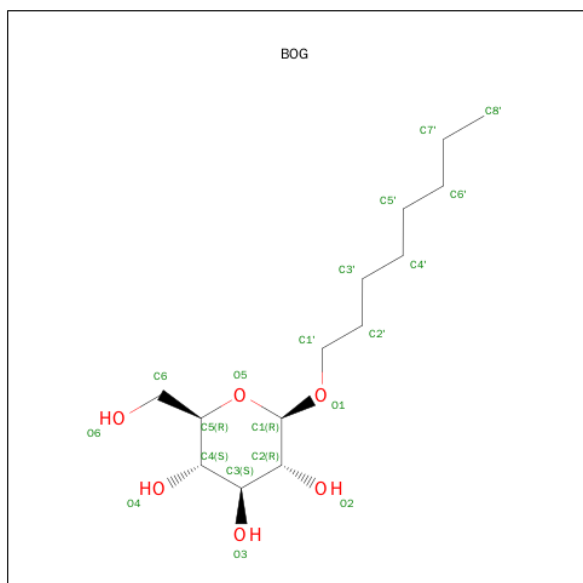
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn		
			1	1	0	0

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

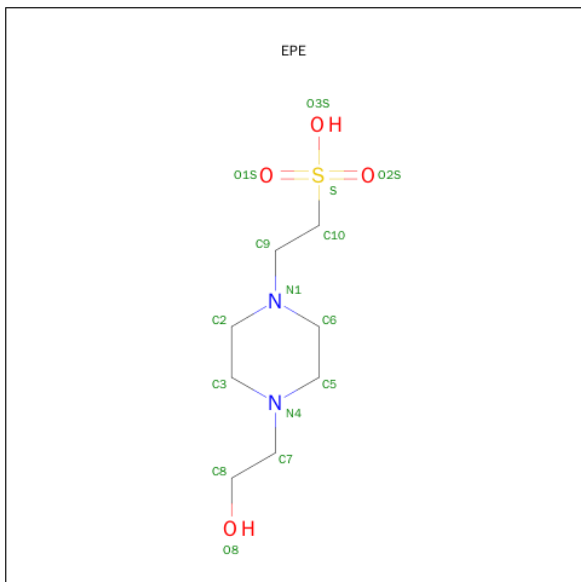
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca		
			1	1	0	0

- Molecule 5 is SUGAR (B-OCTYLGLUCOSIDE) (three-letter code: BOG) (formula: C₁₄H₂₈O₆).



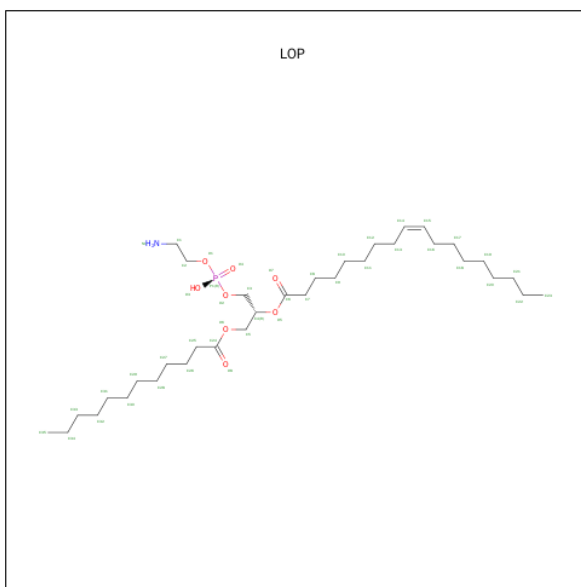
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O		
			20	14	6	0	0
5	A	1	Total	C	O		
			20	14	6	0	0
5	A	1	Total	C	O		
			20	14	6	0	0

- Molecule 6 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 7 is (1R)-2-{[(R)-(2-AMINOETHOXY)(HYDROXY)PHOSPHORYL]OXY}-1-[(DODECANOYLOXY)METHYL]ETHYL (9Z)-OCTADEC-9-ENOATE (three-letter code: LOP) (formula: $C_{35}H_{68}NO_8P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	A	1	Total	C	N	O	P	0	0
			45	35	1	8	1		
7	A	1	Total	C	N	O	P	0	0
			45	35	1	8	1		

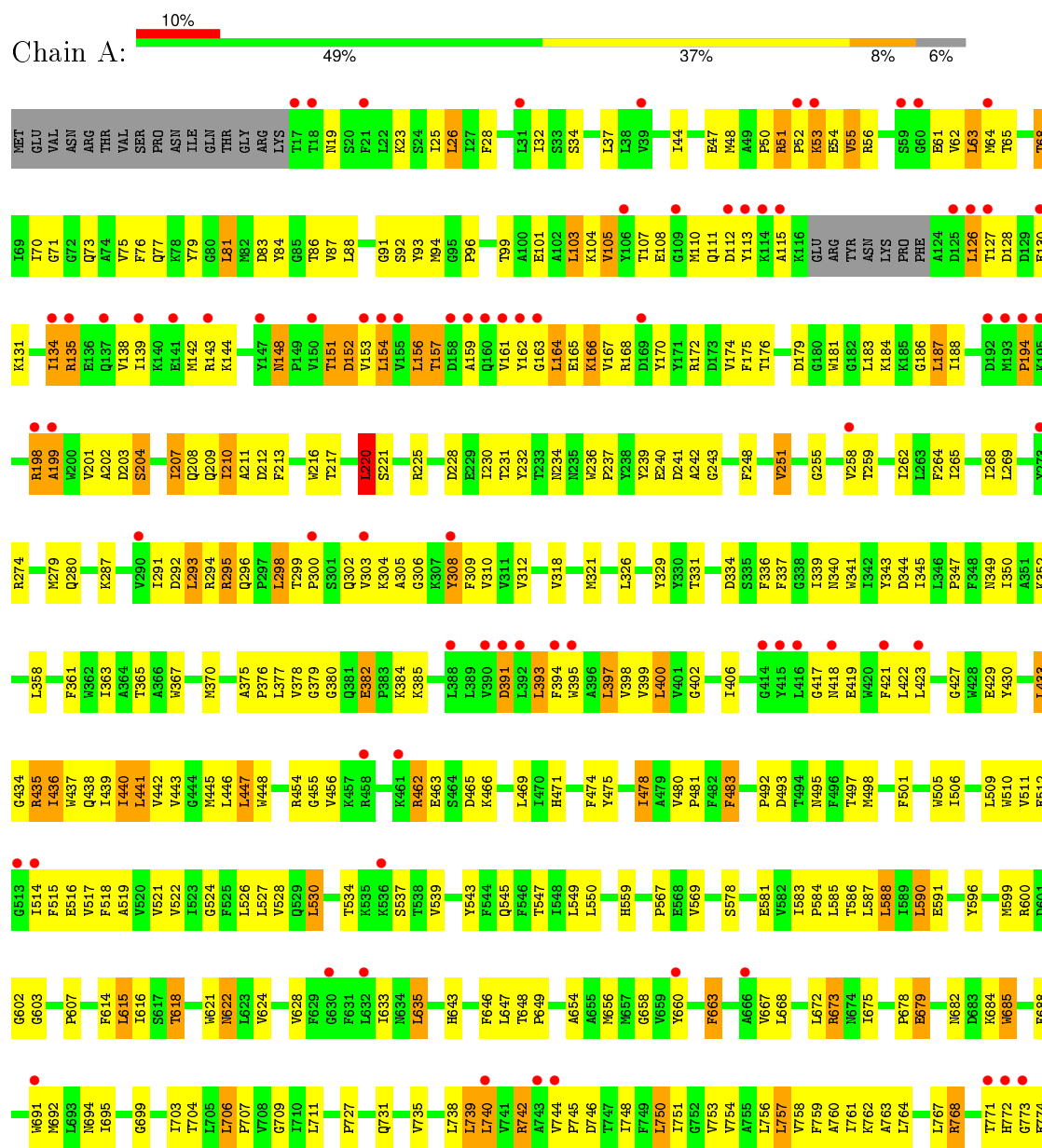
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	124	Total	O	0	0
			124	124		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Nitric oxide reductase



G775			
E776			
E777			
LEU			
PRO			
VAL			
ALA			
ASN			
HIS			
TRP			
MET			
LYS			
ASP			
ARG			
LEU			
LYS			
ASN			
SER			
LEU			
GLU			
HIS			
HIS			
HIS			
HIS			
HIS			

4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	110.41Å 149.65Å 151.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.78 – 2.50 43.53 – 2.51	Depositor EDS
% Data completeness (in resolution range)	98.9 (19.78-2.50) 99.0 (43.53-2.51)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.32 (at 2.51Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.244 , 0.282 0.242 , 0.277	Depositor DCC
R_{free} test set	2122 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	53.5	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 65.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 42695 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6455	wwPDB-VP
Average B, all atoms (Å ²)	64.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.75% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, CA, LOP, HEM, EPE, BOG

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	0.44	0/6262	0.65	2/8517 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	220	LEU	CA-CB-CG	5.51	127.96	115.30
1	A	602	GLY	N-CA-C	-5.08	100.40	113.10

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	6078	0	6095	368	0
2	A	86	0	60	3	0
3	A	1	0	0	0	0
4	A	1	0	0	0	0
5	A	60	0	84	4	0
6	A	15	0	18	0	0
7	A	90	0	134	31	0
8	A	124	0	0	9	0
All	All	6455	0	6391	384	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 30.

All (384) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:198:ARG:HH11	1:A:198:ARG:HG3	0.97	1.12
1:A:172:ARG:HG3	1:A:207:ILE:HD11	1.33	1.04
1:A:293:LEU:H	1:A:293:LEU:HD23	1.28	0.99
1:A:465:ASP:HA	7:A:809:LOP:H11	1.47	0.97
1:A:126:LEU:HD22	1:A:126:LEU:H	1.33	0.93
1:A:56:ARG:HB3	1:A:62:VAL:HA	1.49	0.93
1:A:198:ARG:NH1	1:A:198:ARG:HG3	1.72	0.90
1:A:56:ARG:HA	1:A:63:LEU:HD22	1.54	0.88
1:A:585:LEU:HA	1:A:588:LEU:HD22	1.55	0.87
1:A:198:ARG:HH12	1:A:203:ASP:HA	1.41	0.85
1:A:75:VAL:CG2	1:A:210:ILE:HG12	2.07	0.85
1:A:742:ARG:HD2	1:A:746:ASP:OD2	1.77	0.85
7:A:810:LOP:H112	7:A:810:LOP:H272	1.59	0.84
1:A:172:ARG:HA	1:A:207:ILE:HD12	1.61	0.82
1:A:422:LEU:O	1:A:436:ILE:HG23	1.81	0.81
1:A:543:TYR:O	1:A:547:THR:HG23	1.81	0.81
1:A:293:LEU:H	1:A:293:LEU:CD2	1.94	0.81
1:A:341:TRP:O	1:A:345:ILE:HG22	1.81	0.80
7:A:810:LOP:H292	7:A:810:LOP:H132	1.64	0.79
1:A:624:VAL:HA	1:A:628:VAL:HG13	1.65	0.78
1:A:255:GLY:O	1:A:259:THR:HG23	1.84	0.78
1:A:198:ARG:HH11	1:A:198:ARG:CG	1.87	0.77
1:A:55:VAL:HG13	1:A:64:MET:HB3	1.67	0.77
1:A:104:LYS:O	1:A:108:GLU:HG2	1.85	0.76
7:A:810:LOP:O7	7:A:810:LOP:H91	1.82	0.76
1:A:300:PRO:HD2	1:A:382:GLU:HG3	1.69	0.75
1:A:318:VAL:HG23	1:A:358:LEU:HD13	1.69	0.74
1:A:614:PHE:O	1:A:618:THR:HG22	1.88	0.74
1:A:164:LEU:O	1:A:168:ARG:HG3	1.88	0.73
1:A:126:LEU:HB3	1:A:130:GLU:HG2	1.71	0.73
1:A:517:VAL:O	1:A:521:VAL:HG12	1.89	0.73
1:A:175:PHE:HD1	1:A:187:LEU:HD11	1.52	0.72
1:A:104:LYS:HE2	1:A:108:GLU:OE2	1.90	0.72
1:A:585:LEU:O	1:A:588:LEU:HB2	1.90	0.71
1:A:735:VAL:HG12	1:A:739:LEU:HD22	1.72	0.70
1:A:624:VAL:HG11	7:A:810:LOP:H211	1.73	0.70
1:A:44:ILE:HG12	1:A:567:PRO:HD2	1.72	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:168:ARG:HD3	1:A:208:GLN:NE2	2.06	0.70
1:A:210:ILE:HG22	1:A:211:ALA:N	2.07	0.69
7:A:810:LOP:H112	7:A:810:LOP:H251	1.73	0.69
7:A:810:LOP:O6	7:A:810:LOP:C6	2.40	0.69
1:A:51:ARG:HD2	1:A:495:ASN:ND2	2.08	0.69
1:A:299:THR:HB	1:A:382:GLU:HG2	1.74	0.69
1:A:466:LYS:HB2	7:A:809:LOP:O3	1.92	0.69
1:A:302:GLN:HE22	1:A:377:LEU:HD13	1.58	0.68
1:A:380:GLY:O	1:A:777:GLU:HG2	1.92	0.68
1:A:188:ILE:HG21	1:A:207:ILE:HG22	1.74	0.68
1:A:199:ALA:HB2	1:A:418:ASN:HB3	1.75	0.68
1:A:207:ILE:HG23	8:A:905:HOH:O	1.94	0.68
1:A:198:ARG:NH1	1:A:203:ASP:HA	2.07	0.67
1:A:216:TRP:O	1:A:220:LEU:HD13	1.94	0.67
1:A:194:PRO:O	1:A:198:ARG:HD3	1.94	0.67
1:A:375:ALA:HB3	1:A:376:PRO:HD3	1.76	0.66
1:A:110:MET:HG2	1:A:159:ALA:O	1.94	0.66
1:A:363:ILE:HG22	1:A:515:PHE:CE1	2.30	0.66
1:A:334:ASP:HA	1:A:343:TYR:CD2	2.30	0.65
1:A:168:ARG:HD3	1:A:208:GLN:HE21	1.61	0.65
1:A:363:ILE:HG22	1:A:515:PHE:CZ	2.31	0.65
1:A:75:VAL:HG22	1:A:210:ILE:HG12	1.79	0.65
1:A:321:MET:HE1	1:A:750:LEU:HD11	1.79	0.65
1:A:370:MET:HE1	1:A:526:LEU:HD21	1.79	0.65
1:A:217:THR:HA	1:A:220:LEU:CD1	2.27	0.65
1:A:225:ARG:HE	1:A:232:TYR:HA	1.62	0.65
1:A:93:TYR:HE2	1:A:649:PRO:HG3	1.61	0.64
1:A:157:THR:O	1:A:161:VAL:HG23	1.97	0.64
1:A:135:ARG:O	1:A:139:ILE:HG12	1.97	0.64
1:A:621:TRP:CZ2	7:A:810:LOP:H192	2.33	0.64
7:A:809:LOP:H12	7:A:809:LOP:O4	1.97	0.63
1:A:648:THR:HB	1:A:649:PRO:HD3	1.80	0.63
1:A:65:THR:HG23	1:A:68:THR:H	1.63	0.63
1:A:393:LEU:HD22	1:A:397:LEU:HD21	1.80	0.63
1:A:293:LEU:N	1:A:293:LEU:HD23	2.07	0.63
1:A:142:MET:HE3	1:A:242:ALA:HA	1.80	0.63
1:A:331:THR:HG21	1:A:740:LEU:HD13	1.80	0.62
1:A:400:LEU:HB2	1:A:440:ILE:HD11	1.81	0.62
1:A:217:THR:HA	1:A:220:LEU:HD11	1.80	0.62
1:A:198:ARG:HH12	1:A:203:ASP:CA	2.12	0.62
1:A:302:GLN:NE2	1:A:377:LEU:HD13	2.15	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:347:PRO:HD2	1:A:350:ILE:HD12	1.81	0.62
1:A:436:ILE:O	1:A:440:ILE:HG23	2.00	0.61
1:A:771:THR:HG22	1:A:772:HIS:CD2	2.35	0.61
1:A:107:THR:O	1:A:111:GLN:HG3	2.00	0.61
1:A:225:ARG:NE	1:A:232:TYR:HA	2.16	0.61
1:A:55:VAL:CG1	1:A:64:MET:HB3	2.31	0.61
7:A:809:LOP:O3	7:A:809:LOP:H4	2.00	0.61
1:A:274:ARG:HG3	1:A:274:ARG:O	2.00	0.61
1:A:588:LEU:HD23	1:A:622:ASN:HB3	1.81	0.61
1:A:607:PRO:O	1:A:673:ARG:HD2	2.01	0.61
7:A:810:LOP:C11	7:A:810:LOP:H251	2.31	0.61
1:A:298:LEU:CD1	1:A:303:VAL:HG13	2.31	0.61
1:A:581:GLU:O	1:A:584:PRO:HD2	2.00	0.61
1:A:480:VAL:HB	1:A:481:PRO:CD	2.31	0.60
1:A:569:VAL:HG23	5:A:807:BOG:H3'1	1.83	0.60
1:A:298:LEU:HD12	1:A:303:VAL:HG13	1.84	0.60
1:A:393:LEU:O	1:A:397:LEU:HD22	2.02	0.60
1:A:633:ILE:HD12	2:A:802:HEM:HBD2	1.82	0.60
1:A:309:PHE:HA	1:A:312:VAL:HG13	1.82	0.60
1:A:516:GLU:HG2	1:A:549:LEU:HD21	1.83	0.60
1:A:365:THR:HB	8:A:990:HOH:O	2.01	0.60
1:A:172:ARG:NH2	1:A:208:GLN:OE1	2.31	0.60
1:A:34:SER:OG	7:A:809:LOP:H233	2.00	0.60
1:A:56:ARG:HB2	1:A:61:GLU:O	2.02	0.60
1:A:691:TRP:CE3	1:A:695:ILE:HD11	2.36	0.59
1:A:402:GLY:O	1:A:406:ILE:HG12	2.01	0.59
1:A:179:ASP:OD1	1:A:183:LEU:HB3	2.02	0.59
1:A:172:ARG:HG3	1:A:207:ILE:CD1	2.21	0.59
1:A:304:LYS:HG2	1:A:391:ASP:OD1	2.02	0.59
1:A:86:THR:HG23	1:A:92:SER:O	2.03	0.59
1:A:646:PHE:C	1:A:649:PRO:HD2	2.23	0.59
1:A:93:TYR:CE2	1:A:649:PRO:HG3	2.37	0.59
1:A:694:ASN:HB3	7:A:810:LOP:H312	1.84	0.58
1:A:113:TYR:HB2	1:A:162:TYR:CD2	2.38	0.58
1:A:164:LEU:O	1:A:164:LEU:HD22	2.02	0.58
1:A:692:MET:CE	1:A:748:ILE:HG23	2.34	0.57
1:A:101:GLU:O	1:A:105:VAL:HG23	2.04	0.57
1:A:187:LEU:HD13	1:A:188:ILE:H	1.69	0.57
1:A:151:THR:O	1:A:153:VAL:N	2.34	0.57
1:A:299:THR:HB	1:A:382:GLU:CG	2.33	0.57
1:A:704:THR:HG21	1:A:742:ARG:HG3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:ASP:O	1:A:349:ASN:HA	2.04	0.57
1:A:220:LEU:HD22	1:A:221:SER:N	2.19	0.57
1:A:429:GLU:O	1:A:430:TYR:HB2	2.04	0.57
1:A:291:ILE:CG2	1:A:607:PRO:HG3	2.35	0.57
1:A:148:ASN:O	1:A:151:THR:O	2.23	0.57
1:A:421:PHE:CE1	1:A:492:PRO:HD3	2.40	0.56
1:A:198:ARG:NH1	1:A:202:ALA:O	2.38	0.56
1:A:156:LEU:H	1:A:156:LEU:HD23	1.71	0.56
1:A:691:TRP:HE3	1:A:695:ILE:HD11	1.71	0.56
1:A:395:TRP:HA	1:A:398:VAL:HG12	1.86	0.56
1:A:663:PHE:HB3	8:A:922:HOH:O	2.06	0.56
1:A:433:LEU:HD13	1:A:438:GLN:CG	2.35	0.56
1:A:675:ILE:CG2	1:A:767:LEU:HD22	2.36	0.56
1:A:511:VAL:O	1:A:515:PHE:CD2	2.58	0.55
1:A:181:TRP:CG	1:A:727:PRO:HB3	2.41	0.55
1:A:774:GLU:OE1	1:A:774:GLU:N	2.39	0.55
1:A:62:VAL:HG23	8:A:983:HOH:O	2.07	0.55
1:A:139:ILE:HD13	1:A:142:MET:HE3	1.89	0.55
1:A:156:LEU:N	1:A:156:LEU:HD23	2.21	0.55
1:A:142:MET:CE	1:A:242:ALA:HA	2.37	0.55
1:A:299:THR:CB	1:A:382:GLU:HG2	2.37	0.55
1:A:395:TRP:HA	1:A:398:VAL:CG1	2.36	0.55
1:A:439:ILE:O	1:A:442:VAL:HG22	2.07	0.55
1:A:454:ARG:HH11	1:A:454:ARG:HG2	1.72	0.54
1:A:207:ILE:HG13	1:A:207:ILE:O	2.08	0.54
1:A:139:ILE:HD11	1:A:241:ASP:O	2.08	0.54
1:A:264:PHE:O	1:A:268:ILE:HG12	2.08	0.54
1:A:400:LEU:HG	1:A:440:ILE:CG1	2.38	0.54
1:A:688:PHE:O	1:A:692:MET:HG2	2.08	0.54
1:A:744:VAL:HB	1:A:745:PRO:CD	2.36	0.54
1:A:53:LYS:HE2	1:A:54:GLU:HG3	1.90	0.54
1:A:682:ASN:ND2	1:A:684:LYS:HB3	2.23	0.54
1:A:166:LYS:N	1:A:166:LYS:HE2	2.23	0.54
1:A:175:PHE:CE2	1:A:210:ILE:HG21	2.43	0.53
1:A:203:ASP:HB3	8:A:904:HOH:O	2.07	0.53
1:A:483:PHE:CZ	7:A:809:LOP:H222	2.43	0.53
1:A:682:ASN:HD21	1:A:684:LYS:HB3	1.73	0.53
1:A:378:VAL:HG11	1:A:456:VAL:HG13	1.89	0.53
1:A:539:VAL:HG22	8:A:984:HOH:O	2.08	0.53
1:A:339:ILE:HG22	1:A:340:ASN:N	2.23	0.53
1:A:187:LEU:HD13	1:A:188:ILE:N	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:LEU:CG	1:A:440:ILE:HD11	2.39	0.53
1:A:685:TRP:CE3	1:A:685:TRP:HA	2.43	0.53
1:A:758:VAL:O	1:A:762:LYS:HG2	2.09	0.53
1:A:534:THR:OG1	1:A:537:SER:HB3	2.09	0.53
1:A:113:TYR:CD2	1:A:159:ALA:HA	2.44	0.53
1:A:400:LEU:HG	1:A:440:ILE:HD11	1.91	0.52
1:A:569:VAL:CG2	5:A:807:BOG:H3'1	2.39	0.52
1:A:131:LYS:HD3	1:A:131:LYS:O	2.10	0.52
1:A:760:ALA:O	1:A:763:ALA:HB3	2.09	0.52
1:A:771:THR:HG22	1:A:772:HIS:HD2	1.74	0.51
1:A:291:ILE:HG21	1:A:607:PRO:HG3	1.91	0.51
1:A:378:VAL:HB	1:A:456:VAL:HG22	1.91	0.51
1:A:367:TRP:CZ3	1:A:667:VAL:HG21	2.45	0.51
1:A:203:ASP:O	1:A:204:SER:HB2	2.10	0.51
1:A:515:PHE:HB2	1:A:660:TYR:CE1	2.44	0.51
1:A:395:TRP:O	1:A:399:VAL:HG23	2.09	0.51
1:A:172:ARG:HA	1:A:207:ILE:CD1	2.36	0.51
1:A:393:LEU:HD22	1:A:397:LEU:CD2	2.40	0.51
1:A:203:ASP:O	1:A:204:SER:CB	2.58	0.51
1:A:331:THR:CG2	1:A:740:LEU:HD13	2.41	0.51
1:A:480:VAL:HB	1:A:481:PRO:HD3	1.92	0.51
1:A:534:THR:OG1	1:A:537:SER:CB	2.59	0.51
1:A:434:GLY:O	1:A:437:TRP:HB2	2.11	0.51
1:A:55:VAL:HA	1:A:154:LEU:O	2.11	0.51
1:A:138:VAL:HG22	1:A:142:MET:HE2	1.91	0.51
1:A:699:GLY:O	1:A:703:ILE:HB	2.10	0.51
1:A:76:PHE:HB2	1:A:210:ILE:HD11	1.93	0.51
1:A:201:VAL:CG2	1:A:209:GLN:HE22	2.24	0.50
1:A:64:MET:HE1	1:A:212:ASP:HA	1.91	0.50
1:A:65:THR:HG23	1:A:68:THR:N	2.25	0.50
1:A:19:ASN:O	1:A:23:LYS:HD2	2.11	0.50
1:A:382:GLU:HB2	1:A:773:GLY:O	2.11	0.50
1:A:616:ILE:HD13	7:A:810:LOP:H82	1.93	0.50
1:A:583:ILE:HB	1:A:584:PRO:HD3	1.94	0.50
1:A:56:ARG:HA	1:A:63:LEU:CD2	2.35	0.50
1:A:384:LYS:O	1:A:454:ARG:NH2	2.44	0.50
1:A:52:PRO:HA	1:A:152:ASP:OD1	2.11	0.50
1:A:53:LYS:O	1:A:65:THR:HA	2.12	0.50
1:A:462:ARG:HG2	1:A:462:ARG:HH11	1.77	0.50
1:A:440:ILE:HD12	1:A:440:ILE:O	2.11	0.50
1:A:88:LEU:HA	1:A:236:TRP:HZ3	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:188:ILE:CG2	1:A:207:ILE:HG22	2.40	0.50
1:A:209:GLN:O	1:A:212:ASP:HB2	2.12	0.50
1:A:53:LYS:O	1:A:53:LYS:HD2	2.11	0.50
1:A:23:LYS:NZ	7:A:809:LOP:O4	2.37	0.50
1:A:217:THR:O	1:A:220:LEU:HD22	2.11	0.50
1:A:429:GLU:HG2	1:A:430:TYR:CD2	2.47	0.50
1:A:25:ILE:HD13	5:A:806:BOG:H6'1	1.92	0.50
1:A:518:PHE:O	1:A:522:VAL:HG23	2.12	0.49
1:A:309:PHE:HB3	1:A:668:LEU:HG	1.93	0.49
1:A:55:VAL:HG22	1:A:64:MET:HB2	1.94	0.49
1:A:302:GLN:HE22	1:A:377:LEU:CD1	2.23	0.49
1:A:384:LYS:O	1:A:385:LYS:HB2	2.12	0.49
1:A:65:THR:H	1:A:68:THR:HG1	1.58	0.49
1:A:599:MET:HE2	7:A:810:LOP:H71	1.94	0.49
1:A:56:ARG:HB2	1:A:61:GLU:C	2.33	0.49
1:A:162:TYR:O	1:A:165:GLU:HB3	2.13	0.49
1:A:759:PHE:O	1:A:763:ALA:HB2	2.13	0.49
1:A:441:LEU:HD22	1:A:445:MET:HE2	1.95	0.49
1:A:79:TYR:CE2	1:A:188:ILE:HG12	2.47	0.49
1:A:248:PHE:O	1:A:251:VAL:HG13	2.13	0.49
1:A:615:LEU:O	1:A:618:THR:HG23	2.13	0.48
1:A:339:ILE:C	1:A:340:ASN:HD22	2.17	0.48
1:A:56:ARG:CD	1:A:62:VAL:HG12	2.43	0.48
1:A:475:TYR:CZ	7:A:809:LOP:H281	2.48	0.48
1:A:240:GLU:HB2	8:A:918:HOH:O	2.13	0.48
1:A:163:GLY:O	1:A:167:VAL:HG23	2.12	0.48
1:A:483:PHE:HZ	7:A:809:LOP:H222	1.78	0.48
1:A:441:LEU:HD22	1:A:445:MET:CE	2.43	0.48
1:A:55:VAL:HB	1:A:154:LEU:HD12	1.96	0.48
1:A:505:TRP:O	1:A:509:LEU:HB2	2.12	0.48
1:A:126:LEU:HD23	1:A:131:LYS:HG2	1.96	0.48
1:A:203:ASP:O	1:A:203:ASP:CG	2.52	0.48
1:A:647:LEU:HG	1:A:709:GLY:HA3	1.94	0.48
1:A:293:LEU:HA	1:A:296:GLN:HG3	1.95	0.47
1:A:184:LYS:NZ	1:A:344:ASP:O	2.46	0.47
1:A:675:ILE:O	1:A:768:ARG:HD3	2.14	0.47
1:A:199:ALA:HB2	1:A:418:ASN:CB	2.44	0.47
1:A:305:ALA:O	1:A:308:TYR:HB2	2.14	0.47
1:A:265:ILE:O	1:A:269:LEU:HB2	2.14	0.47
1:A:751:ILE:O	1:A:754:VAL:HG22	2.15	0.47
1:A:599:MET:CE	7:A:810:LOP:H71	2.43	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:675:ILE:HG22	1:A:767:LEU:HD22	1.97	0.47
1:A:26:LEU:HA	1:A:547:THR:HG22	1.97	0.47
1:A:515:PHE:CB	1:A:660:TYR:CE1	2.98	0.47
1:A:280:GLN:N	1:A:537:SER:OG	2.46	0.47
1:A:75:VAL:CG2	1:A:210:ILE:CG1	2.85	0.47
1:A:586:THR:C	1:A:588:LEU:H	2.18	0.47
1:A:635:LEU:HB2	8:A:901:HOH:O	2.15	0.47
1:A:474:PHE:O	1:A:478:ILE:CG2	2.61	0.47
7:A:809:LOP:O7	7:A:809:LOP:O6	2.33	0.47
1:A:139:ILE:CD1	1:A:241:ASP:O	2.63	0.47
1:A:757:LEU:HD22	1:A:761:ILE:HG13	1.96	0.47
1:A:126:LEU:CD2	1:A:126:LEU:H	2.10	0.47
1:A:77:GLN:HB3	1:A:427:GLY:HA3	1.97	0.47
7:A:810:LOP:H181	7:A:810:LOP:C33	2.44	0.47
1:A:298:LEU:HB2	1:A:768:ARG:HH21	1.80	0.47
1:A:445:MET:O	1:A:448:TRP:HB3	2.15	0.46
1:A:70:ILE:HG23	1:A:493:ASP:HA	1.97	0.46
1:A:379:GLY:HA3	1:A:455:GLY:O	2.16	0.46
1:A:400:LEU:CB	1:A:440:ILE:HD11	2.45	0.46
1:A:378:VAL:CB	1:A:456:VAL:HG22	2.46	0.46
1:A:643:HIS:HA	2:A:802:HEM:O1D	2.16	0.46
1:A:73:GLN:HA	1:A:213:PHE:CD2	2.51	0.46
1:A:498:MET:O	1:A:501:PHE:HB3	2.16	0.46
1:A:70:ILE:HD13	1:A:493:ASP:HB2	1.98	0.46
1:A:510:TRP:CZ2	1:A:514:ILE:HD11	2.51	0.46
7:A:810:LOP:H181	7:A:810:LOP:H332	1.98	0.46
1:A:279:MET:HA	1:A:537:SER:OG	2.15	0.46
1:A:154:LEU:CD1	1:A:156:LEU:HD22	2.45	0.46
7:A:809:LOP:C6	7:A:809:LOP:O6	2.64	0.46
1:A:239:TYR:CZ	1:A:241:ASP:HB2	2.51	0.46
1:A:170:TYR:O	1:A:174:VAL:HG23	2.16	0.46
1:A:298:LEU:HD13	1:A:299:THR:H	1.80	0.46
1:A:292:ASP:OD2	1:A:295:ARG:HD2	2.17	0.45
1:A:54:GLU:HA	1:A:64:MET:O	2.16	0.45
1:A:217:THR:HA	1:A:220:LEU:HD13	1.96	0.45
1:A:692:MET:HE1	1:A:748:ILE:HG23	1.97	0.45
1:A:463:GLU:OE2	1:A:471:HIS:HD2	1.99	0.45
1:A:225:ARG:HB2	1:A:228:ASP:CB	2.47	0.45
1:A:81:LEU:HD21	1:A:175:PHE:CE1	2.52	0.45
1:A:111:GLN:CA	1:A:134:ILE:HD11	2.47	0.45
1:A:395:TRP:C	1:A:398:VAL:HG12	2.37	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:THR:O	1:A:103:LEU:HB2	2.16	0.45
1:A:127:THR:HG22	1:A:128:ASP:N	2.32	0.45
1:A:549:LEU:HD13	1:A:549:LEU:O	2.17	0.45
1:A:126:LEU:HB3	1:A:130:GLU:CG	2.44	0.44
1:A:679:GLU:H	1:A:679:GLU:HG3	1.52	0.44
1:A:435:ARG:NH1	1:A:438:GLN:OE1	2.51	0.44
1:A:600:ARG:HA	1:A:600:ARG:HD3	1.55	0.44
1:A:28:PHE:CZ	1:A:32:ILE:HG13	2.52	0.44
1:A:526:LEU:O	1:A:530:LEU:HD13	2.18	0.44
1:A:506:ILE:O	1:A:510:TRP:HB3	2.18	0.44
1:A:94:MET:CE	1:A:329:TYR:HB3	2.46	0.44
1:A:134:ILE:CG1	1:A:135:ARG:N	2.81	0.44
1:A:423:LEU:CD2	1:A:436:ILE:HG12	2.48	0.44
1:A:306:GLY:HA3	1:A:675:ILE:HD13	2.00	0.44
1:A:363:ILE:CG2	1:A:515:PHE:CZ	2.99	0.44
1:A:84:TYR:C	1:A:92:SER:HB2	2.37	0.44
1:A:56:ARG:HD3	1:A:62:VAL:HG12	1.99	0.44
1:A:522:VAL:O	1:A:526:LEU:HD13	2.18	0.44
1:A:112:ASP:O	1:A:115:ALA:HB3	2.16	0.44
1:A:706:LEU:HB3	1:A:707:PRO:CD	2.47	0.44
1:A:55:VAL:HG22	1:A:64:MET:CB	2.46	0.44
1:A:64:MET:HE1	1:A:212:ASP:CB	2.48	0.44
1:A:433:LEU:HD13	1:A:438:GLN:HG3	1.98	0.44
1:A:339:ILE:HG22	1:A:340:ASN:H	1.82	0.44
1:A:236:TRP:CG	1:A:237:PRO:HA	2.53	0.44
1:A:71:GLY:HA3	1:A:209:GLN:OE1	2.18	0.44
1:A:440:ILE:HD12	1:A:440:ILE:C	2.38	0.44
1:A:731:GLN:NE2	8:A:1006:HOH:O	2.51	0.44
1:A:56:ARG:CB	1:A:61:GLU:O	2.65	0.43
1:A:744:VAL:HB	1:A:745:PRO:HD3	1.99	0.43
1:A:524:GLY:O	1:A:528:VAL:HG23	2.18	0.43
1:A:590:LEU:HD23	1:A:590:LEU:C	2.38	0.43
1:A:646:PHE:O	1:A:649:PRO:HD2	2.17	0.43
1:A:442:VAL:HG23	1:A:443:VAL:N	2.32	0.43
1:A:294:ARG:NH2	1:A:678:PRO:HB2	2.33	0.43
1:A:549:LEU:C	1:A:549:LEU:HD13	2.39	0.43
1:A:131:LYS:HA	1:A:134:ILE:HG23	2.00	0.43
1:A:596:TYR:CD1	7:A:810:LOP:H81	2.54	0.43
1:A:762:LYS:O	1:A:762:LYS:HG3	2.17	0.43
1:A:293:LEU:HA	1:A:296:GLN:CD	2.39	0.43
1:A:51:ARG:CD	1:A:495:ASN:ND2	2.80	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:810:LOP:H112	7:A:810:LOP:C27	2.40	0.43
1:A:298:LEU:HD11	1:A:303:VAL:HG13	2.01	0.43
1:A:44:ILE:CG1	1:A:567:PRO:HD2	2.46	0.42
1:A:181:TRP:O	1:A:181:TRP:CD1	2.72	0.42
1:A:64:MET:HE1	1:A:212:ASP:CA	2.49	0.42
1:A:750:LEU:O	1:A:753:VAL:CG1	2.67	0.42
1:A:578:SER:O	1:A:581:GLU:HB2	2.19	0.42
1:A:47:GLU:OE2	5:A:807:BOG:H62	2.19	0.42
1:A:433:LEU:HD13	1:A:438:GLN:HG2	2.01	0.42
1:A:144:LYS:HA	1:A:144:LYS:HZ3	1.83	0.42
1:A:773:GLY:C	1:A:775:GLY:H	2.21	0.42
1:A:685:TRP:HE3	1:A:685:TRP:HA	1.85	0.42
1:A:143:ARG:HD2	1:A:243:GLY:HA3	2.00	0.42
1:A:86:THR:HG22	1:A:91:GLY:C	2.40	0.42
1:A:258:VAL:O	1:A:262:ILE:HG12	2.19	0.42
1:A:331:THR:HG21	1:A:740:LEU:CD1	2.49	0.42
7:A:810:LOP:C10	7:A:810:LOP:H251	2.50	0.42
1:A:646:PHE:HA	1:A:649:PRO:HD2	2.01	0.42
1:A:93:TYR:CE2	1:A:649:PRO:CG	3.02	0.42
1:A:347:PRO:CD	1:A:350:ILE:HD12	2.48	0.42
1:A:367:TRP:CH2	1:A:519:ALA:HB1	2.55	0.42
1:A:336:PHE:O	1:A:337:PHE:HB2	2.20	0.42
1:A:588:LEU:HD12	1:A:588:LEU:HA	1.87	0.41
1:A:691:TRP:CE2	7:A:810:LOP:H282	2.54	0.41
1:A:62:VAL:C	1:A:63:LEU:HD13	2.41	0.41
1:A:370:MET:CE	1:A:526:LEU:HD21	2.49	0.41
1:A:462:ARG:HG2	1:A:462:ARG:NH1	2.35	0.41
1:A:48:MET:SD	1:A:498:MET:HB2	2.61	0.41
1:A:176:THR:O	1:A:186:GLY:N	2.53	0.41
1:A:341:TRP:HE3	1:A:345:ILE:HG21	1.85	0.41
1:A:321:MET:HE2	1:A:750:LEU:HD21	2.01	0.41
1:A:50:PRO:O	1:A:52:PRO:HD3	2.21	0.41
1:A:56:ARG:HB3	1:A:62:VAL:CA	2.36	0.41
1:A:198:ARG:NH2	1:A:204:SER:O	2.52	0.41
1:A:56:ARG:HD2	1:A:62:VAL:HG12	2.03	0.41
1:A:400:LEU:HG	1:A:440:ILE:CD1	2.50	0.41
1:A:113:TYR:HB2	1:A:162:TYR:HD2	1.83	0.41
1:A:187:LEU:H	1:A:187:LEU:CD1	2.34	0.41
1:A:208:GLN:O	1:A:212:ASP:OD1	2.38	0.41
1:A:127:THR:N	1:A:130:GLU:HB3	2.35	0.41
1:A:56:ARG:CB	1:A:62:VAL:HA	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:A:810:LOP:O7	7:A:810:LOP:C9	2.59	0.41
1:A:334:ASP:HA	1:A:343:TYR:CE2	2.55	0.41
1:A:750:LEU:O	1:A:753:VAL:HG13	2.20	0.41
1:A:391:ASP:O	1:A:394:PHE:HB3	2.20	0.41
1:A:654:ALA:O	1:A:658:GLY:HA3	2.21	0.41
1:A:675:ILE:C	1:A:768:ARG:HD3	2.42	0.41
2:A:801:HEM:HBA2	2:A:801:HEM:HHA	2.03	0.41
1:A:81:LEU:HD21	1:A:175:PHE:HE1	1.85	0.40
1:A:309:PHE:HA	1:A:312:VAL:CG1	2.50	0.40
1:A:310:VAL:HG21	1:A:764:LEU:HD21	2.03	0.40
1:A:417:GLY:C	1:A:419:GLU:H	2.23	0.40
1:A:230:ILE:HD12	1:A:234:ASN:HA	2.03	0.40
1:A:239:TYR:CE1	1:A:241:ASP:HB2	2.57	0.40
1:A:393:LEU:HG	1:A:447:LEU:HD13	2.03	0.40
1:A:326:LEU:HD11	1:A:352:LYS:HA	2.04	0.40
1:A:63:LEU:HD13	1:A:63:LEU:N	2.36	0.40
1:A:596:TYR:CD1	7:A:810:LOP:C8	3.04	0.40
1:A:761:ILE:O	1:A:764:LEU:CD2	2.69	0.40
1:A:761:ILE:C	1:A:763:ALA:H	2.25	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	750/800 (94%)	695 (93%)	49 (6%)	6 (1%)	24 41

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	ASP
1	A	157	THR

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Mol	Chain	Res	Type
1	A	199	ALA
1	A	204	SER
1	A	194	PRO
1	A	603	GLY

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	631/675 (94%)	549 (87%)	82 (13%)	5 9

All (82) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	26	LEU
1	A	37	LEU
1	A	51	ARG
1	A	53	LYS
1	A	55	VAL
1	A	63	LEU
1	A	68	THR
1	A	81	LEU
1	A	87	VAL
1	A	96	PRO
1	A	103	LEU
1	A	105	VAL
1	A	126	LEU
1	A	134	ILE
1	A	135	ARG
1	A	148	ASN
1	A	151	THR
1	A	154	LEU
1	A	156	LEU
1	A	164	LEU
1	A	166	LYS
1	A	187	LEU

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Mol	Chain	Res	Type
1	A	198	ARG
1	A	207	ILE
1	A	210	ILE
1	A	220	LEU
1	A	231	THR
1	A	251	VAL
1	A	287	LYS
1	A	293	LEU
1	A	295	ARG
1	A	298	LEU
1	A	308	TYR
1	A	361	PHE
1	A	382	GLU
1	A	391	ASP
1	A	393	LEU
1	A	397	LEU
1	A	400	LEU
1	A	433	LEU
1	A	435	ARG
1	A	436	ILE
1	A	440	ILE
1	A	441	LEU
1	A	446	LEU
1	A	447	LEU
1	A	462	ARG
1	A	469	LEU
1	A	478	ILE
1	A	483	PHE
1	A	497	THR
1	A	512	GLU
1	A	527	LEU
1	A	530	LEU
1	A	545	GLN
1	A	550	LEU
1	A	559	HIS
1	A	587	LEU
1	A	588	LEU
1	A	590	LEU
1	A	591	GLU
1	A	615	LEU
1	A	618	THR
1	A	622	ASN

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Mol	Chain	Res	Type
1	A	635	LEU
1	A	656	MET
1	A	663	PHE
1	A	672	LEU
1	A	673	ARG
1	A	679	GLU
1	A	685	TRP
1	A	706	LEU
1	A	711	LEU
1	A	738	LEU
1	A	739	LEU
1	A	740	LEU
1	A	742	ARG
1	A	750	LEU
1	A	756	LEU
1	A	757	LEU
1	A	768	ARG
1	A	777	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	77	GLN
1	A	148	ASN
1	A	340	ASN
1	A	381	GLN
1	A	471	HIS
1	A	529	GLN
1	A	595	GLN
1	A	622	ASN
1	A	682	ASN
1	A	731	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 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
2	HEM	A	801	1,4	30,50,50	2.66	11 (36%)	24,82,82	2.57	9 (37%)
2	HEM	A	802	1,8,4	30,50,50	2.59	10 (33%)	24,82,82	2.21	8 (33%)
5	BOG	A	805	-	20,20,20	0.89	2 (10%)	25,25,25	0.89	1 (4%)
5	BOG	A	806	-	20,20,20	0.98	2 (10%)	25,25,25	0.93	1 (4%)
5	BOG	A	807	-	20,20,20	0.87	2 (10%)	25,25,25	0.97	1 (4%)
6	EPE	A	808	-	14,15,15	1.05	1 (7%)	18,20,20	2.01	3 (16%)
7	LOP	A	809	-	43,44,44	0.78	2 (4%)	44,49,49	1.27	3 (6%)
7	LOP	A	810	-	43,44,44	0.79	2 (4%)	44,49,49	1.24	4 (9%)

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	HEM	A	801	1,4	-	0/10/54/54	0/0/8/8
2	HEM	A	802	1,8,4	-	0/10/54/54	0/0/8/8
5	BOG	A	805	-	-	0/11/31/31	0/1/1/1
5	BOG	A	806	-	-	0/11/31/31	0/1/1/1
5	BOG	A	807	-	-	0/11/31/31	0/1/1/1
6	EPE	A	808	-	-	0/9/19/19	0/1/1/1
7	LOP	A	809	-	-	0/48/48/48	0/0/0/0
7	LOP	A	810	-	-	0/48/48/48	0/0/0/0

All (32) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	HEM	C3B-C4B	-6.81	1.45	1.51
2	A	801	HEM	C3D-C4D	-5.83	1.44	1.51
2	A	802	HEM	C3B-C4B	-5.75	1.46	1.51
2	A	802	HEM	C3C-CAC	-5.67	1.40	1.51
2	A	802	HEM	C2D-C3D	-5.18	1.39	1.54
2	A	801	HEM	C2D-C3D	-5.14	1.39	1.54
2	A	801	HEM	C3C-CAC	-4.80	1.42	1.51
2	A	802	HEM	C3D-C4D	-3.87	1.46	1.51
2	A	801	HEM	C2C-C1C	-3.63	1.45	1.52
2	A	802	HEM	C2C-C1C	-3.57	1.45	1.52
2	A	801	HEM	C3B-CAB	-3.07	1.45	1.51
2	A	802	HEM	C3B-CAB	-2.94	1.45	1.51
7	A	810	LOP	C16-C15	-2.52	1.39	1.50
7	A	809	LOP	C13-C14	-2.47	1.39	1.50
7	A	810	LOP	C13-C14	-2.46	1.39	1.50
7	A	809	LOP	C16-C15	-2.43	1.39	1.50
2	A	802	HEM	C2B-C1B	-2.21	1.44	1.51
2	A	801	HEM	C2D-C1D	-2.03	1.45	1.51
2	A	801	HEM	C4C-NC	2.00	1.38	1.36
5	A	807	BOG	O5-C1	2.09	1.47	1.41
5	A	806	BOG	O5-C1	2.19	1.47	1.41
5	A	805	BOG	O1-C1	2.24	1.44	1.40
2	A	802	HEM	CBB-CAB	2.25	1.42	1.29
5	A	805	BOG	O5-C1	2.27	1.47	1.41
2	A	801	HEM	CBB-CAB	2.27	1.42	1.29
5	A	807	BOG	O1-C1	2.34	1.44	1.40
2	A	802	HEM	CHD-C4C	2.38	1.42	1.36
2	A	801	HEM	CHD-C4C	2.49	1.42	1.36
6	A	808	EPE	O3S-S	2.77	1.53	1.46
5	A	806	BOG	O1-C1	2.87	1.45	1.40
2	A	801	HEM	FE-NC	4.20	2.12	1.95
2	A	802	HEM	FE-NC	6.01	2.19	1.95

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	809	LOP	C4-O5-C6	-4.22	107.76	117.89
5	A	807	BOG	C1'-O1-C1	-2.84	108.98	113.94
7	A	809	LOP	C5-O6-C24	-2.79	109.04	116.85
6	A	808	EPE	O3S-S-O2S	-2.63	105.49	111.61
5	A	806	BOG	C1'-O1-C1	-2.56	109.46	113.94
6	A	808	EPE	O3S-S-O1S	-2.42	105.98	111.61
7	A	810	LOP	O6-C5-C4	-2.29	102.52	108.69

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	805	BOG	C1'-O1-C1	-2.10	110.27	113.94
7	A	810	LOP	C18-C17-C16	-2.09	105.71	113.86
2	A	802	HEM	C2D-C3D-C4D	2.13	105.12	101.50
2	A	802	HEM	CBD-CAD-C3D	2.26	120.14	113.55
2	A	801	HEM	C2D-C3D-C4D	2.42	105.60	101.50
7	A	810	LOP	O6-C24-C25	2.42	119.28	111.90
2	A	802	HEM	CMD-C2D-C3D	2.57	125.71	114.35
2	A	801	HEM	CMD-C2D-C3D	2.68	126.19	114.35
2	A	802	HEM	C3B-CAB-CBB	2.94	128.97	124.46
2	A	801	HEM	C3B-CAB-CBB	3.03	129.11	124.46
2	A	801	HEM	CAA-C2A-C1A	3.76	131.09	127.01
2	A	801	HEM	CAD-C3D-C4D	3.91	126.25	112.47
7	A	809	LOP	O5-C6-C7	3.93	120.07	111.53
7	A	810	LOP	O5-C6-C7	3.97	120.15	111.53
2	A	801	HEM	CMC-C2C-C3C	4.32	127.31	116.53
2	A	802	HEM	CMC-C2C-C3C	4.38	127.46	116.53
2	A	802	HEM	CAD-C3D-C4D	4.52	128.40	112.47
2	A	801	HEM	CMB-C2B-C3B	4.58	127.96	116.53
2	A	802	HEM	CAD-C3D-C2D	4.62	126.49	113.22
2	A	802	HEM	CMB-C2B-C3B	4.87	128.69	116.53
2	A	801	HEM	CAD-C3D-C2D	5.19	128.15	113.22
2	A	801	HEM	CBA-CAA-C2A	5.24	121.92	112.53
6	A	808	EPE	O1S-S-C10	6.90	112.79	106.91

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 38 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	801	HEM	1	0
2	A	802	HEM	2	0
5	A	806	BOG	1	0
5	A	807	BOG	3	0
7	A	809	LOP	11	0
7	A	810	LOP	20	0

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	754/800 (94%)	0.54	80 (10%) 8 8	34, 62, 93, 104	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	154	LEU	7.2
1	A	113	TYR	6.3
1	A	394	PHE	5.7
1	A	134	ILE	5.5
1	A	416	LEU	5.1
1	A	130	GLU	4.8
1	A	414	GLY	4.6
1	A	158	ASP	4.4
1	A	513	GLY	4.3
1	A	514	ILE	4.3
1	A	155	VAL	4.2
1	A	163	GLY	4.0
1	A	199	ALA	4.0
1	A	776	GLU	3.8
1	A	59	SER	3.8
1	A	139	ILE	3.8
1	A	300	PRO	3.7
1	A	150	VAL	3.6
1	A	115	ALA	3.4
1	A	777	GLU	3.4
1	A	126	LEU	3.4
1	A	192	ASP	3.4
1	A	198	ARG	3.4
1	A	161	VAL	3.3
1	A	743	ALA	3.3
1	A	162	TYR	3.3
1	A	773	GLY	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	127	THR	3.2
1	A	159	ALA	3.2
1	A	141	GLU	3.2
1	A	64	MET	3.1
1	A	273	TYR	3.1
1	A	137	GLN	3.0
1	A	112	ASP	3.0
1	A	21	PHE	2.9
1	A	17	THR	2.8
1	A	194	PRO	2.8
1	A	303	VAL	2.8
1	A	193	MET	2.7
1	A	421	PHE	2.7
1	A	109	GLY	2.7
1	A	114	LYS	2.7
1	A	392	LEU	2.7
1	A	418	ASN	2.7
1	A	135	ARG	2.6
1	A	423	LEU	2.6
1	A	160	GLN	2.5
1	A	153	VAL	2.5
1	A	388	LEU	2.5
1	A	771	THR	2.5
1	A	390	VAL	2.4
1	A	60	GLY	2.4
1	A	290	VAL	2.4
1	A	660	TYR	2.4
1	A	536	LYS	2.4
1	A	391	ASP	2.4
1	A	52	PRO	2.3
1	A	691	TRP	2.3
1	A	195	LYS	2.3
1	A	31	LEU	2.3
1	A	258	VAL	2.2
1	A	772	HIS	2.2
1	A	632	LEU	2.2
1	A	143	ARG	2.2
1	A	395	TRP	2.2
1	A	39	VAL	2.1
1	A	458	ARG	2.1
1	A	125	ASP	2.1
1	A	169	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	740	LEU	2.1
1	A	630	GLY	2.1
1	A	415	TYR	2.1
1	A	53	LYS	2.1
1	A	461	LYS	2.1
1	A	106	TYR	2.1
1	A	308	TYR	2.1
1	A	744	VAL	2.1
1	A	147	TYR	2.1
1	A	18	THR	2.0
1	A	666	ALA	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
6	EPE	A	808	15/15	0.51	0.46	3.82	88,93,109,109	0
5	BOG	A	806	20/20	0.84	0.37	3.81	76,87,90,91	0
7	LOP	A	809	45/45	0.71	0.36	3.45	73,85,101,104	0
7	LOP	A	810	45/45	0.74	0.34	2.86	59,70,102,104	0
5	BOG	A	805	20/20	0.73	0.24	1.98	75,89,93,95	0
4	CA	A	804	1/1	0.98	0.30	1.71	49,49,49,49	0
5	BOG	A	807	20/20	0.77	0.26	1.20	73,85,88,90	0
2	HEM	A	801	43/43	0.95	0.22	0.85	38,46,52,54	0
2	HEM	A	802	43/43	0.97	0.20	-0.36	29,38,50,54	0
3	ZN	A	803	1/1	0.99	0.15	-	55,55,55,55	0

6.5 Other polymers ⓘ

There are no such residues in this entry.