



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 07:31 PM GMT

PDB ID : 1FZH
Title : METHANE MONOOXYGENASE HYDROXYLASE, FORM II PRESSURIZED WITH XENON GAS
Authors : Whittington, D.A.; Rosenzweig, A.C.; Frederick, C.A.; Lippard, S.J.
Deposited on : 2000-10-03
Resolution : 2.60 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

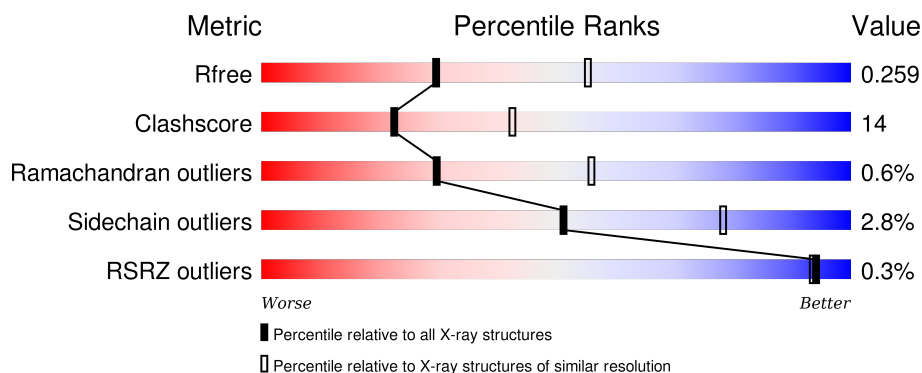
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	527	 68% 28% . .
1	B	527	 69% 27% . .
2	C	389	 80% 19% .
2	D	389	 68% 31% .
3	E	170	 73% 23% . .

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Mol	Chain	Length	Quality of chain
3	F	170	<div> <div></div> <div>%</div> <div>58%</div> <div>39%</div> <div>..</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
6	XE	A	9006	-	-	X	-
6	XE	A	9009	-	-	-	X
6	XE	B	9010	-	-	X	-
6	XE	B	9011	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 18070 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 METHANE MONOOXYGENASE COMPONENT A, ALPHA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	511	Total	C	N	O	S	0	0	0
			4185	2677	721	769	18			
1	B	510	Total	C	N	O	S	0	0	0
			4177	2673	719	767	18			

- Molecule 2 is a protein called METHANE MONOOXYGENASE COMPONENT A, BETA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	388	Total	C	N	O	S	0	0	0
			3193	2054	551	580	8			
2	D	388	Total	C	N	O	S	0	0	0
			3187	2051	548	580	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	370	ARG	ALA	CONFLICT	UNP P18798
D	370	ARG	ALA	CONFLICT	UNP P18798

- Molecule 3 is a protein called METHANE MONOOXYGENASE COMPONENT A, GAMMA CHAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	165	Total	C	N	O	S	0	0	0
			1362	864	245	248	5			
3	F	167	Total	C	N	O	S	0	0	0
			1375	872	247	251	5			

- Molecule 4 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	2	Total	Fe	0	0
			2	2		
4	A	2	Total	Fe	0	0
			2	2		

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	1	Total	Ca	0	0
			1	1		
5	A	1	Total	Ca	0	0
			1	1		
5	C	2	Total	Ca	0	0
			2	2		

- Molecule 6 is XENON (three-letter code: XE) (formula: Xe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	B	5	Total	Xe	0	0
			5	5		
6	A	6	Total	Xe	0	0
			6	6		

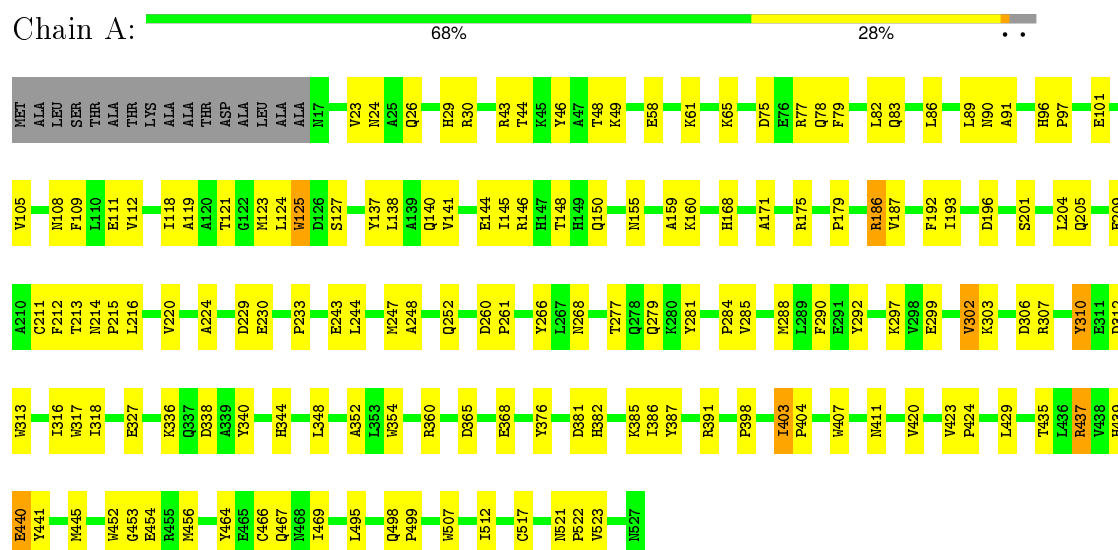
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	133	Total	O	0	0
			133	133		
7	B	134	Total	O	0	0
			134	134		
7	C	154	Total	O	0	0
			154	154		
7	D	67	Total	O	0	0
			67	67		
7	E	63	Total	O	0	0
			63	63		
7	F	21	Total	O	0	0
			21	21		

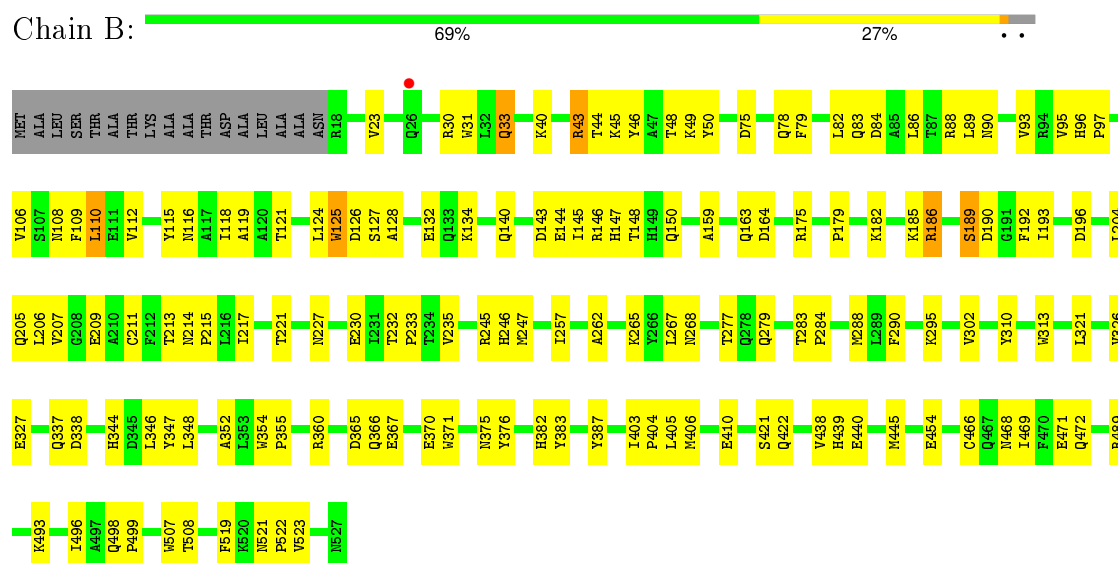
3 Residue-property plots

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.

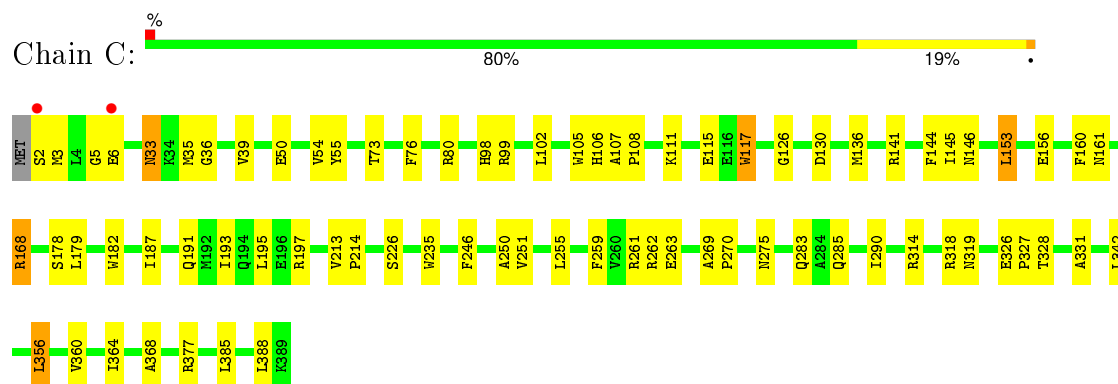
• Molecule 1: METHANE MONOOXYGENASE COMPONENT A, ALPHA CHAIN



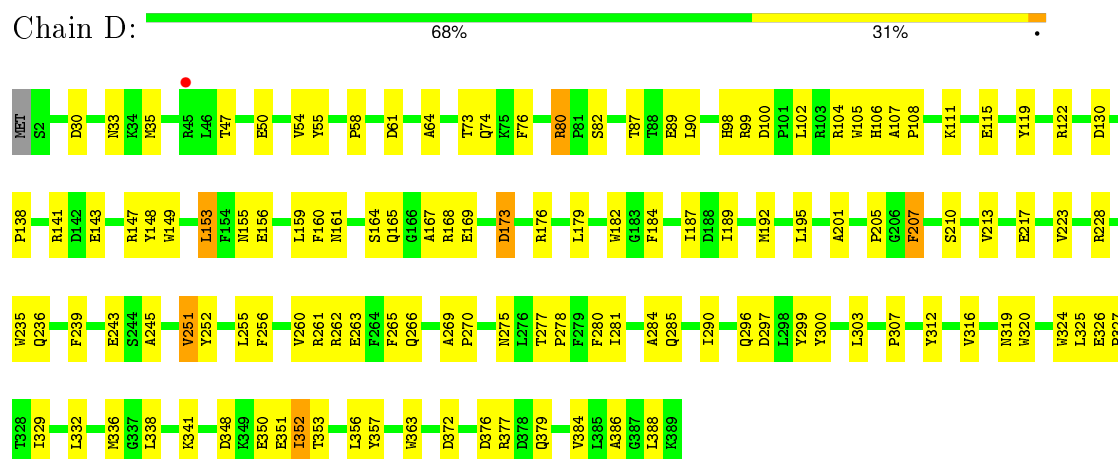
• Molecule 1: METHANE MONOOXYGENASE COMPONENT A, ALPHA CHAIN



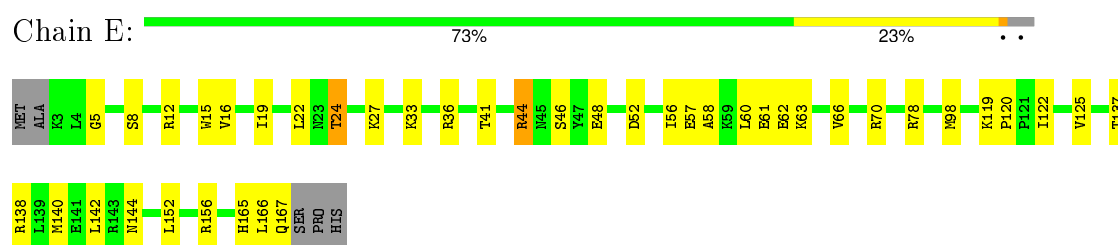
• Molecule 2: METHANE MONOOXYGENASE COMPONENT A, BETA CHAIN



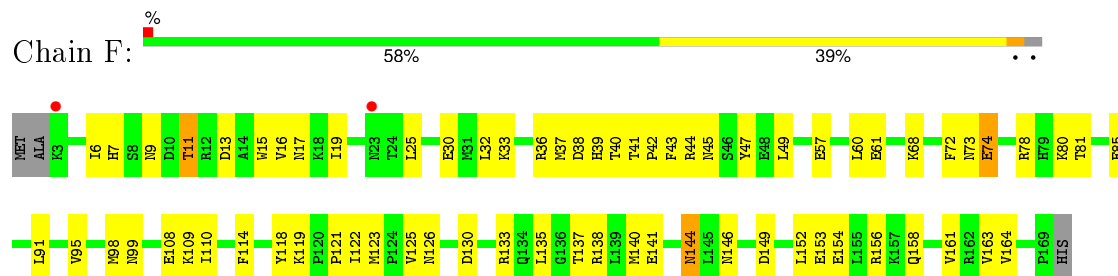
• Molecule 2: METHANE MONOOXYGENASE COMPONENT A, BETA CHAIN



• Molecule 3: METHANE MONOOXYGENASE COMPONENT A, GAMMA CHAIN



• Molecule 3: METHANE MONOOXYGENASE COMPONENT A, GAMMA CHAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.27Å 174.62Å 223.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.00 – 2.60 28.96 – 2.60	Depositor EDS
% Data completeness (in resolution range)	86.3 (29.00-2.60) 86.4 (28.96-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.53 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.206 , 0.260 0.205 , 0.259	Depositor DCC
R_{free} test set	2958 reflections (4.03%)	DCC
Wilson B-factor (Å ²)	30.2	Xtriage
Anisotropy	0.072	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 43.0	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 81726 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	18070	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.43% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CA, FE, XE

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	0.38	0/4310	0.59	0/5853
1	B	0.38	0/4302	0.57	0/5842
2	C	0.42	0/3289	0.59	0/4464
2	D	0.38	0/3283	0.57	0/4457
3	E	0.40	0/1390	0.61	0/1872
3	F	0.34	0/1404	0.54	0/1892
All	All	0.39	0/17978	0.58	0/24380

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4185	0	3981	123	0
1	B	4177	0	3975	139	0
2	C	3193	0	3042	73	0
2	D	3187	0	3031	106	0
3	E	1362	0	1358	27	0
3	F	1375	0	1370	55	0
4	A	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	2	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	C	2	0	0	0	0
6	A	6	0	0	5	0
6	B	5	0	0	5	0
7	A	133	0	0	7	0
7	B	134	0	0	4	0
7	C	154	0	0	5	0
7	D	67	0	0	3	0
7	E	63	0	0	1	0
7	F	21	0	0	0	0
All	All	18070	0	16757	468	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 14.

All (468) 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:44:THR:HG22	1:B:46:TYR:H	1.24	0.96
1:A:78:GLN:HE22	1:A:150:GLN:HE21	1.17	0.93
3:F:41:THR:HG22	3:F:43:PHE:H	1.33	0.93
1:A:352:ALA:HA	1:A:404:PRO:HB2	1.51	0.93
2:C:146:ASN:HD21	2:C:197:ARG:HH21	1.17	0.93
1:A:44:THR:HG22	1:A:46:TYR:H	1.38	0.89
1:B:352:ALA:HA	1:B:404:PRO:HB2	1.56	0.88
1:A:179:PRO:HB3	1:A:469:ILE:HD13	1.56	0.86
1:A:381:ASP:HA	1:A:385:LYS:HE2	1.58	0.84
1:A:214:ASN:HB3	1:A:215:PRO:HD3	1.61	0.83
2:C:261:ARG:HE	2:C:285:GLN:HE22	1.24	0.82
3:E:24:THR:HG22	3:E:27:LYS:H	1.44	0.81
2:D:100:ASP:OD1	2:D:104:ARG:HD3	1.81	0.79
2:D:261:ARG:HE	2:D:285:GLN:HE22	1.30	0.79
1:B:33:GLN:HE21	1:B:33:GLN:HA	1.46	0.78
1:A:23:VAL:HB	2:C:195:LEU:HD11	1.64	0.77
2:D:201:ALA:HA	2:D:207:PHE:HB3	1.64	0.77
2:C:270:PRO:HB3	2:D:270:PRO:HB3	1.67	0.76
1:A:75:ASP:OD2	1:A:146:ARG:NH1	2.20	0.75
3:F:9:ASN:OD1	3:F:11:THR:HG23	1.86	0.74
2:D:138:PRO:HA	2:D:141:ARG:NH1	2.02	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:109:PHE:O	1:B:112:VAL:HG12	1.88	0.73
1:A:193:ILE:HD12	2:C:168:ARG:HH21	1.53	0.73
3:F:41:THR:O	3:F:44:ARG:HD2	1.89	0.72
1:B:78:GLN:HE21	1:B:235:VAL:HA	1.54	0.72
2:D:122:ARG:HD3	7:D:433:HOH:O	1.89	0.72
2:C:364:ILE:HA	2:C:368:ALA:HB3	1.73	0.71
2:D:138:PRO:HA	2:D:141:ARG:HH12	1.56	0.70
3:E:46:SER:OG	3:E:48:GLU:HG2	1.91	0.70
2:C:146:ASN:ND2	2:C:197:ARG:HH21	1.89	0.70
2:C:107:ALA:HB3	2:C:108:PRO:HD3	1.74	0.70
1:B:206:LEU:HD11	1:B:321:LEU:HD11	1.73	0.69
1:B:33:GLN:HE22	1:B:132:GLU:H	1.38	0.69
1:A:148:THR:HG21	6:A:9006:XE:XE	2.71	0.69
2:D:376:ASP:OD2	2:D:379:GLN:HG2	1.93	0.69
2:D:312:TYR:O	2:D:316:VAL:HG23	1.93	0.68
1:A:243:GLU:O	1:A:247:MET:HG2	1.92	0.68
1:B:108:ASN:HD21	1:B:175:ARG:HH11	1.42	0.68
2:C:326:GLU:HB3	2:C:327:PRO:HD3	1.76	0.68
2:D:76:PHE:HB2	2:D:80:ARG:HB3	1.76	0.68
3:F:40:THR:O	3:F:41:THR:HB	1.93	0.67
1:B:211:CYS:HB2	1:B:313:TRP:CD1	2.30	0.67
2:C:102:LEU:CD1	2:C:290:ILE:HG23	2.26	0.66
2:D:102:LEU:CD1	2:D:290:ILE:HG23	2.24	0.66
3:E:22:LEU:O	3:E:63:LYS:HE2	1.95	0.66
3:E:12:ARG:O	3:E:16:VAL:HG23	1.95	0.66
1:A:146:ARG:HB2	2:C:106:HIS:CE1	2.29	0.66
1:A:429:LEU:HG	1:A:429:LEU:O	1.96	0.65
1:B:288:MET:HE3	1:B:346:LEU:HB3	1.78	0.65
1:B:106:VAL:O	1:B:110:LEU:HB2	1.97	0.65
1:A:381:ASP:O	1:A:385:LYS:HD2	1.95	0.65
1:A:49:LYS:HD3	3:E:144:ASN:HD22	1.60	0.65
3:E:57:GLU:O	3:E:61:GLU:HG3	1.96	0.65
1:A:317:TRP:HD1	1:A:318:ILE:HD12	1.61	0.65
2:D:256:PHE:HA	2:D:332:LEU:HD21	1.79	0.64
1:B:472:GLN:OE1	3:F:6:ILE:HG23	1.97	0.64
2:D:90:LEU:HD13	2:D:303:LEU:HD13	1.80	0.64
3:F:130:ASP:OD1	3:F:133:ARG:NH1	2.29	0.64
2:D:47:THR:OG1	2:D:50:GLU:HG3	1.97	0.64
1:A:23:VAL:HB	2:C:195:LEU:CD1	2.27	0.64
2:D:338:LEU:HD12	2:D:341:LYS:HG3	1.80	0.64
3:E:19:ILE:HG12	3:E:60:LEU:HD13	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:PHE:CE2	6:B:9005:XE:XE	3.29	0.64
2:D:98:HIS:HD2	2:D:297:ASP:OD1	1.81	0.63
1:B:82:LEU:HD23	1:B:86:LEU:HD12	1.80	0.63
1:B:360:ARG:HG2	1:B:498:GLN:HB2	1.80	0.63
1:B:214:ASN:HB3	1:B:215:PRO:HD3	1.79	0.63
1:B:186:ARG:HD3	1:B:186:ARG:O	1.98	0.63
2:D:261:ARG:HE	2:D:285:GLN:NE2	1.96	0.63
3:F:32:LEU:HD12	3:F:60:LEU:HD23	1.81	0.63
2:D:324:TRP:O	2:D:327:PRO:HD2	1.98	0.63
2:C:314:ARG:O	2:C:318:ARG:HB2	1.99	0.62
2:C:6:GLU:HG3	7:C:5079:HOH:O	1.99	0.62
1:A:365:ASP:OD2	1:A:368:GLU:HG3	1.98	0.62
1:A:44:THR:CG2	1:A:46:TYR:H	2.11	0.62
1:B:44:THR:OG1	1:B:127:SER:HA	1.99	0.62
1:B:78:GLN:HE22	1:B:150:GLN:HE21	1.48	0.62
3:E:66:VAL:HG12	3:E:70:ARG:HH21	1.65	0.62
3:E:41:THR:O	3:E:44:ARG:HD2	1.99	0.61
1:B:128:ALA:O	1:B:134:LYS:HE2	2.00	0.61
1:A:121:THR:HG21	1:A:140:GLN:HG2	1.81	0.61
1:B:40:LYS:HG3	7:B:9107:HOH:O	2.00	0.61
1:B:108:ASN:HD21	1:B:175:ARG:HD3	1.65	0.61
1:A:310:TYR:CZ	1:A:336:LYS:HD2	2.34	0.61
1:B:186:ARG:HD3	1:B:186:ARG:C	2.21	0.60
3:F:13:ASP:O	3:F:16:VAL:HG22	2.02	0.60
1:B:159:ALA:O	2:D:33:ASN:HB2	2.02	0.60
2:C:2:SER:HB2	7:C:5113:HOH:O	2.02	0.60
2:D:102:LEU:HD12	2:D:290:ILE:HG23	1.82	0.60
1:B:406:MET:O	1:B:410:GLU:HG3	2.01	0.60
1:B:438:VAL:HB	3:F:164:VAL:HG23	1.84	0.60
2:C:161:ASN:HB3	2:C:235:TRP:CE2	2.37	0.59
2:D:213:VAL:HG23	7:D:454:HOH:O	2.01	0.59
2:D:82:SER:O	2:D:168:ARG:NH2	2.34	0.59
1:B:186:ARG:CZ	1:B:277:THR:HG23	2.33	0.59
2:D:325:LEU:O	2:D:329:ILE:HG13	2.03	0.59
1:B:48:THR:O	3:F:137:THR:HG23	2.01	0.59
2:D:107:ALA:HB3	2:D:108:PRO:HD3	1.84	0.59
2:C:33:ASN:HD22	2:C:33:ASN:H	1.50	0.59
1:A:307:ARG:HG2	1:A:312:ASP:OD2	2.03	0.58
1:B:262:ALA:HA	1:B:265:LYS:HE2	1.83	0.58
2:C:213:VAL:HB	2:C:214:PRO:HD3	1.86	0.58
1:A:105:VAL:O	1:A:109:PHE:HB2	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:LYS:HA	2:C:33:ASN:HB2	1.85	0.58
1:A:290:PHE:CE2	6:A:9004:XE:XE	3.35	0.58
1:B:179:PRO:HB3	1:B:469:ILE:HD13	1.86	0.58
2:D:165:GLN:NE2	2:D:239:PHE:O	2.37	0.58
1:A:204:LEU:HG	1:A:205:GLN:HG3	1.86	0.58
1:A:78:GLN:NE2	1:A:150:GLN:HE21	1.97	0.58
2:C:146:ASN:HD22	2:C:197:ARG:HE	1.52	0.58
2:C:144:PHE:CZ	2:C:342:LEU:HD23	2.38	0.58
2:D:153:LEU:HD12	2:D:153:LEU:C	2.24	0.58
1:B:163:GLN:HG2	7:B:9100:HOH:O	2.04	0.57
1:A:517:CYS:HB3	6:A:9008:XE:XE	2.82	0.57
2:D:336:MET:CE	2:D:356:LEU:HD11	2.34	0.57
2:D:184:PHE:O	2:D:187:ILE:HG22	2.05	0.57
2:C:33:ASN:HD22	2:C:33:ASN:N	2.03	0.56
1:A:209:GLU:HA	1:A:213:THR:HB	1.87	0.56
1:B:468:ASN:OD1	1:B:471:GLU:HG3	2.05	0.56
1:A:398:PRO:HG3	1:A:507:TRP:CD1	2.40	0.56
1:B:227:ASN:HD21	1:B:295:LYS:H	1.51	0.56
3:E:44:ARG:HG3	3:E:46:SER:O	2.06	0.56
1:A:91:ALA:HB1	7:A:9012:HOH:O	2.04	0.56
3:F:146:ASN:HB3	3:F:149:ASP:OD2	2.06	0.56
1:A:124:LEU:HB3	1:A:137:TYR:CE1	2.41	0.56
3:F:81:THR:HG23	3:F:85:GLU:O	2.06	0.56
3:F:41:THR:CG2	3:F:43:PHE:H	2.13	0.56
3:F:118:TYR:HB3	3:F:123:MET:HB2	1.88	0.56
1:A:155:ASN:HD22	1:A:168:HIS:HD2	1.52	0.56
2:D:143:GLU:O	2:D:147:ARG:HB3	2.05	0.56
1:A:144:GLU:HA	1:A:144:GLU:OE2	2.05	0.56
1:B:115:TYR:OH	2:D:173:ASP:HA	2.05	0.56
3:F:41:THR:HG22	3:F:43:PHE:N	2.12	0.55
3:F:33:LYS:O	3:F:37:MET:HG2	2.05	0.55
1:B:302:VAL:HG13	1:B:376:TYR:HE2	1.69	0.55
2:C:269:ALA:HB3	2:C:270:PRO:HD3	1.88	0.55
2:D:275:ASN:C	2:D:278:PRO:HD2	2.27	0.55
1:A:44:THR:HG22	1:A:46:TYR:N	2.16	0.55
3:E:58:ALA:O	3:E:62:GLU:HG3	2.07	0.55
1:B:439:HIS:HD2	3:F:163:VAL:HA	1.72	0.55
3:E:98:MET:HE2	3:E:98:MET:O	2.07	0.55
1:B:352:ALA:CA	1:B:404:PRO:HB2	2.35	0.54
1:B:185:LYS:O	1:B:189:SER:HB2	2.07	0.54
1:B:44:THR:HG23	1:B:126:ASP:OD1	2.06	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:23:VAL:HB	2:D:195:LEU:HD21	1.90	0.54
1:B:44:THR:HG22	1:B:46:TYR:N	2.09	0.54
1:B:288:MET:HE1	1:B:346:LEU:HG	1.90	0.54
1:A:268:ASN:HD21	1:A:327:GLU:H	1.55	0.54
1:B:125:TRP:HE1	2:D:161:ASN:HD22	1.54	0.54
2:C:275:ASN:ND2	2:D:266:GLN:HE21	2.06	0.54
2:D:223:VAL:HG11	2:D:338:LEU:HB2	1.89	0.54
2:D:98:HIS:CD2	2:D:99:ARG:H	2.26	0.54
1:B:125:TRP:HE1	2:D:161:ASN:ND2	2.05	0.54
1:A:310:TYR:CE1	1:A:336:LYS:HD2	2.43	0.54
2:C:153:LEU:C	2:C:153:LEU:HD12	2.27	0.54
3:F:41:THR:HG23	3:F:42:PRO:HD2	1.88	0.53
2:D:87:THR:HG21	2:D:169:GLU:OE1	2.07	0.53
1:B:43:ARG:HD2	1:B:43:ARG:C	2.27	0.53
1:B:209:GLU:HA	1:B:213:THR:OG1	2.09	0.53
1:A:302:VAL:HG13	1:A:376:TYR:HE2	1.72	0.53
3:F:81:THR:CG2	3:F:85:GLU:HG3	2.39	0.53
2:C:326:GLU:HG3	7:C:5122:HOH:O	2.09	0.53
2:C:261:ARG:NE	2:C:285:GLN:HE22	1.99	0.53
2:D:102:LEU:HB2	2:D:104:ARG:HD2	1.91	0.53
2:D:352:ILE:HD11	2:D:388:LEU:HD11	1.91	0.53
3:F:39:HIS:CD2	3:F:49:LEU:HD12	2.44	0.53
3:F:32:LEU:HA	3:F:60:LEU:HD23	1.92	0.52
2:D:277:THR:O	2:D:281:ILE:HG13	2.09	0.52
3:F:153:GLU:CD	3:F:153:GLU:H	2.13	0.52
1:B:354:TRP:CH2	1:B:499:PRO:HD3	2.45	0.52
2:D:351:GLU:C	2:D:353:THR:H	2.13	0.52
1:A:437:ARG:HG2	1:A:437:ARG:HH11	1.75	0.51
2:C:54:VAL:HG12	2:C:55:TYR:CD2	2.45	0.51
2:C:261:ARG:HE	2:C:285:GLN:NE2	2.02	0.51
1:A:24:ASN:OD1	1:A:26:GLN:HG3	2.11	0.51
2:D:266:GLN:HE22	2:D:278:PRO:HB3	1.76	0.51
1:B:121:THR:HA	1:B:124:LEU:HD12	1.91	0.51
1:B:125:TRP:O	1:B:125:TRP:CD1	2.64	0.51
1:A:101:GLU:CD	1:A:360:ARG:HH11	2.14	0.51
1:B:144:GLU:HA	1:B:144:GLU:OE2	2.11	0.51
3:F:44:ARG:HD3	3:F:47:TYR:CZ	2.46	0.51
1:A:123:MET:HB2	2:C:168:ARG:HD3	1.93	0.51
1:B:302:VAL:HG13	1:B:376:TYR:CE2	2.45	0.51
1:A:437:ARG:NH1	1:A:454:GLU:OE2	2.44	0.51
1:A:196:ASP:HB2	3:E:140:MET:SD	2.51	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:439:HIS:HE1	1:A:454:GLU:OE1	1.93	0.51
3:E:41:THR:O	3:E:44:ARG:CD	2.59	0.50
2:D:179:LEU:HD23	2:D:182:TRP:CE3	2.45	0.50
1:A:354:TRP:CH2	1:A:499:PRO:HD3	2.46	0.50
1:B:196:ASP:HB2	3:F:140:MET:SD	2.51	0.50
1:A:211:CYS:HB2	1:A:313:TRP:CD1	2.46	0.50
1:B:43:ARG:HD2	1:B:43:ARG:O	2.10	0.50
3:F:15:TRP:O	3:F:19:ILE:HG23	2.11	0.50
1:B:84:ASP:OD1	1:B:88:ARG:NH2	2.44	0.50
2:D:336:MET:HE1	2:D:356:LEU:HD11	1.93	0.50
2:D:263:GLU:OE2	2:D:263:GLU:HA	2.12	0.50
2:C:356:LEU:O	2:C:360:VAL:HG23	2.12	0.50
3:E:152:LEU:O	3:E:156:ARG:HG3	2.11	0.50
1:A:79:PHE:O	1:A:83:GLN:HG3	2.12	0.50
2:D:348:ASP:OD2	2:D:350:GLU:HB2	2.11	0.50
1:A:382:HIS:O	1:A:386:ILE:HG13	2.11	0.50
1:A:360:ARG:HG2	1:A:498:GLN:HB2	1.94	0.50
2:D:149:TRP:HB2	2:D:265:PHE:CE2	2.47	0.50
1:B:33:GLN:NE2	1:B:132:GLU:H	2.07	0.49
1:A:521:ASN:OD1	1:A:523:VAL:HG12	2.12	0.49
1:A:248:ALA:O	1:A:252:GLN:HB2	2.12	0.49
2:C:111:LYS:O	2:C:115:GLU:HG3	2.11	0.49
1:A:108:ASN:HD21	1:A:175:ARG:HH11	1.60	0.49
1:A:119:ALA:O	2:C:168:ARG:HD2	2.12	0.49
1:B:193:ILE:O	2:D:168:ARG:NH1	2.44	0.49
2:D:243:GLU:HG3	2:D:320:TRP:CD1	2.47	0.49
2:D:192:MET:HE3	2:D:280:PHE:CE2	2.47	0.49
1:B:108:ASN:ND2	1:B:175:ARG:HH11	2.08	0.49
3:F:16:VAL:HG23	3:F:17:ASN:N	2.28	0.49
1:B:439:HIS:HB3	3:F:161:VAL:HG21	1.93	0.49
1:A:354:TRP:CZ2	1:A:403:ILE:HD11	2.46	0.49
1:B:213:THR:O	1:B:217:ILE:HG12	2.12	0.49
2:D:255:LEU:HD21	2:D:363:TRP:CG	2.48	0.49
3:E:15:TRP:CD1	3:E:56:ILE:HD13	2.48	0.49
2:C:226:SER:HB2	2:C:331:ALA:HA	1.95	0.49
1:A:495:LEU:HB3	7:A:9081:HOH:O	2.12	0.49
1:B:30:ARG:HG2	1:B:30:ARG:HH11	1.78	0.49
1:B:354:TRP:CG	1:B:355:PRO:HD3	2.48	0.48
1:B:232:THR:HB	1:B:233:PRO:HD3	1.95	0.48
1:B:82:LEU:HD23	1:B:86:LEU:CD1	2.43	0.48
1:A:121:THR:HG21	1:A:140:GLN:CG	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:439:HIS:HB3	3:F:161:VAL:CG2	2.43	0.48
1:A:216:LEU:O	1:A:220:VAL:HG23	2.12	0.48
1:B:214:ASN:HB2	1:B:247:MET:HE2	1.94	0.48
1:B:466:CYS:HB2	2:D:73:THR:HA	1.95	0.48
1:A:118:ILE:HD13	1:A:145:ILE:HG12	1.94	0.48
1:B:33:GLN:NE2	1:B:33:GLN:HA	2.22	0.48
1:B:119:ALA:HB1	2:D:168:ARG:HD2	1.95	0.48
1:A:137:TYR:O	1:A:141:VAL:HG23	2.14	0.48
2:D:262:ARG:HA	2:D:266:GLN:HB3	1.94	0.48
2:D:54:VAL:O	2:D:55:TYR:HB2	2.14	0.48
3:E:165:HIS:CE1	3:E:167:GLN:HG3	2.48	0.48
1:A:44:THR:OG1	1:A:127:SER:HA	2.13	0.48
2:C:263:GLU:OE2	2:C:263:GLU:HA	2.14	0.48
3:F:98:MET:HG3	3:F:138:ARG:HG2	1.96	0.48
3:F:61:GLU:HB3	3:F:121:PRO:HD3	1.95	0.48
2:C:179:LEU:HD12	2:C:182:TRP:CE3	2.49	0.48
1:B:95:VAL:HG12	1:B:96:HIS:N	2.29	0.48
3:F:81:THR:HG21	3:F:85:GLU:HG3	1.95	0.48
1:A:439:HIS:CE1	1:A:454:GLU:OE1	2.67	0.48
3:F:57:GLU:O	3:F:61:GLU:HG3	2.14	0.48
2:D:80:ARG:HB2	7:D:423:HOH:O	2.14	0.48
2:D:336:MET:HE3	2:D:384:VAL:HG12	1.96	0.48
2:C:136:MET:SD	2:C:141:ARG:HB2	2.54	0.48
2:D:235:TRP:CD1	2:D:235:TRP:C	2.87	0.47
1:A:302:VAL:HG23	1:A:303:LYS:H	1.79	0.47
2:C:193:ILE:HA	7:C:5058:HOH:O	2.12	0.47
1:B:31:TRP:CH2	2:D:210:SER:HA	2.49	0.47
2:D:228:ARG:HH11	2:D:228:ARG:HG2	1.79	0.47
2:D:260:VAL:O	2:D:265:PHE:HD1	1.97	0.47
1:B:125:TRP:O	1:B:125:TRP:HD1	1.97	0.47
1:A:101:GLU:OE1	1:A:360:ARG:HD3	2.14	0.47
1:B:140:GLN:HG3	1:B:246:HIS:CE1	2.49	0.47
3:E:165:HIS:HE1	3:E:167:GLN:HG3	1.79	0.47
3:F:38:ASP:HA	3:F:45:ASN:HB2	1.95	0.47
3:E:15:TRP:O	3:E:19:ILE:HG13	2.14	0.47
2:D:98:HIS:CD2	2:D:99:ARG:N	2.82	0.47
1:A:204:LEU:O	1:A:209:GLU:HG3	2.15	0.47
1:B:489:ARG:NH1	1:B:496:ILE:O	2.46	0.47
1:B:30:ARG:NH1	1:B:30:ARG:HG2	2.29	0.47
1:B:366:GLN:O	1:B:370:GLU:HG3	2.15	0.47
2:C:50:GLU:OE1	2:C:99:ARG:NH1	2.48	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:423:VAL:HA	1:A:424:PRO:HD3	1.79	0.47
2:D:326:GLU:HB2	2:D:327:PRO:HD3	1.96	0.47
2:D:179:LEU:HD23	2:D:182:TRP:CZ3	2.50	0.47
3:F:91:LEU:C	3:F:91:LEU:HD23	2.35	0.47
2:D:189:ILE:HD12	2:D:284:ALA:HB2	1.96	0.47
1:B:367:GLU:HG3	7:B:9066:HOH:O	2.15	0.47
1:B:44:THR:HG1	1:B:127:SER:HA	1.78	0.47
1:B:519:PHE:CD2	6:B:9010:XE:XE	3.46	0.47
1:A:48:THR:O	3:E:137:THR:HG23	2.14	0.47
2:D:243:GLU:HB2	2:D:320:TRP:CZ2	2.50	0.47
3:F:109:LYS:HZ2	3:F:109:LYS:HB2	1.78	0.47
1:B:204:LEU:HG	1:B:205:GLN:HG3	1.97	0.47
1:A:77:ARG:HG3	7:A:9079:HOH:O	2.14	0.47
2:D:98:HIS:O	2:D:99:ARG:HG2	2.14	0.47
1:A:186:ARG:CZ	1:A:277:THR:HG23	2.45	0.47
1:A:230:GLU:HG3	1:B:89:LEU:HD21	1.96	0.47
1:B:93:VAL:HG11	2:C:3:MET:HG2	1.96	0.46
1:B:211:CYS:HB2	1:B:313:TRP:CG	2.50	0.46
2:D:336:MET:CE	2:D:384:VAL:HG12	2.45	0.46
3:F:61:GLU:O	3:F:121:PRO:HG2	2.16	0.46
1:B:489:ARG:HB3	2:D:30:ASP:OD2	2.14	0.46
2:C:255:LEU:HB2	2:C:328:THR:HG21	1.96	0.46
1:B:50:TYR:CD2	1:B:257:ILE:HD12	2.50	0.46
2:C:187:ILE:O	2:C:191:GLN:HG3	2.15	0.46
1:B:79:PHE:HB3	1:B:83:GLN:NE2	2.30	0.46
2:D:189:ILE:HD11	2:D:284:ALA:HA	1.96	0.46
1:A:82:LEU:HD23	1:A:86:LEU:HD12	1.97	0.46
2:C:270:PRO:HB3	2:D:270:PRO:CB	2.42	0.46
1:B:288:MET:CE	1:B:346:LEU:HB3	2.43	0.46
2:D:155:ASN:O	2:D:159:LEU:HG	2.15	0.46
1:A:281:TYR:CZ	1:A:285:VAL:HG21	2.50	0.46
1:B:44:THR:HG22	1:B:45:LYS:N	2.30	0.46
2:C:54:VAL:O	2:C:55:TYR:HB2	2.15	0.46
1:B:143:ASP:OD2	1:B:245:ARG:NH2	2.46	0.46
3:E:120:PRO:HG2	3:E:125:VAL:HG12	1.96	0.46
1:A:65:LYS:HB3	2:C:117:TRP:CD2	2.51	0.46
1:A:224:ALA:HB1	1:A:229:ASP:HB3	1.98	0.46
1:A:452:TRP:O	1:A:456:MET:HG3	2.15	0.46
1:B:23:VAL:HB	2:D:195:LEU:CD2	2.45	0.46
2:D:269:ALA:HB3	2:D:270:PRO:HD3	1.97	0.46
2:C:235:TRP:CD1	2:C:235:TRP:C	2.90	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:61:ASP:OD2	3:F:7:HIS:HD2	1.99	0.46
2:D:161:ASN:HB3	2:D:235:TRP:CE2	2.51	0.45
2:C:146:ASN:ND2	2:C:197:ARG:HE	2.14	0.45
1:B:96:HIS:ND1	1:B:97:PRO:HD2	2.32	0.45
1:B:268:ASN:HD21	1:B:327:GLU:H	1.65	0.45
2:C:98:HIS:HE1	2:C:178:SER:OG	2.00	0.45
1:A:407:TRP:CE2	1:A:411:ASN:ND2	2.85	0.45
1:B:288:MET:HE3	1:B:346:LEU:HD23	1.98	0.45
3:F:154:GLU:HG3	3:F:158:GLN:HE21	1.82	0.45
1:A:306:ASP:OD2	1:A:336:LYS:NZ	2.49	0.45
2:C:146:ASN:HD21	2:C:197:ARG:NH2	1.99	0.45
3:F:36:ARG:CZ	3:F:119:LYS:HB3	2.47	0.45
1:A:125:TRP:C	1:A:125:TRP:CD1	2.90	0.45
3:F:137:THR:O	3:F:141:GLU:HG3	2.16	0.45
2:D:89:GLU:CD	3:F:125:VAL:HG13	2.37	0.45
1:A:146:ARG:HB2	2:C:106:HIS:NE2	2.32	0.45
1:B:405:LEU:HD22	6:B:9011:XE:XE	2.95	0.45
1:A:317:TRP:CD1	1:A:318:ILE:HD12	2.48	0.44
1:A:125:TRP:HE1	2:C:161:ASN:ND2	2.15	0.44
1:B:468:ASN:CG	1:B:471:GLU:HG3	2.37	0.44
2:D:319:ASN:OD1	3:F:78:ARG:HD3	2.17	0.44
1:A:58:GLU:HB2	7:A:9140:HOH:O	2.16	0.44
3:F:30:GLU:HA	3:F:30:GLU:OE2	2.16	0.44
3:F:152:LEU:O	3:F:156:ARG:HG3	2.17	0.44
2:C:76:PHE:HZ	2:C:168:ARG:HH12	1.65	0.44
1:A:244:LEU:HA	1:A:247:MET:HG3	1.98	0.44
1:A:159:ALA:O	2:C:33:ASN:HB2	2.17	0.44
1:A:29:HIS:CD2	1:A:61:LYS:HA	2.52	0.44
1:B:82:LEU:HA	1:B:86:LEU:HD12	1.99	0.44
2:D:192:MET:HE3	2:D:280:PHE:HE2	1.82	0.44
2:D:243:GLU:HG3	2:D:320:TRP:NE1	2.32	0.44
2:C:385:LEU:O	2:C:388:LEU:HB2	2.18	0.44
1:B:337:GLN:HG3	1:B:338:ASP:N	2.32	0.44
2:D:296:GLN:O	2:D:300:TYR:HB2	2.17	0.44
3:F:95:VAL:HG12	3:F:99:ASN:HD21	1.82	0.44
3:F:41:THR:HG23	3:F:42:PRO:CD	2.47	0.44
2:D:336:MET:HB3	2:D:388:LEU:HD23	1.98	0.44
1:B:140:GLN:O	1:B:144:GLU:HG2	2.18	0.44
1:A:288:MET:CE	6:A:9002:XE:XE	3.43	0.44
3:E:138:ARG:NH2	3:E:142:LEU:HD21	2.33	0.44
1:A:302:VAL:HG11	1:A:340:TYR:CE1	2.53	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:111:LYS:O	2:D:115:GLU:HG3	2.18	0.44
2:D:54:VAL:HA	2:D:173:ASP:OD1	2.18	0.44
1:A:521:ASN:HA	1:A:522:PRO:HD2	1.82	0.44
1:B:30:ARG:O	1:B:30:ARG:HG2	2.18	0.44
3:F:125:VAL:HG23	3:F:126:ASN:N	2.33	0.44
1:A:96:HIS:ND1	1:A:97:PRO:HD2	2.33	0.43
2:C:259:PHE:CD1	2:C:263:GLU:HB2	2.54	0.43
1:B:493:LYS:HE2	1:B:508:THR:HG21	2.00	0.43
2:C:102:LEU:HD13	2:C:290:ILE:HG23	1.99	0.43
2:C:246:PHE:O	2:C:250:ALA:HB3	2.18	0.43
1:B:371:TRP:CE2	1:B:375:ASN:ND2	2.86	0.43
1:A:192:PHE:CE2	1:A:204:LEU:HA	2.53	0.43
2:D:167:ALA:O	2:D:176:ARG:NH1	2.51	0.43
1:B:207:VAL:HG22	1:B:313:TRP:CZ2	2.54	0.43
1:B:227:ASN:ND2	1:B:295:LYS:H	2.16	0.43
3:F:73:ASN:O	3:F:74:GLU:C	2.57	0.43
1:B:49:LYS:HE3	3:F:144:ASN:HD22	1.83	0.43
1:A:317:TRP:HD1	1:A:318:ILE:CD1	2.30	0.43
1:A:89:LEU:HD21	1:B:230:GLU:HG3	2.00	0.43
2:D:251:VAL:HG12	2:D:252:TYR:N	2.34	0.43
1:B:288:MET:HE2	1:B:347:TYR:N	2.33	0.43
7:A:9022:HOH:O	3:E:144:ASN:HB3	2.17	0.43
1:A:521:ASN:CG	1:A:523:VAL:HG12	2.39	0.43
1:A:187:VAL:HG12	1:A:277:THR:HG22	2.00	0.43
1:B:521:ASN:OD1	1:B:523:VAL:HG12	2.19	0.43
2:D:236:GLN:OE1	2:D:236:GLN:HA	2.17	0.43
1:B:125:TRP:O	1:B:134:LYS:HG2	2.19	0.43
1:B:344:HIS:HE1	1:B:376:TYR:CD2	2.35	0.43
1:B:75:ASP:OD2	1:B:146:ARG:NH1	2.52	0.43
3:F:25:LEU:HD22	3:F:68:LYS:HA	2.01	0.43
2:D:105:TRP:O	2:D:108:PRO:HD2	2.19	0.43
1:B:164:ASP:OD1	1:B:489:ARG:NH2	2.52	0.43
1:A:440:GLU:HG3	1:A:441:TYR:N	2.31	0.43
1:A:266:TYR:HB3	7:A:9022:HOH:O	2.18	0.43
2:D:245:ALA:HB3	2:D:299:TYR:OH	2.19	0.42
1:B:125:TRP:C	1:B:125:TRP:CD1	2.92	0.42
2:D:269:ALA:N	2:D:270:PRO:CD	2.83	0.42
1:B:489:ARG:NH1	1:B:496:ILE:HA	2.34	0.42
1:B:148:THR:HG21	6:B:9007:XE:XE	2.97	0.42
1:A:65:LYS:HB3	2:C:117:TRP:CG	2.54	0.42
2:C:126:GLY:O	2:C:130:ASP:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:118:ILE:HD13	1:B:145:ILE:HG12	2.01	0.42
1:A:109:PHE:O	1:A:112:VAL:HG12	2.19	0.42
1:A:212:PHE:O	1:A:216:LEU:HB2	2.20	0.42
1:B:268:ASN:ND2	1:B:327:GLU:H	2.17	0.42
1:B:33:GLN:CA	1:B:33:GLN:HE21	2.17	0.42
1:A:420:VAL:HG13	1:A:464:TYR:CE2	2.54	0.42
1:B:365:ASP:OD2	1:B:365:ASP:C	2.58	0.42
1:A:148:THR:CG2	6:A:9006:XE:XE	3.45	0.42
1:B:116:ASN:HD22	1:B:193:ILE:HD13	1.84	0.42
2:C:33:ASN:ND2	2:C:33:ASN:H	2.16	0.42
2:D:164:SER:O	2:D:167:ALA:HB3	2.20	0.42
3:F:114:PHE:CD2	3:F:135:LEU:HD12	2.55	0.42
1:A:96:HIS:HA	1:A:97:PRO:HD3	1.92	0.42
1:A:453:GLY:HA3	7:A:9024:HOH:O	2.20	0.41
2:D:102:LEU:CB	2:D:104:ARG:HD2	2.49	0.41
2:D:148:TYR:CD1	2:D:338:LEU:HD11	2.55	0.41
1:A:101:GLU:CD	1:A:360:ARG:HD3	2.41	0.41
1:A:146:ARG:HB2	2:C:106:HIS:CD2	2.55	0.41
2:C:105:TRP:O	2:C:108:PRO:HD2	2.20	0.41
1:A:244:LEU:HD23	1:A:247:MET:HG3	2.02	0.41
1:B:217:ILE:O	1:B:221:THR:HG23	2.20	0.41
1:B:403:ILE:O	1:B:403:ILE:HG13	2.19	0.41
3:E:33:LYS:HE2	7:E:206:HOH:O	2.20	0.41
2:C:36:GLY:O	2:C:39:VAL:HG23	2.19	0.41
1:B:382:HIS:HD2	1:B:383:TYR:CE1	2.39	0.41
1:B:112:VAL:HG23	2:D:58:PRO:HG3	2.02	0.41
1:A:212:PHE:O	1:A:216:LEU:CB	2.68	0.41
1:B:519:PHE:CG	6:B:9010:XE:XE	3.52	0.41
1:A:186:ARG:NH1	1:A:277:THR:HG23	2.35	0.41
1:A:292:TYR:OH	1:A:344:HIS:HD2	2.03	0.41
1:B:112:VAL:CG2	2:D:58:PRO:HG3	2.50	0.41
1:A:124:LEU:HD21	1:A:201:SER:HB2	2.01	0.41
1:B:439:HIS:HE1	1:B:454:GLU:OE1	2.04	0.41
1:A:297:LYS:HD2	1:A:297:LYS:N	2.36	0.41
1:A:138:LEU:O	1:A:141:VAL:HB	2.21	0.41
1:A:495:LEU:HD11	1:A:512:ILE:CG1	2.51	0.41
1:B:190:ASP:HB3	2:D:74:GLN:HB3	2.03	0.41
1:A:260:ASP:HA	1:A:261:PRO:HD3	1.95	0.41
2:C:5:GLY:HA3	7:C:5151:HOH:O	2.21	0.41
2:D:357:TYR:HE2	2:D:377:ARG:HE	1.67	0.41
1:B:438:VAL:HG12	3:F:164:VAL:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:437:ARG:HG2	1:A:437:ARG:NH1	2.35	0.41
1:A:171:ALA:O	1:A:175:ARG:HD3	2.20	0.41
1:A:466:CYS:HB2	2:C:73:THR:HA	2.03	0.41
2:C:146:ASN:O	2:C:214:PRO:HG3	2.21	0.41
2:D:324:TRP:HA	2:D:327:PRO:HD2	2.03	0.41
2:D:147:ARG:HH11	2:D:217:GLU:HB2	1.86	0.41
1:B:115:TYR:CE2	2:D:173:ASP:HB3	2.56	0.41
1:A:186:ARG:HD3	1:A:186:ARG:C	2.40	0.41
1:B:267:LEU:HD21	1:B:326:VAL:HG22	2.03	0.41
2:D:156:GLU:HA	2:D:156:GLU:OE2	2.21	0.41
2:C:141:ARG:O	2:C:145:ILE:HB	2.20	0.40
1:A:186:ARG:HA	2:C:73:THR:OG1	2.20	0.40
1:B:147:HIS:CE1	7:B:9145:HOH:O	2.75	0.40
1:A:348:LEU:HD23	1:A:387:TYR:CZ	2.56	0.40
2:D:76:PHE:HB2	2:D:80:ARG:CB	2.49	0.40
1:B:192:PHE:CE2	1:B:204:LEU:HA	2.56	0.40
1:B:283:THR:HB	1:B:284:PRO:HD3	2.03	0.40
1:B:507:TRP:CD1	1:B:507:TRP:N	2.89	0.40
3:E:52:ASP:O	3:E:56:ILE:HG13	2.21	0.40
1:A:108:ASN:O	1:A:111:GLU:HB3	2.21	0.40
3:F:98:MET:HE2	3:F:110:ILE:HB	2.03	0.40
1:B:521:ASN:HA	1:B:522:PRO:HD2	1.95	0.40
1:B:146:ARG:HB2	2:D:106:HIS:CE1	2.56	0.40
2:C:283:GLN:HG3	2:D:119:TYR:OH	2.21	0.40
1:B:348:LEU:HD23	1:B:387:TYR:CE2	2.56	0.40
2:C:156:GLU:OE2	2:C:156:GLU:HA	2.21	0.40
1:A:244:LEU:HA	1:A:247:MET:CG	2.52	0.40
1:B:288:MET:HE1	1:B:346:LEU:C	2.41	0.40
1:A:230:GLU:C	1:A:233:PRO:HD2	2.42	0.40
2:C:319:ASN:OD1	3:E:78:ARG:HD3	2.22	0.40
3:F:32:LEU:HA	3:F:60:LEU:CD2	2.52	0.40
2:C:179:LEU:HA	2:C:179:LEU:HD12	1.89	0.40
1:B:421:SER:O	1:B:422:GLN:HB2	2.22	0.40
3:F:72:PHE:CE1	3:F:80:LYS:HB3	2.55	0.40
2:C:262:ARG:HD3	2:D:130:ASP:OD2	2.21	0.40
1:B:182:LYS:HA	1:B:182:LYS:HD3	1.92	0.40
3:E:36:ARG:NH2	3:E:119:LYS:HD2	2.37	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	509/527 (97%)	483 (95%)	25 (5%)	1 (0%)	52	77
1	B	508/527 (96%)	480 (94%)	28 (6%)	0	100	100
2	C	386/389 (99%)	371 (96%)	14 (4%)	1 (0%)	46	72
2	D	386/389 (99%)	356 (92%)	24 (6%)	6 (2%)	12	24
3	E	163/170 (96%)	153 (94%)	8 (5%)	2 (1%)	16	33
3	F	165/170 (97%)	143 (87%)	19 (12%)	3 (2%)	11	21
All	All	2117/2172 (98%)	1986 (94%)	118 (6%)	13 (1%)	30	56

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	F	74	GLU
2	D	251	VAL
3	E	5	GLY
3	F	122	ILE
2	D	64	ALA
2	D	352	ILE
3	F	144	ASN
2	D	205	PRO
2	D	386	ALA
1	A	284	PRO
2	D	307	PRO
2	C	251	VAL
3	E	122	ILE

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	433/442 (98%)	415 (96%)	18 (4%)	36	65
1	B	432/442 (98%)	421 (98%)	11 (2%)	55	81
2	C	322/323 (100%)	313 (97%)	9 (3%)	51	78
2	D	321/323 (99%)	314 (98%)	7 (2%)	60	83
3	E	143/147 (97%)	139 (97%)	4 (3%)	51	78
3	F	145/147 (99%)	143 (99%)	2 (1%)	74	90
All	All	1796/1824 (98%)	1745 (97%)	51 (3%)	51	78

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ARG
1	A	43	ARG
1	A	90	ASN
1	A	125	TRP
1	A	186	ARG
1	A	279	GLN
1	A	299	GLU
1	A	302	VAL
1	A	310	TYR
1	A	316	ILE
1	A	338	ASP
1	A	391	ARG
1	A	403	ILE
1	A	435	THR
1	A	437	ARG
1	A	440	GLU
1	A	445	MET
1	A	467	GLN
1	B	33	GLN
1	B	43	ARG
1	B	90	ASN
1	B	110	LEU
1	B	125	TRP
1	B	186	ARG
1	B	189	SER
1	B	279	GLN
1	B	310	TYR

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Mol	Chain	Res	Type
1	B	440	GLU
1	B	445	MET
2	C	33	ASN
2	C	35	MET
2	C	80	ARG
2	C	117	TRP
2	C	153	LEU
2	C	160	PHE
2	C	168	ARG
2	C	356	LEU
2	C	377	ARG
2	D	35	MET
2	D	80	ARG
2	D	153	LEU
2	D	160	PHE
2	D	173	ASP
2	D	207	PHE
2	D	372	ASP
3	E	8	SER
3	E	24	THR
3	E	44	ARG
3	E	166	LEU
3	F	11	THR
3	F	108	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (66) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	78	GLN
1	A	90	ASN
1	A	108	ASN
1	A	155	ASN
1	A	168	HIS
1	A	227	ASN
1	A	249	ASN
1	A	252	GLN
1	A	268	ASN
1	A	273	ASN
1	A	278	GLN
1	A	279	GLN
1	A	343	HIS

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Mol	Chain	Res	Type
1	A	344	HIS
1	A	382	HIS
1	A	412	ASN
1	A	439	HIS
1	A	442	ASN
1	B	26	GLN
1	B	33	GLN
1	B	78	GLN
1	B	83	GLN
1	B	90	ASN
1	B	100	ASN
1	B	108	ASN
1	B	116	ASN
1	B	227	ASN
1	B	249	ASN
1	B	259	ASN
1	B	268	ASN
1	B	273	ASN
1	B	278	GLN
1	B	279	GLN
1	B	343	HIS
1	B	344	HIS
1	B	382	HIS
1	B	413	HIS
1	B	439	HIS
1	B	451	GLN
1	B	516	ASN
1	B	527	ASN
2	C	33	ASN
2	C	98	HIS
2	C	146	ASN
2	C	161	ASN
2	C	285	GLN
2	C	301	ASN
2	D	98	HIS
2	D	106	HIS
2	D	155	ASN
2	D	161	ASN
2	D	266	GLN
2	D	285	GLN
2	D	296	GLN
2	D	301	ASN

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Mol	Chain	Res	Type
3	E	34	GLN
3	E	45	ASN
3	E	144	ASN
3	E	165	HIS
3	F	7	HIS
3	F	45	ASN
3	F	79	HIS
3	F	99	ASN
3	F	158	GLN
3	F	167	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 19 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

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

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

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	511/527 (96%)	-0.51	0 100 100	17, 30, 47, 60	0
1	B	510/527 (96%)	-0.59	1 (0%) 95 95	15, 30, 48, 56	0
2	C	388/389 (99%)	-0.71	2 (0%) 91 90	13, 23, 36, 52	0
2	D	388/389 (99%)	-0.38	1 (0%) 94 93	19, 36, 54, 66	0
3	E	165/170 (97%)	-0.66	0 100 100	15, 26, 39, 50	0
3	F	167/170 (98%)	0.04	2 (1%) 81 77	32, 44, 60, 69	0
All	All	2129/2172 (98%)	-0.51	6 (0%) 94 93	13, 30, 50, 69	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	F	3	LYS	3.7
3	F	23	ASN	3.5
2	C	2	SER	3.4
2	C	6	GLU	2.7
1	B	26	GLN	2.0
2	D	45	ARG	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

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	XE	A	9009	1/1	0.98	0.26	5.54	32,32,32,32	1
6	XE	B	9011	1/1	0.97	0.21	3.87	32,32,32,32	1
6	XE	B	9007	1/1	0.99	0.15	1.82	32,32,32,32	1
6	XE	B	9005	1/1	0.97	0.18	0.93	32,32,32,32	1
6	XE	A	9004	1/1	0.98	0.17	0.86	32,32,32,32	1
6	XE	A	9006	1/1	0.99	0.11	0.25	32,32,32,32	1
5	CA	A	5005	1/1	0.88	0.10	-1.35	52,52,52,52	0
6	XE	A	9001	1/1	1.00	0.07	-1.84	32,32,32,32	0
6	XE	B	9003	1/1	1.00	0.08	-2.11	32,32,32,32	0
6	XE	A	9002	1/1	0.99	0.07	-3.36	32,32,32,32	1
4	FE	B	5003	1/1	0.99	0.03	-4.37	28,28,28,28	0
4	FE	A	5001	1/1	0.99	0.02	-4.57	27,27,27,27	0
4	FE	B	5004	1/1	0.97	0.04	-4.93	36,36,36,36	0
4	FE	A	5002	1/1	0.99	0.02	-5.38	31,31,31,31	0
6	XE	B	9010	1/1	0.98	0.13	-	32,32,32,32	1
5	CA	B	5008	1/1	0.90	0.06	-	45,45,45,45	0
6	XE	A	9008	1/1	0.96	0.17	-	32,32,32,32	1
5	CA	C	5006	1/1	0.91	0.06	-	52,52,52,52	0
5	CA	C	5007	1/1	0.85	0.11	-	70,70,70,70	0

6.5 Other polymers

There are no such residues in this entry.