



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 19, 2017 – 05:03 PM EST

PDB ID : 5TE8
Title : Crystal structure of the midazolam-bound human CYP3A4
Authors : Sevrioukova, I.; Poulos, T.
Deposited on : 2016-09-20
Resolution : 2.70 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
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) : rb-20028442

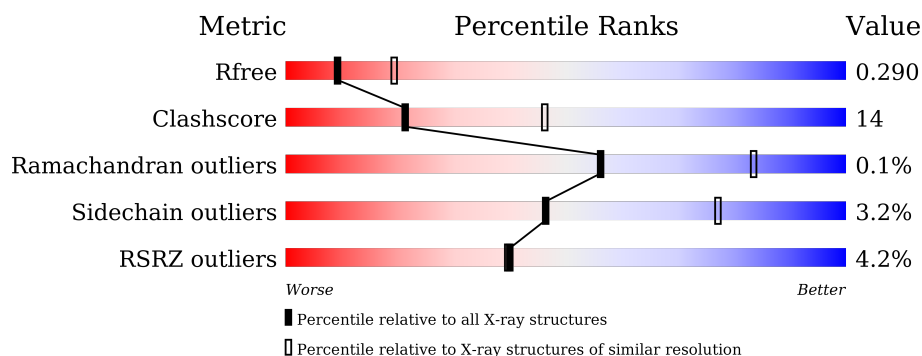
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	487	<div> <div>0%</div> <div> <div></div> <div>72%</div> <div>24%</div> <div>..</div> </div> </div>
1	B	487	<div> <div>2%</div> <div> <div></div> <div>74%</div> <div>22%</div> <div>..</div> </div> </div>
1	C	487	<div> <div>9%</div> <div> <div></div> <div>60%</div> <div>34%</div> <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
3	08J	A	602	-	-	X	-
3	08J	C	602	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11681 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.

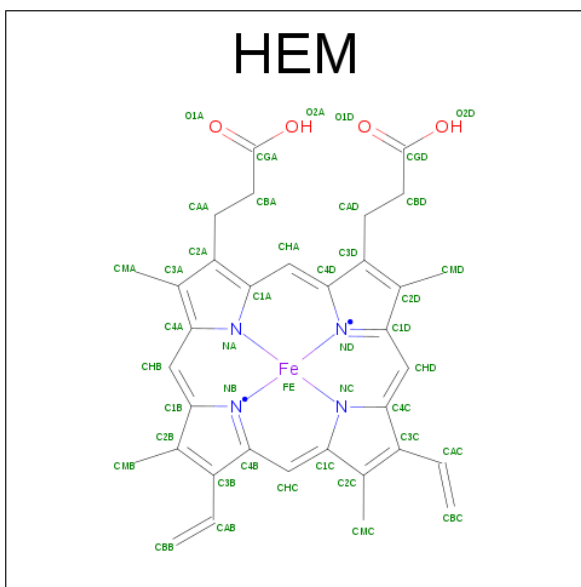
- Molecule 1 is a protein called Cytochrome P450 3A4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	470	Total	C	N	O	S	0	1	0
			3796	2470	626	676	24			
1	B	471	Total	C	N	O	S	0	0	0
			3797	2469	626	678	24			
1	C	469	Total	C	N	O	S	0	0	0
			3779	2459	622	674	24			

There are 18 discrepancies between the modelled and reference sequences:

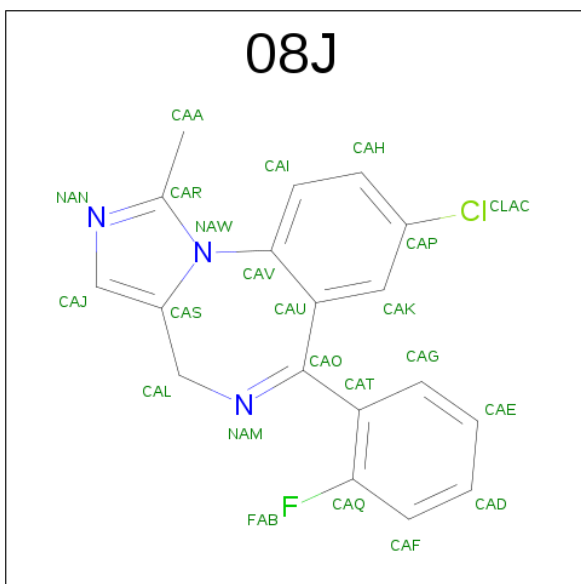
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	see remark 999	UNP P08684
A	2	ALA	-	see remark 999	UNP P08684
A	504	HIS	-	expression tag	UNP P08684
A	505	HIS	-	expression tag	UNP P08684
A	506	HIS	-	expression tag	UNP P08684
A	507	HIS	-	expression tag	UNP P08684
B	1	MET	-	see remark 999	UNP P08684
B	2	ALA	-	see remark 999	UNP P08684
B	504	HIS	-	expression tag	UNP P08684
B	505	HIS	-	expression tag	UNP P08684
B	506	HIS	-	expression tag	UNP P08684
B	507	HIS	-	expression tag	UNP P08684
C	1	MET	-	see remark 999	UNP P08684
C	2	ALA	-	see remark 999	UNP P08684
C	504	HIS	-	expression tag	UNP P08684
C	505	HIS	-	expression tag	UNP P08684
C	506	HIS	-	expression tag	UNP P08684
C	507	HIS	-	expression tag	UNP P08684

- 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 43	C 34	Fe 1	N 4	O 4	0	0
2	B	1	Total 43	C 34	Fe 1	N 4	O 4	0	0
2	C	1	Total 43	C 34	Fe 1	N 4	O 4	0	0

- Molecule 3 is 8-chloro-6-(2-fluorophenyl)-1-methyl-4H-imidazo[1,5-a][1,4]benzodiazepine (three-letter code: 08J) (formula: C₁₈H₁₃ClFN₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total 23	C 18	Cl 1	F 1	N 3	0	0
3	B	1	Total 23	C 18	Cl 1	F 1	N 3	0	0
3	C	1	Total 23	C 18	Cl 1	F 1	N 3	0	0

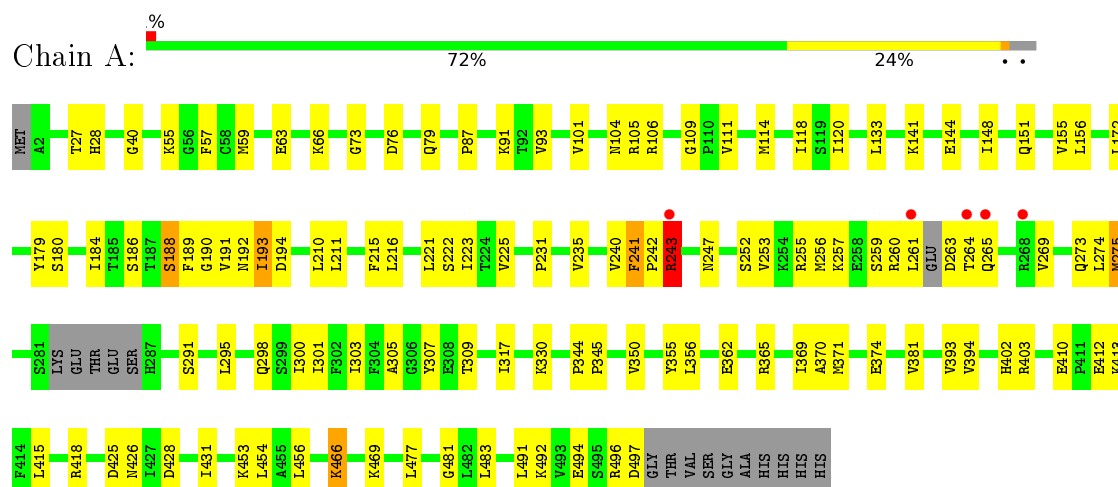
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	53	Total 53	O 53	0	0
4	B	42	Total 42	O 42	0	0
4	C	16	Total 16	O 16	0	0

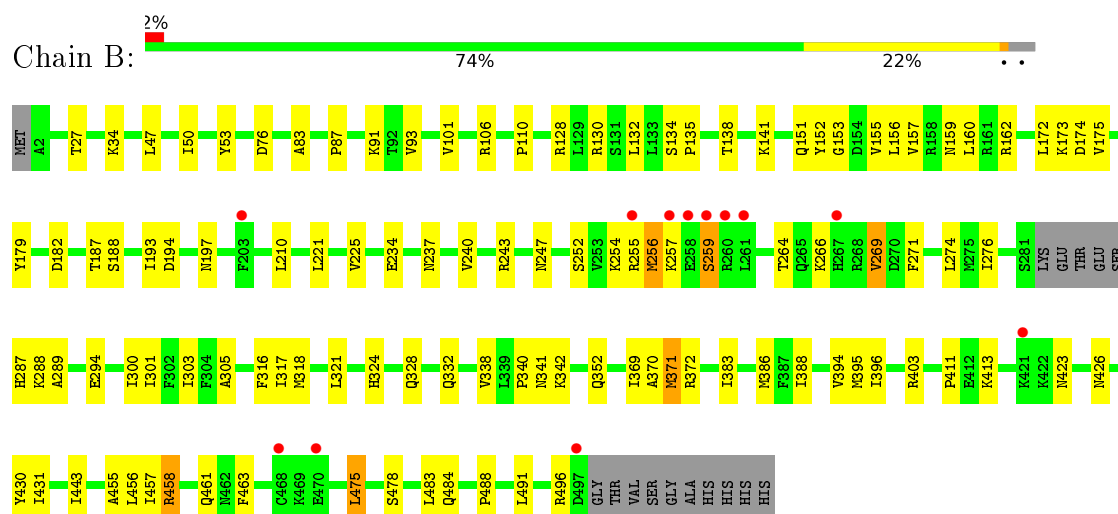
3 Residue-property plots [i](#)

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: Cytochrome P450 3A4



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S495	V395	L321	V240	V146	MET
R496	I396	A322	F241	I149	A2
ASP	H402	T323	L249	Y152	Y23
GLY	R403	H324	K251	R158	L24
THR	D404	V327	S252	M159	T27
VAL	P405	Q328	K254	L160	L32
SER	P408	Q329	R257	R161	P39
GLY	P411	K330	E258	E162	I50
ALA	P412	L331	S259	E163	I51
HIS	F413	Q332	R260	A164	S52
HIS	F414	E333	E165	T166	Y53
HIS	F415	E334	L261	L172	C58
HIS	P416	I335	E262	V175	M59
HIS	R417	A337	T264	F176	F60
HIS	E418	V338	Q265	Y179	E63
HIS	F419	L339	H267	V183	Y68
HIS	S420	P340	R268	I186	V71
HIS	K424	K342	V269	S186	I84
HIS	D425	A343	I276	F189	P87
HIS	M426	P344	L281	G190	D88
HIS	T427	P345	L283	T191	M89
HIS	D428	T346	L288	N192	T92
HIS	P429	Y347	L289	I193	V93
HIS	Y430	V350	K288	D194	K96
HIS	I431	L351	A289	D201	Y99
HIS	P434	Q352	L290	F202	S100
HIS	T443	M353	S291	V204	V101
HIS	M451	E354	D292	K209	F102
HIS	M452	Y355	L293	L210	T103
HIS	K453	M358	L294	L211	N104
HIS	L454	V359	Q298	R212	P110
HIS	A455	M361	S299	F215	V111
HIS	L456	E362	I300	L221	A117
HIS	L457	T363	F302	S222	I118
HIS	M458	L364	I303	I223	S119
HIS	V459	R365	T309	T224	K127
HIS	L460	L366	V313	V225	R128
HIS	Q461	F367	L314	F226	L129
HIS	M462	P368	S315	F228	R130
HIS	F463	I369	F316	L229	S131
HIS	S464	M371	I317	I230	L132
HIS	P465	R372	M318	P231	L133
HIS	K466	L373	Y319	E234	K143
HIS	P467	K379	E320		
HIS	C468	D380			
HIS	K469	V381			
HIS	L475	M386			
HIS	K476	K390			
HIS	L477	V394			
HIS	V493				
HIS	E494				

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	64.29Å 117.98Å 205.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	102.34 – 2.70 61.36 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (102.34-2.70) 98.8 (61.36-2.70)	Depositor EDS
R_{merge}	0.17	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.55 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.224 , 0.292 0.235 , 0.290	Depositor DCC
R_{free} test set	2178 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	50.5	Xtriage
Anisotropy	0.479	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	11681	wwPDB-VP
Average B, all atoms (Å ²)	73.0	wwPDB-VP

Xtriage'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.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: HEM, 08J

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	0/3889	0.62	2/5260 (0.0%)
1	B	0.38	0/3891	0.61	2/5264 (0.0%)
1	C	0.39	0/3872	0.62	3/5238 (0.1%)
All	All	0.38	0/11652	0.62	7/15762 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	2

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	243	ARG	CB-CA-C	-7.67	95.07	110.40
1	C	163	GLU	N-CA-CB	6.95	123.11	110.60
1	B	259	SER	N-CA-C	6.50	128.56	111.00
1	C	341	ASN	N-CA-C	-5.94	94.97	111.00
1	B	210	LEU	CA-CB-CG	5.78	128.59	115.30
1	C	454	LEU	CA-CB-CG	5.60	128.18	115.30
1	A	265	GLN	CB-CA-C	-5.19	100.01	110.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	333	GLU	Peptide
1	C	418	ARG	Sidechain

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	3796	0	3876	100	0
1	B	3797	0	3873	75	0
1	C	3779	0	3862	141	1
2	A	43	0	30	3	0
2	B	43	0	30	3	0
2	C	43	0	30	9	0
3	A	23	0	13	8	0
3	B	23	0	13	2	0
3	C	23	0	13	13	0
4	A	53	0	0	6	0
4	B	42	0	0	2	0
4	C	16	0	0	2	0
All	All	11681	0	11740	331	1

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 (331) 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:C:369:ILE:HD11	3:C:602:08J:CLAC	1.32	1.59
1:C:369:ILE:CD1	3:C:602:08J:CLAC	2.03	1.41
1:C:362:GLU:HG3	1:C:418:ARG:NH2	1.83	0.93
1:C:369:ILE:HD13	3:C:602:08J:CLAC	2.07	0.91
1:C:309:THR:HG21	3:C:602:08J:CLAC	2.10	0.88
1:A:242:PRO:O	1:A:243:ARG:HB2	1.72	0.87
1:A:260:ARG:O	1:A:263:ASP:O	1.92	0.87
3:C:602:08J:H5	3:C:602:08J:H3	1.55	0.87
1:C:413:LYS:HG3	1:C:418:ARG:NH1	1.90	0.86
1:A:111:VAL:HG12	1:A:114:MET:HB2	1.58	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:339:LEU:HB3	1:C:343:ALA:HB3	1.60	0.84
1:C:254:LYS:O	1:C:258:GLU:HB2	1.79	0.82
1:B:252:SER:O	1:B:256:MET:HB2	1.79	0.81
1:C:257:LYS:HA	1:C:260:ARG:HG3	1.62	0.81
1:C:331:LEU:HG	1:C:334:GLU:HB3	1.63	0.79
1:B:287:HIS:CD2	1:B:288:LYS:HD2	2.19	0.76
1:C:424:LYS:HB3	1:C:427:ILE:HD13	1.66	0.76
1:C:329:GLN:HA	1:C:332:GLN:HB2	1.66	0.76
1:C:373:LEU:HB2	1:C:396:ILE:HB	1.68	0.75
1:B:287:HIS:HD2	1:B:288:LYS:HD2	1.52	0.74
1:C:87:PRO:HG3	1:C:431:ILE:HD11	1.70	0.74
1:C:261:LEU:HD12	1:C:268:ARG:HH11	1.52	0.74
1:B:338:VAL:HG21	1:B:352:GLN:HG2	1.69	0.73
1:B:300:ILE:HA	1:B:303:ILE:HD12	1.71	0.72
1:C:362:GLU:HG2	1:C:416:PRO:HA	1.71	0.72
1:B:478:SER:OG	1:B:484:GLN:HB3	1.89	0.72
1:C:379:LYS:HA	1:C:390:LYS:HB2	1.71	0.72
1:C:110:PRO:HG3	1:C:234:GLU:HG3	1.70	0.71
1:A:141:LYS:HD2	1:A:274:LEU:HD22	1.71	0.71
2:C:601:HEM:HMB2	2:C:601:HEM:HBB2	1.71	0.71
3:C:602:08J:CAA	3:C:602:08J:H3	2.20	0.71
1:B:371:MET:O	1:B:371:MET:HG2	1.91	0.70
1:A:210:LEU:HD21	1:A:300:ILE:HG23	1.74	0.69
1:B:76:ASP:OD2	1:B:106:ARG:NH2	2.25	0.69
1:B:160:LEU:HD13	1:B:175:VAL:HG21	1.74	0.69
1:A:63:GLU:HA	1:A:66:LYS:HE3	1.74	0.69
1:C:418:ARG:NH2	4:C:701:HOH:O	2.20	0.69
1:B:237:ASN:HB3	4:B:719:HOH:O	1.93	0.69
1:B:157:VAL:HG23	1:B:463:PHE:CE2	2.28	0.68
1:C:415:LEU:H	1:C:418:ARG:HH12	1.42	0.67
1:A:371:MET:HE1	1:A:481:GLY:C	2.15	0.66
1:C:111:VAL:HG21	1:C:215:PHE:CZ	2.31	0.66
1:C:99:TYR:HD1	1:C:127:LYS:HE2	1.60	0.65
1:C:369:ILE:HD11	3:C:602:08J:CAP	2.26	0.65
1:A:370:ALA:O	1:A:371:MET:HB2	1.96	0.64
1:C:152:TYR:OH	1:C:192:ASN:HA	1.98	0.64
1:A:172:LEU:HD11	1:A:491:LEU:HD12	1.80	0.64
1:A:55:LYS:HB3	1:A:59:MET:HB2	1.79	0.64
1:B:152:TYR:CD1	1:B:182:ASP:HB3	2.34	0.63
1:C:413:LYS:HG3	1:C:418:ARG:HH12	1.62	0.63
1:A:141:LYS:HD2	1:A:274:LEU:CD2	2.28	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:128:ARG:NH2	1:B:289:ALA:O	2.32	0.62
1:C:179:TYR:CZ	1:C:455:ALA:HB2	2.35	0.62
1:C:23:TYR:OH	1:C:32:LEU:HD21	1.99	0.62
1:C:419:PHE:C	1:C:424:LYS:HG3	2.20	0.62
1:C:336:ASP:O	1:C:340:PRO:HB3	1.99	0.62
1:C:226:PHE:CE1	1:C:228:PHE:HB2	2.34	0.62
1:C:290:LEU:HD23	1:C:291:SER:O	1.99	0.62
1:C:336:ASP:OD2	1:C:341:ASN:HB2	1.98	0.62
1:A:242:PRO:O	1:A:243:ARG:CB	2.44	0.62
1:A:118:ILE:H	1:A:298:GLN:HE22	1.47	0.61
1:B:369:ILE:HA	1:B:483:LEU:HB2	1.83	0.61
1:C:143:LYS:O	1:C:146:VAL:HG22	2.01	0.61
1:B:324:HIS:NE2	1:B:413:LYS:NZ	2.48	0.60
1:A:269:VAL:HG22	1:A:269:VAL:O	2.02	0.60
1:A:87:PRO:HG3	1:A:431:ILE:HD11	1.83	0.60
1:C:128:ARG:O	1:C:132:LEU:HG	2.02	0.60
1:C:290:LEU:HG	1:C:294:GLU:HB3	1.84	0.60
1:B:340:PRO:O	1:B:341:ASN:HB2	2.01	0.60
3:C:602:08J:CAA	3:C:602:08J:CAI	2.79	0.59
1:A:106:ARG:HD2	1:A:374:GLU:OE1	2.03	0.59
1:A:496:ARG:O	1:A:497:ASP:HB2	2.03	0.59
1:C:186:SER:HA	1:C:191:VAL:H	1.66	0.59
1:A:264:THR:HG22	1:A:264:THR:O	2.03	0.58
1:B:156:LEU:HD13	1:B:179:TYR:HB2	1.84	0.58
1:C:317:ILE:HG21	1:C:456:LEU:HD11	1.84	0.58
1:A:63:GLU:HG2	1:A:66:LYS:HE3	1.85	0.58
1:B:47:LEU:O	1:B:50:ILE:HG23	2.02	0.58
1:C:221:LEU:HD21	1:C:240:VAL:HG11	1.85	0.58
1:C:363:THR:O	1:C:367:PHE:N	2.34	0.58
1:A:317:ILE:HD13	1:A:456:LEU:HD11	1.85	0.57
1:C:309:THR:CG2	3:C:602:08J:CLAC	2.88	0.57
1:B:328:GLN:O	1:B:332:GLN:HB2	2.05	0.57
1:B:87:PRO:HG3	1:B:431:ILE:HD11	1.85	0.57
1:C:341:ASN:O	1:C:342:LYS:HB2	2.05	0.56
1:C:413:LYS:CG	1:C:418:ARG:NH1	2.67	0.56
1:B:172:LEU:HD11	1:B:491:LEU:HD12	1.88	0.56
1:A:253:VAL:O	1:A:257:LYS:HG2	2.06	0.56
1:A:101:VAL:HG21	1:A:381:VAL:HG11	1.86	0.56
2:A:601:HEM:HAA1	3:A:602:08J:H8	1.88	0.55
1:A:257:LYS:N	4:A:701:HOH:O	2.39	0.55
1:A:415:LEU:O	1:A:418:ARG:HG3	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:180:SER:O	1:A:184[A]:ILE:HG13	2.07	0.55
1:B:288:LYS:O	1:B:289:ALA:HB3	2.06	0.55
1:C:146:VAL:HG21	1:C:347:TYR:HB2	1.89	0.55
1:A:305:ALA:HB2	3:A:602:08J:CAA	2.37	0.55
1:A:57:PHE:HD1	1:A:57:PHE:H	1.53	0.54
1:C:335:ILE:HD11	1:C:457:ILE:HA	1.89	0.54
1:A:243:ARG:HG3	1:A:243:ARG:O	2.07	0.54
1:C:292:ASP:O	1:C:295:LEU:HB3	2.07	0.54
2:A:601:HEM:HBC2	2:A:601:HEM:HMC1	1.89	0.54
2:C:601:HEM:HBD2	2:C:601:HEM:HMD2	1.89	0.54
1:C:260:ARG:HG2	1:C:261:LEU:H	1.73	0.54
1:A:148:ILE:N	1:A:148:ILE:HD12	2.23	0.54
1:A:189:PHE:CE2	1:A:303:ILE:HD11	2.43	0.53
1:A:257:LYS:HG3	4:A:701:HOH:O	2.09	0.53
1:C:179:TYR:OH	1:C:455:ALA:HB2	2.09	0.53
1:A:221:LEU:HD21	1:A:240:VAL:HG11	1.90	0.53
1:C:161:ARG:HG3	1:C:463:PHE:HZ	1.73	0.53
1:A:191:VAL:HG12	1:A:192:ASN:N	2.24	0.53
1:C:172:LEU:HD23	1:C:176:PHE:CE2	2.44	0.53
1:A:466:LYS:NZ	1:A:494:GLU:HB2	2.23	0.53
1:B:317:ILE:HG21	1:B:456:LEU:HD11	1.91	0.53
1:A:189:PHE:HE2	1:A:303:ILE:HD11	1.74	0.52
1:B:443:ILE:HG22	2:B:601:HEM:HMD2	1.92	0.52
1:C:324:HIS:O	1:C:327:VAL:HG22	2.10	0.52
1:C:111:VAL:HG21	1:C:215:PHE:HZ	1.74	0.52
1:C:365:ARG:HA	1:C:402:HIS:ND1	2.25	0.52
2:A:601:HEM:HBC2	2:A:601:HEM:CMC	2.40	0.52
1:B:269:VAL:O	1:B:269:VAL:HG13	2.10	0.52
1:B:132:LEU:HD21	1:B:288:LYS:HA	1.92	0.52
1:A:371:MET:HE1	1:A:481:GLY:CA	2.40	0.52
1:B:386:MET:HA	4:B:732:HOH:O	2.09	0.52
1:A:369:ILE:HA	1:A:483:LEU:HB3	1.92	0.52
1:A:261:LEU:HD12	1:A:264:THR:OG1	2.10	0.52
1:C:101:VAL:HG11	1:C:381:VAL:HG21	1.92	0.52
1:A:428:ASP:HB3	1:A:431:ILE:HG12	1.92	0.51
1:B:316:PHE:HE1	1:B:475:LEU:HD21	1.75	0.51
1:C:443:ILE:HG22	2:C:601:HEM:HMD3	1.92	0.51
1:B:179:TYR:CZ	1:B:455:ALA:HB2	2.45	0.51
1:C:183:VAL:HG11	1:C:451:ASN:ND2	2.25	0.51
1:A:261:LEU:CD1	1:A:264:THR:OG1	2.58	0.51
1:B:287:HIS:CD2	1:B:288:LYS:HB2	2.45	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:364:LEU:HD22	1:C:434:PRO:HB2	1.93	0.51
1:B:338:VAL:C	1:B:340:PRO:HD3	2.30	0.51
1:A:362:GLU:OE2	1:A:362:GLU:HA	2.11	0.51
1:B:342:LYS:O	1:B:458:ARG:NH1	2.44	0.51
1:C:221:LEU:HD21	1:C:240:VAL:CG1	2.41	0.51
1:B:423:ASN:HB3	1:B:426:ASN:HD21	1.76	0.51
1:C:321:LEU:HB3	1:C:328:GLN:HE21	1.75	0.51
1:A:109:GLY:O	1:A:111:VAL:HG23	2.11	0.50
1:C:160:LEU:HD13	1:C:175:VAL:HG21	1.92	0.50
3:A:602:08J:H3	3:A:602:08J:H5	1.93	0.50
1:B:151:GLN:O	1:B:155:VAL:HG23	2.11	0.50
1:C:119:SER:OG	3:C:602:08J:H4	2.11	0.50
3:B:602:08J:H5	3:B:602:08J:H3	1.92	0.50
1:B:110:PRO:HG3	1:B:234:GLU:HG3	1.92	0.49
1:A:156:LEU:HD13	1:A:179:TYR:HB2	1.94	0.49
1:C:84:ILE:HD12	1:C:89:MET:HB3	1.95	0.49
1:B:179:TYR:CE2	1:B:455:ALA:HB2	2.46	0.49
1:C:111:VAL:HG21	1:C:215:PHE:CE2	2.46	0.49
1:C:251:LYS:HG3	1:C:254:LYS:HD3	1.94	0.49
1:C:333:GLU:HA	1:C:335:ILE:HG22	1.94	0.49
1:C:413:LYS:CE	1:C:418:ARG:HD3	2.43	0.49
1:C:102:PHE:CE1	1:C:394:VAL:HG21	2.48	0.49
1:A:371:MET:CE	1:A:481:GLY:C	2.80	0.49
1:B:287:HIS:CA	1:B:288:LYS:HB2	2.43	0.49
1:C:362:GLU:HG3	1:C:418:ARG:CZ	2.41	0.49
1:C:313:VAL:HB	1:C:452:MET:SD	2.53	0.49
1:A:184[A]:ILE:O	1:A:188:SER:HB2	2.12	0.48
1:A:184[A]:ILE:HG21	1:A:303:ILE:HA	1.95	0.48
1:A:477:LEU:HD13	1:A:483:LEU:HD11	1.95	0.48
1:C:210:LEU:HD11	1:C:241:PHE:HZ	1.77	0.48
1:C:365:ARG:NH1	1:C:402:HIS:O	2.46	0.48
1:C:413:LYS:NZ	1:C:418:ARG:HD3	2.29	0.48
1:A:231:PRO:O	1:A:235:VAL:HG23	2.14	0.48
1:A:105:ARG:NH1	3:A:602:08J:H7	2.28	0.48
1:A:151:GLN:O	1:A:155:VAL:HG23	2.13	0.48
1:A:243:ARG:O	1:A:247:ASN:CG	2.51	0.48
1:C:201:ASP:HB3	1:C:204:VAL:HG23	1.96	0.48
1:C:210:LEU:HD21	1:C:300:ILE:HG23	1.96	0.48
1:C:210:LEU:CD1	1:C:241:PHE:HZ	2.26	0.48
1:C:366:LEU:O	1:C:403:ARG:NH2	2.29	0.48
1:C:260:ARG:HG2	1:C:261:LEU:N	2.28	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:ASP:OD2	1:A:106:ARG:NH2	2.46	0.47
1:C:92:THR:HA	1:C:96:LYS:HB2	1.95	0.47
1:A:256:MET:O	1:A:260:ARG:HG3	2.14	0.47
1:A:93:VAL:HG21	1:A:394:VAL:HG11	1.97	0.47
1:B:396:ILE:HD12	1:B:396:ILE:N	2.29	0.47
1:B:305:ALA:HB2	3:B:602:08J:CAA	2.44	0.47
1:B:193:ILE:HG22	1:B:194:ASP:N	2.29	0.47
1:C:117:ALA:HB1	1:C:301:ILE:CG1	2.44	0.47
1:C:413:LYS:CD	1:C:418:ARG:HH11	2.27	0.47
2:C:601:HEM:C4D	3:C:602:08J:H3	2.49	0.47
1:B:370:ALA:O	1:B:371:MET:HB3	2.14	0.47
1:B:173:LYS:HD3	1:B:488:PRO:HG3	1.96	0.47
1:B:153:GLY:O	1:B:458:ARG:HG2	2.14	0.47
1:A:118:ILE:HD12	1:A:133:LEU:HD12	1.96	0.47
1:C:413:LYS:HE3	1:C:418:ARG:HD3	1.96	0.47
1:C:358:MET:HG2	1:C:419:PHE:HB3	1.96	0.47
1:B:287:HIS:CB	1:B:288:LYS:HB2	2.45	0.47
1:C:24:LEU:O	1:C:27:THR:HB	2.15	0.47
1:C:342:LYS:HA	1:C:461:GLN:NE2	2.30	0.47
1:B:255:ARG:O	1:B:259:SER:OG	2.22	0.47
1:C:309:THR:HG22	1:C:369:ILE:HD13	1.97	0.47
1:B:403:ARG:HA	1:B:411:PRO:HB3	1.97	0.47
1:C:464:SER:OG	1:C:494:GLU:HB2	2.15	0.47
1:A:104:ASN:HB2	4:A:731:HOH:O	2.14	0.46
1:A:111:VAL:O	1:A:111:VAL:HG12	2.15	0.46
1:A:186:SER:HA	1:A:191:VAL:O	2.15	0.46
1:B:93:VAL:HG21	1:B:394:VAL:HG11	1.96	0.46
1:C:128:ARG:NH1	1:C:289:ALA:O	2.47	0.46
1:C:369:ILE:CG1	3:C:602:08J:CLAC	2.93	0.46
1:B:457:ILE:O	1:B:461:GLN:HG3	2.15	0.46
1:C:223:ILE:HD12	1:C:230:ILE:CG1	2.45	0.46
1:C:260:ARG:HB3	1:C:262:GLU:HB2	1.98	0.46
1:C:320:GLU:O	1:C:324:HIS:HB2	2.16	0.46
1:A:79:GLN:NE2	1:A:393:VAL:HG23	2.31	0.46
1:C:443:ILE:CG2	2:C:601:HEM:HMD3	2.45	0.46
1:C:50:ILE:HA	1:C:53:TYR:HD2	1.80	0.46
1:B:91:LYS:HG3	1:B:430:TYR:CZ	2.51	0.46
1:C:260:ARG:NH2	1:C:276:ILE:HG23	2.31	0.46
2:B:601:HEM:HH C	2:B:601:HEM:HBB2	1.98	0.46
1:C:257:LYS:HG3	1:C:276:ILE:HG12	1.97	0.46
1:C:93:VAL:HA	1:C:102:PHE:CD2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:166:THR:HG22	1:C:166:THR:O	2.15	0.45
1:A:221:LEU:HD12	1:A:223:ILE:HD11	1.98	0.45
1:A:309:THR:CG2	3:A:602:08J:CLAC	3.02	0.45
1:A:403:ARG:NH1	1:A:412:GLU:OE1	2.48	0.45
1:C:117:ALA:HB1	1:C:301:ILE:HG13	1.98	0.45
1:B:134:SER:HB3	1:B:135:PRO:HD3	1.97	0.45
1:B:130:ARG:NH1	2:B:601:HEM:O1D	2.50	0.45
1:B:157:VAL:HG23	1:B:463:PHE:CZ	2.51	0.45
1:C:468:CYS:SG	1:C:469:LYS:N	2.89	0.45
1:C:119:SER:OG	3:C:602:08J:NAN	2.44	0.45
1:A:144:GLU:O	1:A:269:VAL:HG11	2.15	0.45
1:B:288:LYS:HG2	1:B:289:ALA:N	2.32	0.45
1:B:426:ASN:OD1	1:B:426:ASN:N	2.50	0.45
2:C:601:HEM:HMC2	2:C:601:HEM:HBC2	1.97	0.45
1:A:263:ASP:HB2	1:C:158:ARG:NH1	2.32	0.45
1:C:316:PHE:HB3	1:C:363:THR:HG23	1.98	0.45
1:A:350:VAL:HG21	1:A:454:LEU:HD23	1.98	0.45
1:B:386:MET:HE3	1:B:388:ILE:HD11	1.99	0.45
1:C:209:LYS:HG3	1:C:212:ARG:NH2	2.32	0.45
1:C:39:PRO:HG2	1:C:68:TYR:HB3	1.99	0.44
1:A:120:ILE:HD11	1:A:215:PHE:HE2	1.83	0.44
1:A:256:MET:N	4:A:701:HOH:O	2.50	0.44
1:A:120:ILE:HD11	1:A:215:PHE:CE2	2.52	0.44
1:A:211:LEU:HD21	1:A:303:ILE:HG22	1.99	0.44
1:B:301:ILE:HD12	1:B:301:ILE:HA	1.86	0.44
1:A:148:ILE:HD12	1:A:148:ILE:H	1.83	0.44
1:A:193:ILE:HG22	1:A:194:ASP:H	1.81	0.44
1:C:257:LYS:HG2	1:C:257:LYS:O	2.18	0.44
1:C:344:PRO:HA	1:C:345:PRO:HD3	1.84	0.44
1:C:161:ARG:CG	1:C:463:PHE:HZ	2.30	0.44
1:C:71:VAL:HG21	1:C:386:MET:SD	2.58	0.44
1:A:193:ILE:HG22	1:A:194:ASP:N	2.32	0.44
1:A:40:GLY:HA3	1:A:73:GLY:O	2.18	0.44
1:C:408:TRP:HD1	1:C:413:LYS:HZ1	1.65	0.43
1:A:259:SER:O	1:A:263:ASP:HB3	2.17	0.43
1:B:138:THR:OG1	1:B:141:LYS:HG2	2.18	0.43
1:C:428:ASP:C	1:C:430:TYR:H	2.21	0.43
1:B:159:ASN:HA	1:B:162:ARG:HD2	2.00	0.43
1:B:243:ARG:HG2	1:B:247:ASN:HD21	1.84	0.43
1:B:83:ALA:HA	1:B:395:MET:O	2.19	0.43
1:C:456:LEU:O	1:C:459:VAL:HG22	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:601:HEM:CMB	2:C:601:HEM:HBB2	2.46	0.43
1:A:91:LYS:NZ	4:A:707:HOH:O	2.51	0.43
1:B:257:LYS:HG2	1:B:276:ILE:HD11	1.99	0.43
1:A:252:SER:O	1:A:255:ARG:HG2	2.19	0.43
1:A:330:LYS:HD3	1:A:355:TYR:CZ	2.54	0.43
1:B:383:ILE:HG13	1:B:383:ILE:O	2.19	0.43
1:C:152:TYR:OH	1:C:186:SER:HB3	2.18	0.43
1:C:331:LEU:HD12	1:C:355:TYR:HB3	2.01	0.43
1:A:186:SER:O	1:A:190:GLY:HA2	2.19	0.43
1:A:27:THR:CG2	1:A:28:HIS:N	2.81	0.43
1:A:252:SER:O	1:A:256:MET:HG3	2.19	0.42
1:B:194:ASP:OD2	1:B:197:ASN:HB2	2.18	0.42
1:C:294:GLU:O	1:C:298:GLN:HG2	2.19	0.42
1:C:343:ALA:HA	1:C:344:PRO:HD3	1.94	0.42
1:A:111:VAL:HG11	1:A:215:PHE:HZ	1.84	0.42
1:A:275:MET:HB3	1:A:295:LEU:CD1	2.49	0.42
1:C:223:ILE:HD13	1:C:229:LEU:HD23	2.01	0.42
1:C:419:PHE:CA	1:C:424:LYS:HG3	2.49	0.42
1:A:133:LEU:HD11	1:A:298:GLN:HE21	1.85	0.42
1:A:309:THR:HG22	3:A:602:08J:CLAC	2.56	0.42
1:B:318:MET:HE2	1:B:321:LEU:HD12	2.00	0.42
1:C:172:LEU:HD23	1:C:176:PHE:HE2	1.84	0.42
1:C:189:PHE:CZ	1:C:249:LEU:HD23	2.54	0.42
1:C:331:LEU:HD12	1:C:355:TYR:HD2	1.82	0.42
1:B:287:HIS:HA	1:B:288:LYS:HB2	2.01	0.42
1:A:298:GLN:O	1:A:301:ILE:HG22	2.19	0.42
1:C:413:LYS:HE3	1:C:418:ARG:CD	2.49	0.42
1:C:111:VAL:HG23	1:C:241:PHE:HB3	2.02	0.42
1:C:130:ARG:HD2	1:C:443:ILE:HD12	2.02	0.42
1:C:111:VAL:HG23	1:C:241:PHE:CB	2.50	0.42
1:A:305:ALA:HB2	3:A:602:08J:H5	2.02	0.42
1:C:265:GLN:HE21	1:C:267:HIS:HB2	1.85	0.42
1:A:410:GLU:OE2	1:A:413:LYS:HE3	2.20	0.42
1:B:318:MET:CE	1:B:321:LEU:HD12	2.50	0.42
1:B:50:ILE:O	1:B:53:TYR:HB2	2.20	0.42
1:A:344:PRO:HA	1:A:345:PRO:HD3	1.92	0.42
1:B:221:LEU:HD11	1:B:240:VAL:HG21	2.02	0.42
1:C:362:GLU:HG3	4:C:701:HOH:O	2.19	0.42
1:C:420:SER:O	1:C:424:LYS:HE2	2.20	0.42
1:C:405:PRO:HA	1:C:411:PRO:HG3	2.02	0.41
1:C:161:ARG:HG3	1:C:463:PHE:CZ	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:356:LEU:HD21	1:A:453:LYS:HB3	2.02	0.41
1:B:187:THR:O	1:B:271:PHE:N	2.36	0.41
1:A:260:ARG:HD3	1:A:273:GLN:OE1	2.20	0.41
1:B:318:MET:HA	1:B:318:MET:HE2	2.01	0.41
1:A:184[A]:ILE:HD11	1:A:307:TYR:HA	2.02	0.41
1:A:492:LYS:NZ	4:A:711:HOH:O	2.54	0.41
1:A:496:ARG:O	1:A:497:ASP:CB	2.69	0.41
1:B:128:ARG:HH12	1:B:294:GLU:CD	2.24	0.41
1:C:52:SER:HB3	1:C:60:PHE:CD1	2.55	0.41
1:A:133:LEU:HD11	1:A:298:GLN:NE2	2.35	0.41
1:A:365:ARG:O	1:A:402:HIS:HB3	2.21	0.41
1:B:372:ARG:HG2	1:B:395:MET:SD	2.60	0.41
1:B:413:LYS:HD2	1:B:413:LYS:HA	1.97	0.41
1:C:300:ILE:HA	1:C:303:ILE:HD12	2.03	0.41
1:C:324:HIS:CE1	1:C:414:PHE:HB3	2.56	0.41
1:B:264:THR:O	1:B:266:LYS:HG3	2.21	0.41
1:C:58:CYS:SG	1:C:371:MET:HG2	2.61	0.41
2:C:601:HEM:CMD	2:C:601:HEM:CBD	2.99	0.41
1:C:118:ILE:HD12	1:C:133:LEU:HD12	2.03	0.41
1:C:346:THR:O	1:C:347:TYR:C	2.59	0.41
1:B:254:LYS:HB2	1:B:254:LYS:HE3	1.89	0.40
1:C:230:ILE:HB	1:C:231:PRO:CD	2.51	0.40
2:C:601:HEM:CMD	2:C:601:HEM:HBD2	2.51	0.40
1:A:241:PHE:HA	1:A:242:PRO:HD3	1.85	0.40
1:A:184[B]:ILE:CG2	1:A:303:ILE:HG12	2.51	0.40
1:A:57:PHE:CD1	1:A:57:PHE:N	2.89	0.40
1:C:340:PRO:O	1:C:340:PRO:CG	2.69	0.40
1:C:102:PHE:HE1	1:C:394:VAL:HG21	1.84	0.40
1:C:415:LEU:H	1:C:418:ARG:NH1	2.15	0.40
1:A:191:VAL:CG1	1:A:192:ASN:N	2.83	0.40
1:A:216:LEU:HD13	3:A:602:08J:CAR	2.52	0.40
1:C:111:VAL:HG22	1:C:111:VAL:O	2.22	0.40
1:C:159:ASN:O	1:C:162:ARG:CB	2.70	0.40
1:C:253:VAL:O	1:C:257:LYS:N	2.55	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:354:GLU:OE2	1:C:466:LYS:CE[4_545]	2.18	0.02

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	465/487 (96%)	435 (94%)	29 (6%)	1 (0%)	52	80
1	B	467/487 (96%)	424 (91%)	43 (9%)	0	100	100
1	C	465/487 (96%)	402 (86%)	62 (13%)	1 (0%)	52	80
All	All	1397/1461 (96%)	1261 (90%)	134 (10%)	2 (0%)	56	83

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	243	ARG
1	C	347	TYR

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	430/443 (97%)	419 (97%)	11 (3%)	54	83
1	B	430/443 (97%)	417 (97%)	13 (3%)	48	79
1	C	428/443 (97%)	411 (96%)	17 (4%)	38	69
All	All	1288/1329 (97%)	1247 (97%)	41 (3%)	46	77

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	188	SER

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Mol	Chain	Res	Type
1	A	193	ILE
1	A	222	SER
1	A	225	VAL
1	A	241	PHE
1	A	275	MET
1	A	291	SER
1	A	425	ASP
1	A	426	ASN
1	A	466	LYS
1	A	469	LYS
1	B	27	THR
1	B	34	LYS
1	B	101	VAL
1	B	174	ASP
1	B	188	SER
1	B	225	VAL
1	B	256	MET
1	B	269	VAL
1	B	274	LEU
1	B	371	MET
1	B	458	ARG
1	B	475	LEU
1	B	496	ARG
1	C	63	GLU
1	C	104	ASN
1	C	149	ILE
1	C	203	PHE
1	C	225	VAL
1	C	261	LEU
1	C	264	THR
1	C	294	GLU
1	C	301	ILE
1	C	315	SER
1	C	331	LEU
1	C	362	GLU
1	C	380	ASP
1	C	419	PHE
1	C	454	LEU
1	C	460	LEU
1	C	477	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	54	HIS
1	A	298	GLN
1	B	287	HIS
1	B	341	ASN
1	C	151	GLN
1	C	265	GLN
1	C	279	GLN
1	C	324	HIS
1	C	328	GLN
1	C	332	GLN
1	C	461	GLN

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 carbohydrates 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	$\# Z > 2$
2	HEM	A	601	1	24,50,50	0.77	1 (4%)	16,82,82	1.54	2 (12%)
3	08J	A	602	-	20,26,26	0.87	0	26,38,38	4.11	8 (30%)
2	HEM	B	601	1	24,50,50	0.73	1 (4%)	16,82,82	1.41	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	08J	B	602	-	20,26,26	0.99	1 (5%)	26,38,38	2.31	7 (26%)
2	HEM	C	601	1	24,50,50	0.74	1 (4%)	16,82,82	1.24	2 (12%)
3	08J	C	602	-	20,26,26	1.36	2 (10%)	26,38,38	7.38	10 (38%)

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	601	1	-	0/6/54/54	0/0/8/8
3	08J	A	602	-	-	0/4/17/17	0/3/4/4
2	HEM	B	601	1	-	0/6/54/54	0/0/8/8
3	08J	B	602	-	-	0/4/17/17	0/3/4/4
2	HEM	C	601	1	-	0/6/54/54	0/0/8/8
3	08J	C	602	-	-	0/4/17/17	0/3/4/4

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	602	08J	CAO-NAM	-4.60	1.22	1.28
2	A	601	HEM	C3B-C2B	-2.27	1.37	1.40
2	B	601	HEM	C3B-C2B	-2.18	1.37	1.40
2	C	601	HEM	C3B-C2B	-2.06	1.37	1.40
3	B	602	08J	CAP-CLAC	2.09	1.79	1.74
3	C	602	08J	CAU-CAV	2.56	1.42	1.39

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	602	08J	CAU-CAO-NAM	-16.01	96.73	125.06
3	C	602	08J	CAV-CAU-CAO	-7.35	111.83	122.82
3	A	602	08J	CAU-CAO-NAM	-5.48	115.36	125.06
2	A	601	HEM	CBA-CAA-C2A	-3.78	105.84	112.49
2	B	601	HEM	C3C-CAC-CBC	-3.65	119.07	126.40
3	B	602	08J	CAK-CAU-CAO	-3.41	114.58	118.98
3	A	602	08J	CAV-CAU-CAO	-2.63	118.89	122.82
2	C	601	HEM	C3C-CAC-CBC	-2.35	121.67	126.40
3	C	602	08J	CAF-CAQ-CAT	-2.28	120.64	123.16
3	B	602	08J	CAU-CAO-NAM	-2.19	121.18	125.06
2	A	601	HEM	C3B-CAB-CBB	-2.12	122.13	126.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	HEM	CMA-C3A-C4A	-2.00	124.90	128.31
3	B	602	08J	CAS-NAW-CAR	2.13	111.97	109.64
3	A	602	08J	CAT-CAO-CAU	2.18	121.09	117.81
3	B	602	08J	CAG-CAT-CAQ	2.25	119.19	116.61
3	A	602	08J	CAS-NAW-CAR	2.30	112.16	109.64
3	C	602	08J	CAK-CAU-CAO	2.48	122.18	118.98
3	C	602	08J	CAG-CAT-CAQ	2.80	119.81	116.61
3	C	602	08J	CAH-CAI-CAV	2.85	124.11	119.46
3	A	602	08J	CAG-CAT-CAQ	2.92	119.95	116.61
3	A	602	08J	CAT-CAO-NAM	3.25	121.61	116.66
3	B	602	08J	CAH-CAI-CAV	3.26	124.78	119.46
3	B	602	08J	CAK-CAU-CAV	4.03	122.08	117.33
3	A	602	08J	CAK-CAU-CAV	6.10	124.52	117.33
3	C	602	08J	CAK-CAU-CAV	7.33	125.97	117.33
3	C	602	08J	CAT-CAO-CAU	7.37	128.89	117.81
3	B	602	08J	CAL-NAM-CAO	8.26	127.99	117.53
3	C	602	08J	CAT-CAO-NAM	11.57	134.26	116.66
3	A	602	08J	CAL-NAM-CAO	17.64	139.87	117.53
3	C	602	08J	CAL-NAM-CAO	28.67	153.83	117.53

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 36 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	HEM	3	0
3	A	602	08J	8	0
2	B	601	HEM	3	0
3	B	602	08J	2	0
2	C	601	HEM	9	0
3	C	602	08J	13	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	470/487 (96%)	-0.14	5 (1%) 82 83	25, 48, 90, 163	0
1	B	471/487 (96%)	0.08	12 (2%) 61 61	25, 63, 121, 167	0
1	C	469/487 (96%)	0.56	42 (8%) 12 9	38, 96, 163, 186	0
All	All	1410/1461 (96%)	0.17	59 (4%) 40 39	25, 65, 145, 186	0

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	263	ASP	5.4
1	C	269	VAL	4.8
1	C	165	GLU	4.7
1	C	162	ARG	4.4
1	C	351	LEU	4.3
1	B	497	ASP	4.0
1	C	288	LYS	4.0
1	A	264	THR	3.8
1	B	267	HIS	3.8
1	C	338	VAL	3.7
1	C	347	TYR	3.5
1	A	265	GLN	3.5
1	C	354	GLU	3.4
1	C	258	GLU	3.4
1	C	360	VAL	3.4
1	C	335	ILE	3.3
1	C	329	GLN	3.2
1	C	426	ASN	3.2
1	B	260	ARG	3.2
1	C	456	LEU	2.9
1	C	350	VAL	2.9
1	C	189	PHE	2.9
1	C	462	ASN	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	454	LEU	2.8
1	C	417	GLU	2.7
1	C	99	TYR	2.6
1	B	470	GLU	2.6
1	B	255	ARG	2.6
1	C	408	TRP	2.6
1	B	468	CYS	2.6
1	C	323	THR	2.5
1	C	493	VAL	2.5
1	C	333	GLU	2.4
1	C	203	PHE	2.4
1	C	190	GLY	2.4
1	A	268	ARG	2.3
1	C	427	ILE	2.3
1	C	281	SER	2.3
1	B	257	LYS	2.2
1	B	261	LEU	2.2
1	C	192	ASN	2.2
1	B	203	PHE	2.2
1	C	194	ASP	2.2
1	C	186	SER	2.2
1	C	262	GLU	2.2
1	C	419	PHE	2.2
1	C	316	PHE	2.2
1	B	259	SER	2.2
1	B	258	GLU	2.1
1	C	363	THR	2.1
1	C	319	TYR	2.1
1	C	143	LYS	2.1
1	C	475	LEU	2.1
1	B	421	LYS	2.1
1	A	261	LEU	2.1
1	C	352	GLN	2.1
1	C	494	GLU	2.1
1	A	243	ARG	2.0
1	C	289	ALA	2.0

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

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(\AA^2)	Q<0.9
3	08J	C	602	23/23	0.88	0.26	1.76	73,87,95,115	0
3	08J	A	602	23/23	0.96	0.17	0.78	32,34,37,37	0
3	08J	B	602	23/23	0.96	0.15	0.08	39,40,42,44	0
2	HEM	C	601	43/43	0.95	0.19	-0.23	58,62,67,70	0
2	HEM	A	601	43/43	0.98	0.13	-0.31	22,25,30,31	0
2	HEM	B	601	43/43	0.97	0.14	-0.39	29,37,41,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.