



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:22 PM GMT

PDB ID : 3R5K
Title : A designed redox-controlled caspase-7
Authors : Witkowski, W.A.; Hardy, J.A.
Deposited on : 2011-03-18
Resolution : 2.86 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

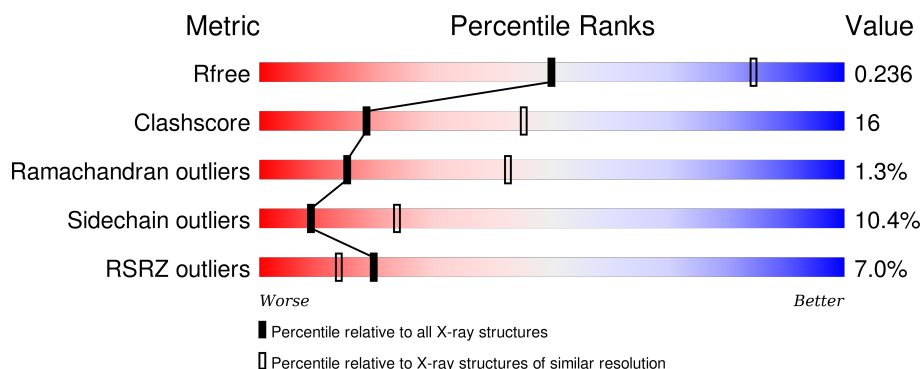
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.86 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	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

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	312	<div> <div>7%</div> <div>50%</div> <div>22%</div> <div>•</div> <div>25%</div> </div>
1	B	312	<div> <div>4%</div> <div>56%</div> <div>14%</div> <div>5%</div> <div>•</div> <div>24%</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
2	FMT	A	312	-	-	X	-
2	FMT	A	313	-	-	X	-
2	FMT	B	4	-	-	X	X
2	FMT	B	7	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3900 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.

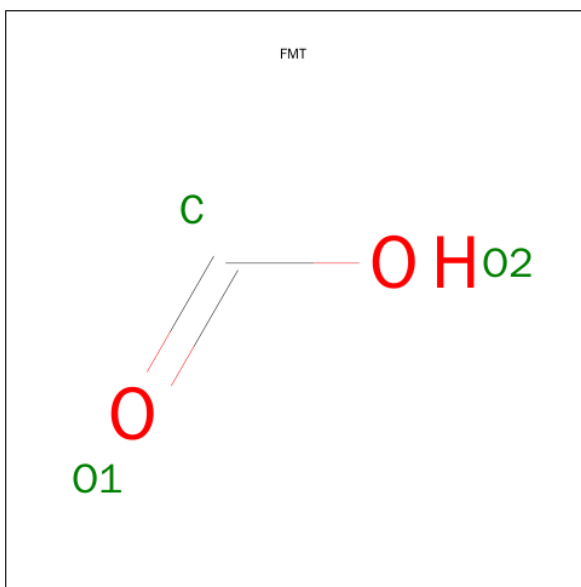
- Molecule 1 is a protein called Caspase-7.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	234	Total	C	N	O	S	0	0	0
			1874	1190	318	351	15			
1	B	237	Total	C	N	O	S	0	1	0
			1904	1209	322	357	16			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	196C	MET	-	EXPRESSION TAG	UNP P55210
A	210	CYS	ARG	ENGINEERED MUTATION	UNP P55210
A	246	SER	CYS	ENGINEERED MUTATION	UNP P55210
A	304	LEU	-	EXPRESSION TAG	UNP P55210
A	305	GLU	-	EXPRESSION TAG	UNP P55210
A	306	HIS	-	EXPRESSION TAG	UNP P55210
A	307	HIS	-	EXPRESSION TAG	UNP P55210
A	308	HIS	-	EXPRESSION TAG	UNP P55210
A	309	HIS	-	EXPRESSION TAG	UNP P55210
A	310	HIS	-	EXPRESSION TAG	UNP P55210
A	311	HIS	-	EXPRESSION TAG	UNP P55210
B	496C	MET	-	EXPRESSION TAG	UNP P55210
B	510	CYS	ARG	ENGINEERED MUTATION	UNP P55210
B	546	SER	CYS	ENGINEERED MUTATION	UNP P55210
B	604	LEU	-	EXPRESSION TAG	UNP P55210
B	605	GLU	-	EXPRESSION TAG	UNP P55210
B	606	HIS	-	EXPRESSION TAG	UNP P55210
B	607	HIS	-	EXPRESSION TAG	UNP P55210
B	608	HIS	-	EXPRESSION TAG	UNP P55210
B	609	HIS	-	EXPRESSION TAG	UNP P55210
B	610	HIS	-	EXPRESSION TAG	UNP P55210
B	611	HIS	-	EXPRESSION TAG	UNP P55210

- Molecule 2 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 3 1 2	0	0
2	A	1	Total C O 3 1 2	0	0
2	B	1	Total C O 3 1 2	0	0
2	B	1	Total C O 3 1 2	0	0
2	B	1	Total C O 3 1 2	0	0
2	B	1	Total C O 3 1 2	0	0

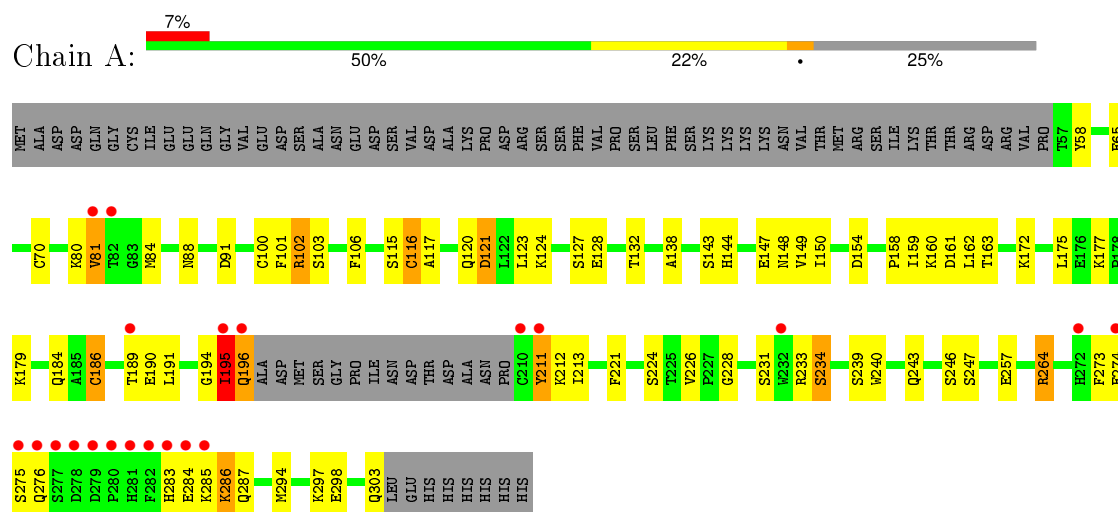
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	53	Total O 53 53	0	0
3	B	51	Total O 51 51	0	0

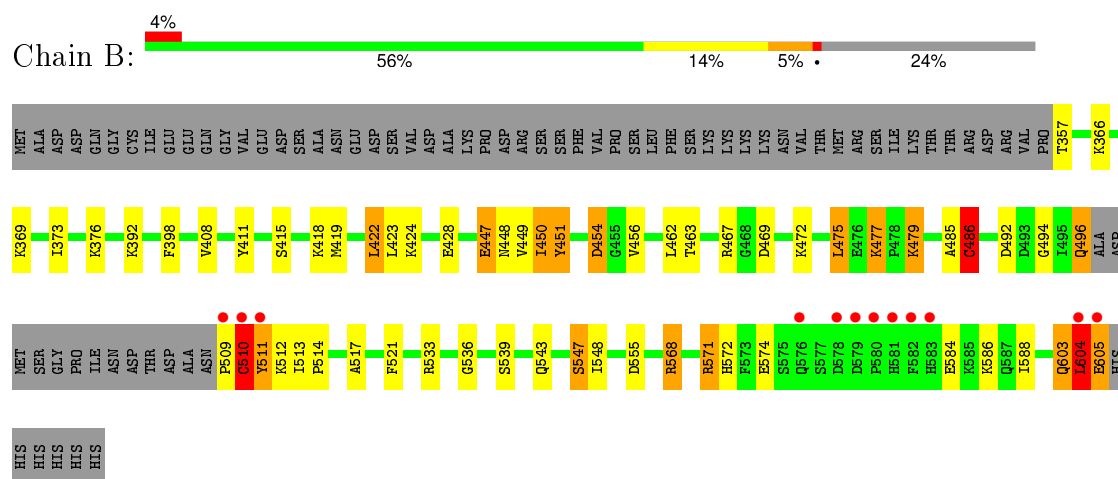
3 Residue-property plots

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: Caspase-7



• Molecule 1: Caspase-7



4 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, α , β , γ	89.85Å 89.85Å 185.91Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.00 – 2.86 48.48 – 2.86	Depositor EDS
% Data completeness (in resolution range)	98.1 (48.00-2.86) 98.4 (48.48-2.86)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.86Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.188 , 0.251 0.185 , 0.236	Depositor DCC
R_{free} test set	1049 reflections (5.43%)	DCC
Wilson B-factor (Å ²)	63.6	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 53.2	EDS
Estimated twinning fraction	0.032 for -h,-k,l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 20383 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3900	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.19% 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: FMT

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	0.48	0/1914	0.57	0/2576
1	B	0.52	0/1945	0.61	0/2618
All	All	0.50	0/3859	0.59	0/5194

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	1
1	B	0	3
All	All	0	4

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	189	THR	Peptide
1	B	451	TYR	Peptide
1	B	454	ASP	Peptide
1	B	510	CYS	Peptide

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	1874	0	1831	71	0
1	B	1904	0	1860	55	0
2	A	6	0	2	4	0
2	B	12	0	4	4	0
3	A	53	0	0	14	0
3	B	51	0	0	8	0
All	All	3900	0	3697	117	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 16.

All (117) 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:264:ARG:HG3	1:A:264:ARG:HH11	1.15	1.11
1:A:186:CYS:HB2	3:A:366:HOH:O	1.49	1.09
1:A:150:ILE:HG23	1:A:159:ILE:HD11	1.31	1.07
1:A:274:GLU:HB3	1:B:511:TYR:HE2	1.20	1.05
1:A:274:GLU:HB3	1:B:511:TYR:CE2	2.05	0.92
1:A:264:ARG:CG	1:A:264:ARG:HH11	1.86	0.88
1:A:274:GLU:OE2	1:A:284:GLU:HG2	1.77	0.85
1:B:513:ILE:HG13	1:B:514:PRO:HD2	1.56	0.84
1:A:234:SER:HB3	3:A:318:HOH:O	1.78	0.83
1:A:123:LEU:HD12	1:A:162:LEU:HB3	1.64	0.80
1:B:571:ARG:HB3	1:B:572:HIS:CD2	2.18	0.78
1:A:276:GLN:HA	1:A:283:HIS:HD2	1.48	0.78
1:B:392:LYS:HE3	1:B:536:GLY:O	1.85	0.76
1:B:477:LYS:O	1:B:479:LYS:HE2	1.85	0.76
1:B:513:ILE:HD11	3:B:100:HOH:O	1.85	0.75
1:A:264:ARG:HG3	1:A:264:ARG:NH1	1.90	0.75
1:B:568:ARG:CG	1:B:568:ARG:HH11	1.99	0.74
1:A:81:VAL:HG23	3:A:329:HOH:O	1.87	0.74
1:A:274:GLU:HG3	3:A:338:HOH:O	1.87	0.74
1:B:424:LYS:HE3	1:B:428:GLU:OE2	1.87	0.74
1:B:588:ILE:H	2:B:4:FMT:H	1.53	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:509:PRO:HA	1:B:510:CYS:C	2.09	0.72
1:B:411:TYR:CE2	1:B:422:LEU:HD11	2.25	0.71
1:B:415:SER:HB2	1:B:454:ASP:OD2	1.93	0.68
1:A:116:CYS:O	1:A:117:ALA:HB3	1.95	0.67
1:A:158:PRO:HG2	1:A:161:ASP:OD2	1.94	0.67
1:A:211:TYR:HE2	1:B:571:ARG:HG3	1.59	0.66
1:B:357:THR:CG2	3:B:28:HOH:O	2.43	0.66
1:A:120:GLN:HG2	3:A:341:HOH:O	1.95	0.66
1:B:603:GLN:O	1:B:605:GLU:HG2	1.97	0.65
1:B:357:THR:HG22	3:B:28:HOH:O	1.95	0.65
1:A:162:LEU:HD12	1:A:162:LEU:H	1.63	0.64
1:A:191:LEU:HD22	1:A:285:LYS:HG3	1.79	0.63
1:B:568:ARG:HH11	1:B:568:ARG:HG2	1.63	0.63
1:B:447:GLU:O	1:B:448:ASN:HB2	1.98	0.63
1:A:149:VAL:HA	1:A:158:PRO:HA	1.81	0.63
1:A:124:LYS:HE3	1:A:128:GLU:OE2	1.99	0.62
1:B:450:ILE:HD11	1:B:462:LEU:CD1	2.31	0.61
1:B:418:LYS:O	1:B:422:LEU:HB2	2.01	0.61
1:B:485:ALA:O	1:B:486[B]:CYS:C	2.39	0.61
1:A:91:ASP:HB2	2:A:312:FMT:C	2.31	0.60
1:B:373:ILE:HD13	1:B:419:MET:HG2	1.84	0.60
1:B:568:ARG:CG	1:B:568:ARG:NH1	2.62	0.60
1:A:177:LYS:O	1:A:179:LYS:HE2	2.01	0.60
1:B:588:ILE:HG22	2:B:4:FMT:H	1.84	0.60
1:B:357:THR:HA	3:B:49:HOH:O	2.02	0.60
1:A:276:GLN:HA	1:A:283:HIS:CD2	2.35	0.59
1:B:450:ILE:HD11	1:B:462:LEU:HD11	1.84	0.59
1:A:91:ASP:HB2	2:A:312:FMT:O1	2.03	0.59
1:A:70:CYS:HA	1:A:138:ALA:O	2.02	0.58
1:A:190:GLU:O	1:A:191:LEU:HB2	2.02	0.58
1:A:273:PHE:O	1:A:286:LYS:CE	2.52	0.57
1:B:450:ILE:CD1	1:B:462:LEU:HD11	2.34	0.57
1:B:574:GLU:OE2	1:B:584:GLU:HG2	2.05	0.57
1:B:513:ILE:CD1	3:B:100:HOH:O	2.49	0.57
1:A:163:THR:HG21	1:A:221:PHE:HE1	1.69	0.57
1:A:195:ILE:HG21	1:B:475:LEU:HD11	1.87	0.56
1:A:65:GLU:HG2	3:A:332:HOH:O	2.04	0.56
1:A:121:ASP:HB3	3:A:322:HOH:O	2.04	0.56
1:A:297:LYS:HE2	3:B:48:HOH:O	2.05	0.56
1:A:274:GLU:CB	1:B:511:TYR:CE2	2.86	0.56
1:B:513:ILE:CG1	1:B:514:PRO:HD2	2.33	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:ILE:HA	1:A:162:LEU:HD13	1.88	0.55
1:A:195:ILE:H	1:B:512:LYS:HB3	1.73	0.53
1:A:212:LYS:HE2	1:B:494:GLY:HA3	1.91	0.53
1:A:273:PHE:O	1:A:286:LYS:HE3	2.08	0.52
1:A:257:GLU:HG3	1:A:298:GLU:HB3	1.91	0.52
1:B:533:ARG:HA	1:B:539:SER:HA	1.92	0.52
1:B:568:ARG:HG3	1:B:568:ARG:NH1	2.24	0.51
1:A:275:SER:O	1:A:284:GLU:N	2.42	0.51
1:A:211:TYR:CE2	1:B:571:ARG:HG3	2.43	0.51
1:B:423:LEU:HD12	1:B:462:LEU:HD22	1.92	0.50
1:B:588:ILE:H	2:B:4:FMT:C	2.21	0.50
1:A:240:TRP:CE3	1:A:273:PHE:HB3	2.46	0.50
1:B:411:TYR:CD2	1:B:422:LEU:HD11	2.46	0.49
1:B:604:LEU:C	1:B:605:GLU:HG2	2.30	0.49
1:B:543:GLN:O	1:B:547:SER:HB3	2.13	0.49
1:A:233:ARG:HH12	2:A:313:FMT:C	2.26	0.48
1:A:239:SER:O	1:A:243:GLN:HG3	2.13	0.48
1:B:448:ASN:CG	3:B:54:HOH:O	2.52	0.48
3:A:324:HOH:O	1:B:496:GLN:C	2.52	0.48
1:B:467:ARG:HH21	1:B:469:ASP:CG	2.16	0.48
1:B:451:TYR:CE2	1:B:456:VAL:HG23	2.49	0.47
1:A:190:GLU:HB2	1:A:228:GLY:O	2.14	0.47
1:A:194:GLY:O	1:A:195:ILE:HB	2.13	0.47
1:A:115:SER:HB2	1:A:154:ASP:OD1	2.14	0.47
1:A:88:ASN:HB3	3:A:321:HOH:O	2.16	0.46
1:A:285:LYS:HD3	1:A:285:LYS:HA	1.83	0.46
1:A:100:CYS:O	1:A:103:SER:HB2	2.15	0.46
1:A:116:CYS:O	1:A:117:ALA:CB	2.60	0.46
1:A:143:SER:O	2:A:313:FMT:H	2.16	0.45
1:A:160:LYS:HE3	3:A:363:HOH:O	2.16	0.45
1:A:196:GLN:HB2	3:A:336:HOH:O	2.16	0.45
1:B:463:THR:HG21	1:B:521:PHE:HE2	1.82	0.45
1:A:240:TRP:HB2	3:A:359:HOH:O	2.16	0.45
1:B:492:ASP:HB3	1:B:586:LYS:O	2.17	0.44
1:A:101:PHE:O	1:A:106:PHE:HB2	2.18	0.44
1:B:357:THR:HG23	3:B:28:HOH:O	2.14	0.44
1:A:159:ILE:N	1:A:159:ILE:HD12	2.33	0.44
1:B:485:ALA:O	1:B:486[A]:CYS:C	2.54	0.43
1:A:287:GLN:HA	3:A:357:HOH:O	2.17	0.43
1:A:84:MET:HB3	1:A:144:HIS:CD2	2.53	0.43
1:A:117:ALA:N	3:A:341:HOH:O	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ARG:HD2	1:A:102:ARG:HA	1.82	0.43
1:B:485:ALA:O	1:B:486[B]:CYS:O	2.36	0.43
1:A:195:ILE:HD13	1:B:469:ASP:HA	2.00	0.43
1:A:58:TYR:O	1:A:298:GLU:HG3	2.19	0.42
1:A:162:LEU:HD12	1:A:162:LEU:N	2.30	0.42
1:A:184:GLN:HA	1:A:224:SER:HB3	2.01	0.42
1:A:123:LEU:CD1	1:A:162:LEU:HB3	2.43	0.42
1:B:514:PRO:HG2	1:B:517:ALA:HB2	2.01	0.41
1:A:100:CYS:SG	1:A:246:SER:HA	2.61	0.41
1:A:147:GLU:O	1:A:148:ASN:HB2	2.20	0.41
1:A:160:LYS:HA	1:A:160:LYS:HD2	1.89	0.41
1:A:149:VAL:HG12	1:A:158:PRO:HB3	2.02	0.41
1:B:588:ILE:N	2:B:4:FMT:H	2.28	0.41
1:A:172:LYS:HB3	1:A:172:LYS:HE2	1.91	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	230/312 (74%)	214 (93%)	13 (6%)	3 (1%)	15	42
1	B	234/312 (75%)	218 (93%)	12 (5%)	4 (2%)	11	35
All	All	464/624 (74%)	432 (93%)	25 (5%)	7 (2%)	15	38

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	195	ILE
1	B	486[A]	CYS
1	B	486[B]	CYS
1	B	604	LEU

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Mol	Chain	Res	Type
1	B	511	TYR
1	A	81	VAL
1	A	132	THR

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	206/276 (75%)	187 (91%)	19 (9%)	11	30
1	B	210/276 (76%)	185 (88%)	25 (12%)	6	17
All	All	416/552 (75%)	372 (89%)	44 (11%)	9	22

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	80	LYS
1	A	102	ARG
1	A	116	CYS
1	A	121	ASP
1	A	127	SER
1	A	175	LEU
1	A	186	CYS
1	A	195	ILE
1	A	196	GLN
1	A	211	TYR
1	A	213	ILE
1	A	226	VAL
1	A	231	SER
1	A	234	SER
1	A	247	SER
1	A	264	ARG
1	A	286	LYS
1	A	294	MET
1	A	303	GLN
1	B	366	LYS

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Mol	Chain	Res	Type
1	B	369	LYS
1	B	376	LYS
1	B	398	PHE
1	B	408	VAL
1	B	422	LEU
1	B	447	GLU
1	B	449	VAL
1	B	450	ILE
1	B	472	LYS
1	B	475	LEU
1	B	477	LYS
1	B	479	LYS
1	B	486[A]	CYS
1	B	486[B]	CYS
1	B	496	GLN
1	B	510	CYS
1	B	547	SER
1	B	548	ILE
1	B	555	ASP
1	B	568	ARG
1	B	571	ARG
1	B	603	GLN
1	B	604	LEU
1	B	605	GLU

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	281	HIS
1	A	283	HIS
1	B	359	GLN
1	B	572	HIS

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

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	FMT	A	312	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	A	313	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	B	2	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	B	4	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	B	5	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	B	7	-	0,2,2	0.00	-	0,1,1	0.00	-

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	FMT	A	312	-	-	0/0/0/0	0/0/0/0
2	FMT	A	313	-	-	0/0/0/0	0/0/0/0
2	FMT	B	2	-	-	0/0/0/0	0/0/0/0
2	FMT	B	4	-	-	0/0/0/0	0/0/0/0
2	FMT	B	5	-	-	0/0/0/0	0/0/0/0
2	FMT	B	7	-	-	0/0/0/0	0/0/0/0

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.

3 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	312	FMT	2	0
2	A	313	FMT	2	0
2	B	4	FMT	4	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	234/312 (75%)	0.17	21 (8%) 12 7	35, 61, 96, 109	0
1	B	237/312 (75%)	-0.06	12 (5%) 32 25	34, 49, 85, 108	0
All	All	471/624 (75%)	0.06	33 (7%) 19 13	34, 53, 95, 109	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	509	PRO	6.2
1	B	510	CYS	6.1
1	A	278	ASP	5.3
1	A	277	SER	4.9
1	A	210	CYS	4.8
1	B	511	TYR	4.8
1	B	580	PRO	4.6
1	A	276	GLN	4.1
1	A	275	SER	3.7
1	A	196	GLN	3.6
1	A	280	PRO	3.6
1	A	281	HIS	3.3
1	B	605	GLU	3.2
1	B	578	ASP	3.1
1	A	274	GLU	2.9
1	A	279	ASP	2.8
1	A	283	HIS	2.7
1	A	282	PHE	2.7
1	A	81	VAL	2.6
1	A	272	HIS	2.5
1	A	82	THR	2.4
1	A	211	TYR	2.4
1	A	284	GLU	2.2
1	B	582	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	579	ASP	2.2
1	A	285	LYS	2.2
1	B	576	GLN	2.1
1	B	583	HIS	2.1
1	A	189	THR	2.1
1	B	604	LEU	2.1
1	B	581	HIS	2.1
1	A	232	TRP	2.1
1	A	195	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
2	FMT	B	4	3/3	0.90	0.31	4.89	87,87,88,88	0
2	FMT	B	7	3/3	0.97	0.24	3.50	66,66,67,69	0
2	FMT	A	312	3/3	0.94	0.21	0.34	82,82,82,82	0
2	FMT	B	5	3/3	0.83	0.27	-0.08	76,76,76,76	0
2	FMT	A	313	3/3	0.93	0.18	-0.28	82,82,83,83	0
2	FMT	B	2	3/3	0.84	0.14	-1.99	87,87,88,88	0

6.5 Other polymers [i](#)

There are no such residues in this entry.