



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 01:13 PM UTC

PDB ID : 3R5K / pdb_00003r5k
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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

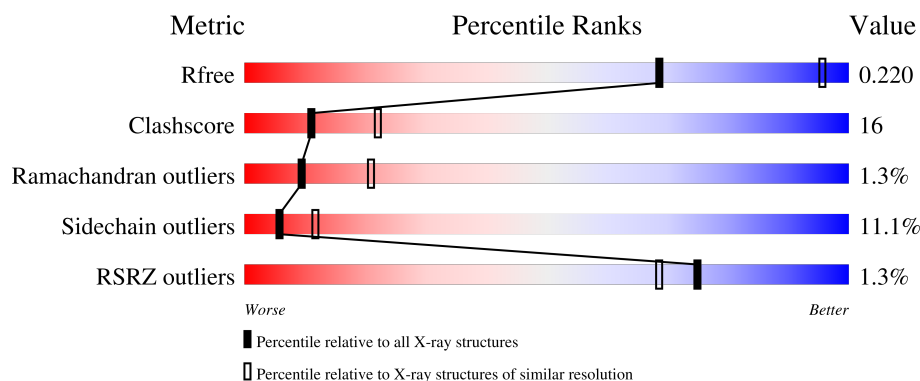
1 Overall quality at a glance

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}	180053	1407 (2.88-2.84)
Clashscore	190562	1446 (2.88-2.84)
Ramachandran outliers	187476	1406 (2.88-2.84)
Sidechain outliers	187428	1407 (2.88-2.84)
RSRZ outliers	180081	1408 (2.88-2.84)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	10% 50% 21% • 25%
1	B	312	10% 54% 15% 6% • 24%

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	-

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 (CCD ID: FMT) (formula: CH₂O₂).

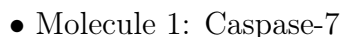


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			3	1	2		
2	A	1	Total	C	O	0	0
			3	1	2		
2	B	1	Total	C	O	0	0
			3	1	2		
2	B	1	Total	C	O	0	0
			3	1	2		
2	B	1	Total	C	O	0	0
			3	1	2		
2	B	1	Total	C	O	0	0
			3	1	2		

- Molecule 3 is water.

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

- 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 48.00 – 2.86	Depositor EDS
% Data completeness (in resolution range)	98.1 (48.00-2.86) 98.3 (48.00-2.86)	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 (Not available) , 0.220	Depositor DCC
R_{free} test set	1050 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	63.6	Xtriage
Anisotropy	0.181	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	0.032 for -h,-k,l	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, 0.333 respectively for untwinned datasets, and 0.375, 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	0.58	0/1914	0.88	3/2576 (0.1%)
1	B	0.60	0/1945	0.87	2/2618 (0.1%)
All	All	0.59	0/3859	0.88	5/5194 (0.1%)

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.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	190	GLU	N-CA-C	9.12	120.91	110.97
1	B	453	LYS	CA-C-N	5.66	128.91	120.31
1	B	453	LYS	C-N-CA	5.66	128.91	120.31
1	A	213	ILE	CA-C-N	5.45	125.46	119.90
1	A	213	ILE	C-N-CA	5.45	125.46	119.90

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	189	THR	Peptide

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Mol	Chain	Res	Type	Group
1	B	451	TYR	Peptide
1	B	454	ASP	Peptide
1	B	510	CYS	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	1874	0	1831	71	0
1	B	1904	0	1860	61	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	9	0
All	All	3900	0	3697	123	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 (123) 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:HH11	1:A:264:ARG:HG3	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:HH11	1:A:264:ARG:CG	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:509:PRO:HA	1:B:510:CYS:C	2.09	0.77
1:B:392:LYS:HE3	1:B:536:GLY:O	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HH11	1:B:568:ARG:CG	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
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:485:ALA:O	1:B:486[B]:CYS:C	2.39	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:H	1:A:162:LEU:HD12	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: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:A:177:LYS:O	1:A:179:LYS:HE2	2.01	0.60
1:B:568:ARG:CG	1:B:568:ARG:NH1	2.62	0.60
1:B:357:THR:HA	3:B:49:HOH:O	2.02	0.60
1:B:588:ILE:HG22	2:B:4:FMT:H	1.84	0.60
1:A:276:GLN:HA	1:A:283:HIS:CD2	2.35	0.59
1:B:384:MET:HA	1:B:384:MET:HE2	1.83	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:65:GLU:HG2	3:A:332:HOH:O	2.04	0.56
1:A:195:ILE:HG21	1:B:475:LEU:HD11	1.87	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
1:B:604:LEU:C	1:B:605:GLU:HG2	2.30	0.55
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:B:448:ASN:CG	3:B:54:HOH:O	2.52	0.53
1:A:273:PHE:O	1:A:286:LYS:HE3	2.08	0.52
3:A:324:HOH:O	1:B:496:GLN:C	2.52	0.52
1:A:257:GLU:HG3	1:A:298:GLU:HB3	1.91	0.52
1:B:467:ARG:HH21	1:B:469:ASP:CG	2.16	0.52
1:B:533:ARG:HA	1:B:539:SER:HA	1.92	0.52
1:B:568:ARG:NH1	1:B:568:ARG:HG3	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: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:509:PRO:CA	1:B:510:CYS:C	2.86	0.47
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:B:485:ALA:O	1:B:486[A]:CYS:C	2.54	0.47
1:A:115:SER:HB2	1:A:154:ASP:OD1	2.14	0.47
1:B:360:TYR:OH	1:B:518:ASP:OD1	2.30	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:B:453:LYS:NZ	3:B:109:HOH:O	2.48	0.45
1:A:143:SER:O	2:A:313:FMT:H	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:HD12	1:A:159:ILE:N	2.33	0.44
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:102:ARG:HA	1:A:102:ARG:HD2	1.82	0.43
1:A:117:ALA:N	3:A:341:HOH:O	2.38	0.43
1:A:195:ILE:HD13	1:B:469:ASP:HA	2.00	0.43
1:B:485:ALA:O	1:B:486[B]:CYS:O	2.36	0.43
1:A:58:TYR:O	1:A:298:GLU:HG3	2.19	0.42
1:B:552:HIS:O	1:B:553:GLY:C	2.62	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:HD2	1:A:160:LYS:HA	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
1:B:398:PHE:CD1	1:B:398:PHE:C	2.98	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	230/312 (74%)	214 (93%)	13 (6%)	3 (1%)	9	21
1	B	234/312 (75%)	218 (93%)	12 (5%)	4 (2%)	7	16
All	All	464/624 (74%)	432 (93%)	25 (5%)	7 (2%)	9	18

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
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%)	8	19
1	B	210/276 (76%)	182 (87%)	28 (13%)	4	7
All	All	416/552 (75%)	369 (89%)	47 (11%)	6	11

All (47) 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	150	ILE
1	A	175	LEU
1	A	186	CYS
1	A	195	ILE

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Mol	Chain	Res	Type
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	294	MET
1	A	303	GLN
1	B	363	ASN
1	B	366	LYS
1	B	369	LYS
1	B	376	LYS
1	B	380	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	456	VAL
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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	120	GLN
1	A	243	GLN
1	A	252	HIS
1	A	272	HIS
1	A	281	HIS
1	A	283	HIS
1	B	359	GLN
1	B	420	GLN
1	B	444	HIS
1	B	484	GLN
1	B	552	HIS
1	B	572	HIS

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 oligosaccharides 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	FMT	A	313	-	2,2,2	0.61	0	1,1,1	0.62	0
2	FMT	B	5	-	2,2,2	0.62	0	1,1,1	0.53	0
2	FMT	B	4	-	2,2,2	0.65	0	1,1,1	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	FMT	B	7	-	2,2,2	0.61	0	1,1,1	0.79	0
2	FMT	A	312	-	2,2,2	0.63	0	1,1,1	0.51	0
2	FMT	B	2	-	2,2,2	0.65	0	1,1,1	0.53	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	313	FMT	2	0
2	B	4	FMT	4	0
2	A	312	FMT	2	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 [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	234/312 (75%)	-0.05	3 (1%) 75 68	35, 61, 96, 109	0
1	B	237/312 (75%)	-0.39	3 (1%) 75 68	26, 49, 85, 108	1 (0%)
All	All	471/624 (75%)	-0.22	6 (1%) 75 68	26, 53, 95, 109	1 (0%)

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	604	LEU	5.0
1	B	509	PRO	4.0
1	A	189	THR	2.9
1	A	211	TYR	2.9
1	B	486[A]	CYS	2.9
1	A	235	PRO	2.1

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 oligosaccharides 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. 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	B-factors($\text{\AA}^2$)	Q<0.9
2	FMT	B	2	3/3	0.83	0.26	87,87,88,88	0
2	FMT	A	312	3/3	0.85	0.20	82,82,82,82	0
2	FMT	A	313	3/3	0.87	0.15	82,82,83,83	0
2	FMT	B	4	3/3	0.88	0.18	87,87,88,88	0
2	FMT	B	5	3/3	0.92	0.17	76,76,76,76	0
2	FMT	B	7	3/3	0.93	0.19	66,66,67,69	0

6.5 Other polymers [i](#)

There are no such residues in this entry.