



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 01:18 PM GMT

PDB ID : 3TJS
Title : Crystal Structure of the complex between human cytochrome P450 3A4 and desthiazolylmethyloxycarbonyl ritonavir
Authors : Sevrioukova, I.F.; Poulos, T.L.
Deposited on : 2011-08-24
Resolution : 2.25 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

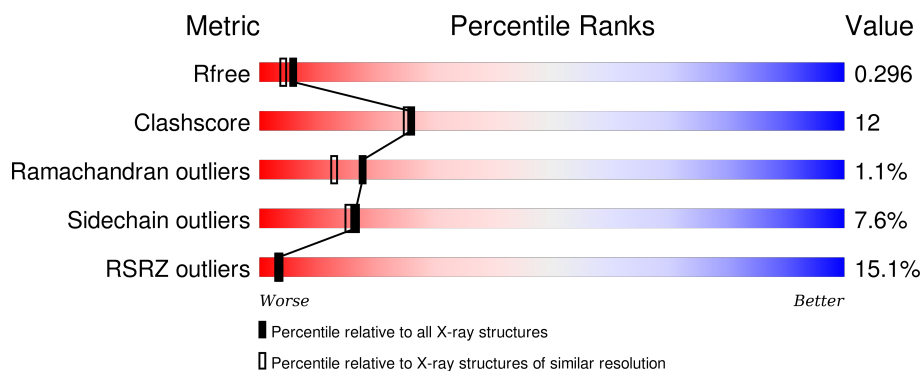
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.25 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	1640 (2.28-2.24)
Clashscore	102246	1095 (2.26-2.26)
Ramachandran outliers	100387	1063 (2.26-2.26)
Sidechain outliers	100360	1063 (2.26-2.26)
RSRZ outliers	91569	1647 (2.28-2.24)

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	

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	D0R	A	600	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3751 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
			Total	C	N	O	S			
1	A	449	3617	2354	597	642	24	0	1	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
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

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

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- Chemical structure of DOR (Dorazepam) is shown. The structure features a benzodiazepine core. The benzene ring is substituted with a 2-chlorophenyl group at position 5 and a 2-(4-chlorophenyl)-2-methyl-5-oxo-1,3-dihydro-4H-benzodiazepin-4-yl group at position 1. The structure is labeled with atom names (C1, C2, N1, etc.) and includes stereochemistry at C3 and C4.

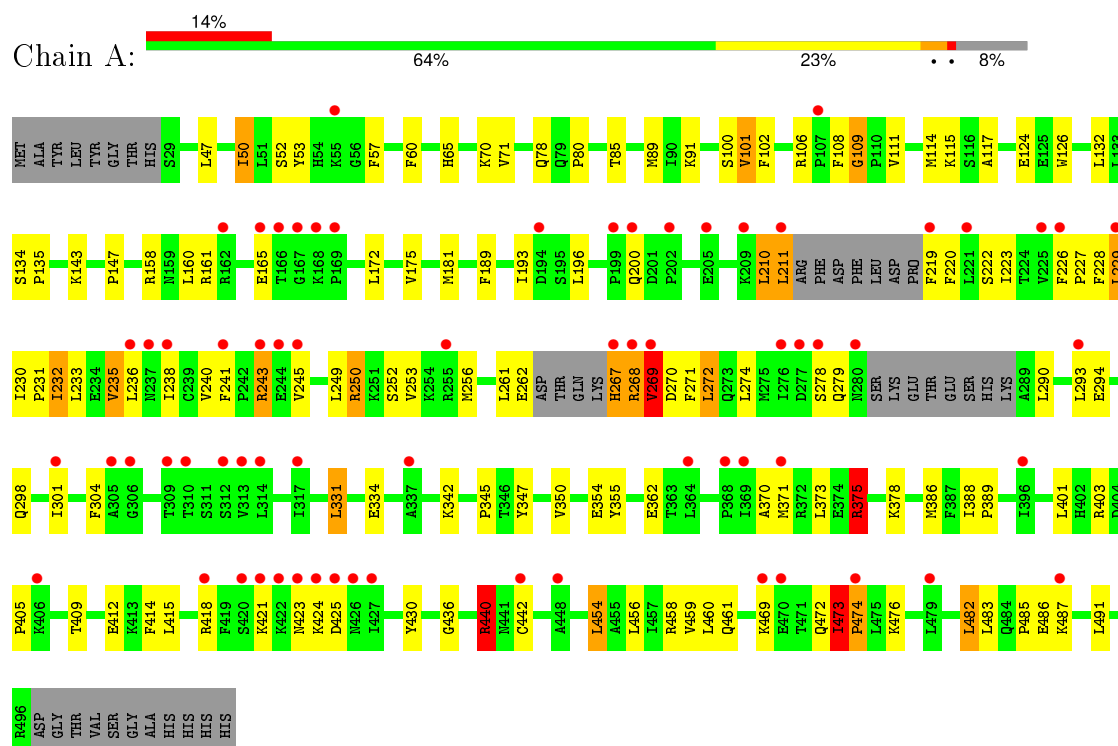
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	50	Total O 50 50	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 ($\text{RSRZ} > 2$). 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



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	78.79 Å 98.60 Å 125.07 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.40 – 2.25 38.40 – 2.25	Depositor EDS
% Data completeness (in resolution range)	98.5 (38.40-2.25) 98.4 (38.40-2.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.23 (at 2.24 Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.228 , 0.297 0.228 , 0.296	Depositor DCC
R_{free} test set	1178 reflections (5.36%)	DCC
Wilson B-factor (Å ²)	45.3	Xtriage
Anisotropy	0.458	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 58.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 23179 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	3751	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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: HEM, D0R

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	0.93	1/3705 (0.0%)	0.98	13/5008 (0.3%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	262	GLU	CG-CD	6.40	1.61	1.51

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	375	ARG	NE-CZ-NH2	-17.14	111.73	120.30
1	A	440	ARG	NE-CZ-NH1	-12.62	113.99	120.30
1	A	375	ARG	NE-CZ-NH1	10.94	125.77	120.30
1	A	440	ARG	NE-CZ-NH2	10.06	125.33	120.30
1	A	440	ARG	CD-NE-CZ	8.21	135.09	123.60
1	A	375	ARG	CG-CD-NE	-8.05	94.90	111.80
1	A	440	ARG	CG-CD-NE	-6.81	97.50	111.80
1	A	473	ILE	C-N-CD	-5.99	107.42	120.60
1	A	375	ARG	CD-NE-CZ	5.73	131.62	123.60
1	A	270	ASP	N-CA-C	5.70	126.38	111.00
1	A	269	VAL	O-C-N	-5.42	114.03	122.70
1	A	373	LEU	CB-CG-CD1	-5.34	101.91	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	261	LEU	CA-CB-CG	5.05	126.91	115.30

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	267	HIS	Peptide
1	A	269	VAL	Mainchain
1	A	473	ILE	Peptide

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	3617	0	3715	89	0
2	A	43	0	30	2	0
3	A	41	0	44	7	0
4	A	50	0	0	3	0
All	All	3751	0	3789	93	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 12.

All (93) 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:250:ARG:HH11	1:A:250:ARG:HG2	1.12	1.15
1:A:269:VAL:O	1:A:269:VAL:HG12	1.69	0.91
1:A:250:ARG:NH1	1:A:250:ARG:HG2	1.85	0.86
1:A:304:PHE:HB3	3:A:600:D0R:H48	1.68	0.76
1:A:269:VAL:O	1:A:269:VAL:CG1	2.35	0.74
1:A:230:ILE:HB	1:A:231:PRO:HD3	1.69	0.74
1:A:409:THR:O	1:A:418[A]:ARG:NH2	2.20	0.74
3:A:600:D0R:C18	3:A:600:D0R:H52	2.19	0.72
1:A:210:LEU:HD21	3:A:600:D0R:H49	1.72	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:210:LEU:HB2	1:A:245:VAL:HG11	1.74	0.70
1:A:71:VAL:HG21	1:A:386:MET:HE1	1.73	0.70
1:A:172:LEU:HD11	1:A:491:LEU:HD12	1.75	0.69
1:A:354:GLU:OE2	4:A:642:HOH:O	2.11	0.68
1:A:126:TRP:CZ2	1:A:440:ARG:HG2	2.31	0.66
1:A:268:ARG:O	1:A:269:VAL:HB	1.97	0.63
1:A:211:LEU:HD21	1:A:482:LEU:HD21	1.81	0.63
1:A:375:ARG:HD2	4:A:604:HOH:O	1.99	0.62
1:A:267:HIS:ND1	1:A:268:ARG:HB3	2.16	0.59
1:A:161:ARG:O	1:A:165:GLU:HG2	2.01	0.59
1:A:229:LEU:O	1:A:232:ILE:HG22	2.03	0.58
1:A:132:LEU:HD11	1:A:278:SER:HB3	1.83	0.58
1:A:222:SER:O	1:A:226:PHE:CD2	2.57	0.58
1:A:345:PRO:HD2	1:A:458:ARG:HH11	1.68	0.58
1:A:331:LEU:HD13	1:A:460:LEU:CD1	2.34	0.58
1:A:101:VAL:HG22	1:A:102:PHE:CD1	2.39	0.57
1:A:304:PHE:CB	3:A:600:DOR:H48	2.35	0.57
1:A:371:MET:HE2	1:A:483:LEU:HD13	1.87	0.56
1:A:124:GLU:H	1:A:124:GLU:CD	2.08	0.55
1:A:108:PHE:O	1:A:109:GLY:O	2.26	0.54
1:A:485:PRO:HB2	1:A:487:LYS:O	2.08	0.54
1:A:250:ARG:CG	1:A:250:ARG:HH11	2.00	0.53
1:A:226:PHE:HB3	1:A:229:LEU:HD22	1.91	0.52
1:A:342:LYS:HD2	1:A:461:GLN:HB3	1.92	0.52
1:A:442:CYS:HB2	2:A:508:HEM:NA	2.25	0.51
1:A:228:PHE:CD1	1:A:229:LEU:HD13	2.46	0.51
1:A:370:ALA:O	1:A:371:MET:HB2	2.10	0.50
1:A:415:LEU:HB2	1:A:418[A]:ARG:NH1	2.27	0.49
1:A:91:LYS:HG3	1:A:430:TYR:CZ	2.47	0.49
1:A:134:SER:OG	1:A:135:PRO:HD3	2.12	0.49
1:A:473:ILE:HG22	1:A:474:PRO:CD	2.43	0.49
1:A:143:LYS:HG2	1:A:347:TYR:CG	2.48	0.48
1:A:294:GLU:O	1:A:298:GLN:HG2	2.13	0.48
1:A:334:GLU:OE1	1:A:355:TYR:N	2.37	0.48
1:A:228:PHE:CE1	1:A:229:LEU:HD13	2.49	0.48
1:A:65:HIS:HD2	4:A:607:HOH:O	1.97	0.47
1:A:85:THR:HB	1:A:401:LEU:HD21	1.97	0.47
1:A:222:SER:O	1:A:226:PHE:HD2	1.96	0.47
1:A:53:TYR:CE2	1:A:57:PHE:CD1	3.03	0.47
1:A:181:MET:HG3	1:A:193:ILE:HD11	1.97	0.47
1:A:371:MET:HE2	1:A:483:LEU:CD1	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:GLU:O	1:A:487:LYS:HE3	2.15	0.46
1:A:108:PHE:HD2	1:A:111:VAL:HG11	1.81	0.46
1:A:143:LYS:HE3	1:A:347:TYR:CD1	2.50	0.46
1:A:243:ARG:HH21	1:A:243:ARG:HB2	1.81	0.46
1:A:226:PHE:CB	1:A:229:LEU:HD22	2.46	0.46
1:A:233:LEU:HA	1:A:236:LEU:HD12	1.96	0.46
3:A:600:D0R:H14A	3:A:600:D0R:C28	2.44	0.46
1:A:101:VAL:HG22	1:A:102:PHE:CE1	2.52	0.45
1:A:403:ARG:O	1:A:405:PRO:HD3	2.17	0.45
1:A:268:ARG:O	1:A:269:VAL:CB	2.64	0.45
3:A:600:D0R:N58	3:A:600:D0R:O76	2.50	0.45
1:A:436:GLY:HA3	2:A:508:HEM:O2A	2.17	0.45
1:A:279:GLN:HG2	1:A:290:LEU:O	2.17	0.44
1:A:354:GLU:OE1	1:A:421:LYS:HD3	2.17	0.44
1:A:253:VAL:HG22	1:A:256:MET:HE3	2.00	0.44
1:A:47:LEU:O	1:A:50:ILE:HB	2.17	0.44
1:A:78:GLN:O	1:A:80:PRO:HD3	2.17	0.43
1:A:100:SER:O	1:A:378:LYS:HE2	2.18	0.43
3:A:600:D0R:H52	3:A:600:D0R:N58	2.32	0.43
1:A:472:GLN:NE2	1:A:476:LYS:H	2.15	0.43
1:A:423:ASN:C	1:A:425:ASP:N	2.72	0.43
1:A:232:ILE:CG2	1:A:233:LEU:N	2.81	0.42
1:A:160:LEU:HD21	1:A:175:VAL:HG21	2.01	0.42
1:A:117:ALA:HB1	1:A:301:ILE:HG13	2.00	0.42
1:A:70:LYS:HG3	1:A:71:VAL:HG23	2.01	0.42
1:A:235:VAL:HG12	1:A:236:LEU:N	2.34	0.42
1:A:223:ILE:O	1:A:226:PHE:C	2.58	0.42
1:A:487:LYS:CE	1:A:487:LYS:HA	2.49	0.42
1:A:388:ILE:HA	1:A:389:PRO:HD3	1.87	0.41
1:A:52:SER:HB3	1:A:60:PHE:CD2	2.55	0.41
1:A:423:ASN:C	1:A:425:ASP:H	2.24	0.41
1:A:227:PRO:C	1:A:229:LEU:H	2.22	0.41
1:A:189:PHE:HD2	1:A:272:LEU:HG	1.86	0.41
1:A:423:ASN:O	1:A:425:ASP:N	2.53	0.41
1:A:293:LEU:HA	1:A:293:LEU:HD23	1.82	0.41
1:A:220:PHE:HD2	1:A:223:ILE:HD11	1.86	0.41
1:A:53:TYR:CE2	1:A:57:PHE:HD1	2.39	0.41
1:A:362:GLU:HG3	1:A:414:PHE:CD1	2.55	0.41
1:A:111:VAL:O	1:A:114:MET:HB2	2.20	0.41
1:A:252:SER:O	1:A:256:MET:HG3	2.21	0.40
1:A:226:PHE:HB3	1:A:228:PHE:CZ	2.56	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:350:VAL:HG21	1:A:454:LEU:HD13	2.02	0.40
1:A:219:PHE:HZ	1:A:240:VAL:HA	1.86	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	442/487 (91%)	417 (94%)	20 (4%)	5 (1%)	17 13

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	269	VAL
1	A	474	PRO
1	A	109	GLY
1	A	424	LYS
1	A	271	PHE

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	411/443 (93%)	380 (92%)	31 (8%)	17 16

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	ILE
1	A	89	MET
1	A	101	VAL
1	A	106	ARG
1	A	115	LYS
1	A	147	PRO
1	A	158	ARG
1	A	196	LEU
1	A	200	GLN
1	A	210	LEU
1	A	211	LEU
1	A	229	LEU
1	A	232	ILE
1	A	235	VAL
1	A	238	ILE
1	A	241	PHE
1	A	243	ARG
1	A	249	LEU
1	A	250	ARG
1	A	268	ARG
1	A	272	LEU
1	A	274	LEU
1	A	331	LEU
1	A	375	ARG
1	A	412	GLU
1	A	440	ARG
1	A	454	LEU
1	A	456	LEU
1	A	459	VAL
1	A	469	LYS
1	A	482	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	247	ASN
1	A	451	ASN
1	A	461	GLN
1	A	472	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 ⓘ

2 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	508	1,3	30,50,50	2.13	11 (36%)	24,82,82	2.63	10 (41%)
3	D0R	A	600	2	40,43,43	1.21	3 (7%)	44,58,58	2.80	14 (31%)

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	508	1,3	-	0/10/54/54	0/0/8/8
3	D0R	A	600	2	-	0/42/44/44	0/3/3/3

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	508	HEM	C3B-C4B	-6.52	1.46	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	600	D0R	C95-N74	-4.87	1.27	1.45
2	A	508	HEM	C3D-C4D	-3.57	1.47	1.51
2	A	508	HEM	C2D-C1D	-2.54	1.43	1.51
2	A	508	HEM	C2C-C1C	-2.30	1.48	1.52
2	A	508	HEM	C2B-C1B	-2.16	1.44	1.51
2	A	508	HEM	C2A-C3A	-2.03	1.31	1.37
3	A	600	D0R	C80-S81	2.28	1.74	1.70
3	A	600	D0R	C13-C12	2.33	1.55	1.53
2	A	508	HEM	CMD-C2D	2.44	1.58	1.53
2	A	508	HEM	C3C-CAC	2.46	1.55	1.51
2	A	508	HEM	C3B-CAB	2.96	1.56	1.51
2	A	508	HEM	FE-ND	3.02	2.13	1.97
2	A	508	HEM	CAA-C2A	4.05	1.58	1.52

All (24) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	600	D0R	C26-C12-C13	-8.92	96.20	111.95
3	A	600	D0R	C19-C18-N58	-4.91	105.62	116.44
2	A	508	HEM	CBA-CAA-C2A	-4.69	104.12	112.53
3	A	600	D0R	C14-C15-N58	-3.42	101.14	110.66
2	A	508	HEM	CBD-CAD-C3D	-3.21	104.21	113.55
2	A	508	HEM	CMA-C3A-C4A	-3.03	123.36	128.36
2	A	508	HEM	C3B-CAB-CBB	-2.32	120.90	124.46
3	A	600	D0R	O76-C21-N74	-2.29	118.19	122.18
3	A	600	D0R	C44-C15-N58	2.33	115.80	110.56
3	A	600	D0R	C14-C15-C44	2.51	119.15	111.08
3	A	600	D0R	C28-C26-C12	2.52	118.84	113.53
3	A	600	D0R	O41-C13-C12	2.70	113.48	109.49
2	A	508	HEM	C2D-C3D-C4D	2.96	106.52	101.50
2	A	508	HEM	CMD-C2D-C3D	3.11	128.11	114.35
3	A	600	D0R	O61-C18-C19	3.33	127.53	120.68
3	A	600	D0R	C19-N20-C21	4.03	129.83	121.46
2	A	508	HEM	CAD-C3D-C2D	4.06	124.89	113.22
2	A	508	HEM	CMC-C2C-C3C	4.12	126.81	116.53
2	A	508	HEM	CAD-C3D-C4D	4.57	128.58	112.47
3	A	600	D0R	C18-C19-N20	4.74	123.46	110.59
2	A	508	HEM	CMB-C2B-C3B	5.23	129.59	116.53
3	A	600	D0R	C85-C82-N83	5.68	135.15	124.27
3	A	600	D0R	C15-N58-C18	5.77	132.14	123.18
3	A	600	D0R	C45-C44-C15	7.16	129.76	114.32

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	508	HEM	2	0
3	A	600	D0R	7	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	449/487 (92%)	0.74	68 (15%) 3 3	33, 54, 91, 108	0

All (68) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	236	LEU	6.3
1	A	165	GLU	5.6
1	A	200	GLN	5.3
1	A	221	LEU	4.6
1	A	278	SER	4.5
1	A	424	LYS	4.5
1	A	226	PHE	4.4
1	A	423	ASN	4.4
1	A	199	PRO	4.2
1	A	255	ARG	4.0
1	A	305	ALA	4.0
1	A	313	VAL	3.9
1	A	479	LEU	3.8
1	A	309	THR	3.5
1	A	219	PHE	3.5
1	A	310	THR	3.5
1	A	167	GLY	3.4
1	A	225	VAL	3.4
1	A	245	VAL	3.4
1	A	369	ILE	3.4
1	A	169	PRO	3.3
1	A	280	ASN	3.3
1	A	238	ILE	3.2
1	A	243	ARG	3.2
1	A	244	GLU	3.1
1	A	314	LEU	3.0
1	A	267	HIS	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	469	LYS	2.9
1	A	211	LEU	2.8
1	A	470	GLU	2.8
1	A	166	THR	2.8
1	A	162	ARG	2.8
1	A	293	LEU	2.7
1	A	425	ASP	2.7
1	A	268	ARG	2.7
1	A	269	VAL	2.7
1	A	426	ASN	2.6
1	A	364	LEU	2.6
1	A	205	GLU	2.6
1	A	301	ILE	2.6
1	A	237	ASN	2.6
1	A	337	ALA	2.5
1	A	421	LYS	2.5
1	A	420	SER	2.5
1	A	487	LYS	2.5
1	A	209	LYS	2.4
1	A	276	ILE	2.4
1	A	312	SER	2.4
1	A	229	LEU	2.4
1	A	422	LYS	2.4
1	A	202	PRO	2.3
1	A	168	LYS	2.3
1	A	418[A]	ARG	2.3
1	A	448	ALA	2.2
1	A	474	PRO	2.2
1	A	55	LYS	2.2
1	A	107	PRO	2.1
1	A	277	ASP	2.1
1	A	368	PRO	2.1
1	A	194	ASP	2.1
1	A	442	CYS	2.0
1	A	406	LYS	2.0
1	A	396	ILE	2.0
1	A	306	GLY	2.0
1	A	371	MET	2.0
1	A	317	ILE	2.0
1	A	427	ILE	2.0
1	A	241	PHE	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(\AA^2)	Q<0.9
3	D0R	A	600	41/41	0.79	0.37	2.54	40,72,97,101	0
2	HEM	A	508	43/43	0.97	0.22	0.08	26,34,39,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.