



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 05:11 PM UTC

PDB ID : 1XMD / pdb_00001xmd
Title : M335V mutant structure of mouse carnitine octanoyltransferase
Authors : Jogl, G.; Hsiao, Y.S.; Tong, L.
Deposited on : 2004-10-01
Resolution : 2.10 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

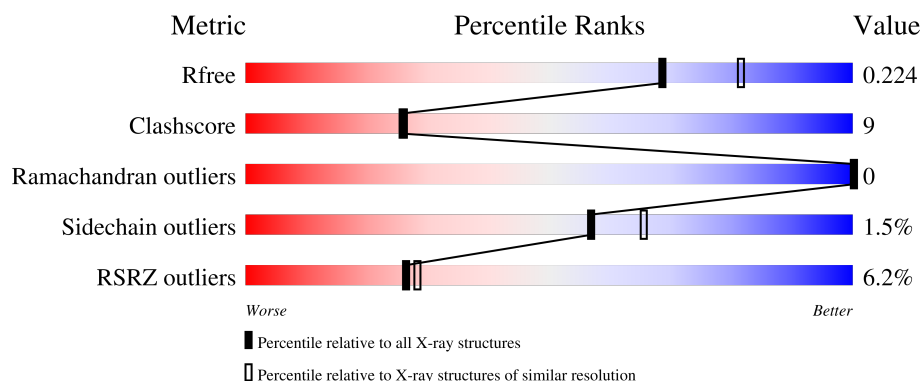
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	612	9% 72% 24% ..
1	B	612	3% 78% 18% ..

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 10230 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.

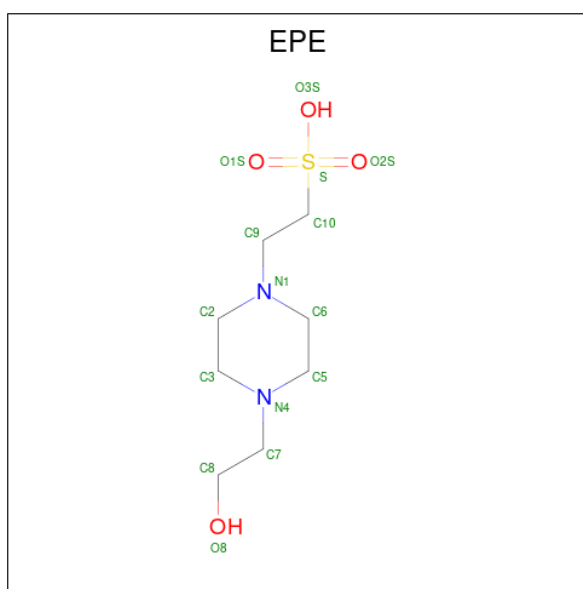
- Molecule 1 is a protein called Peroxisomal carnitine O-octanoyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	591	Total	C	N	O	S	0	0	0
			4775	3042	829	872	32			
1	B	600	Total	C	N	O	S	0	0	0
			4842	3085	839	886	32			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	335	VAL	MET	engineered mutation	UNP Q9DC50
B	335	VAL	MET	engineered mutation	UNP Q9DC50

- Molecule 2 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (CCD ID: EPE) (formula: C₈H₁₈N₂O₄S).



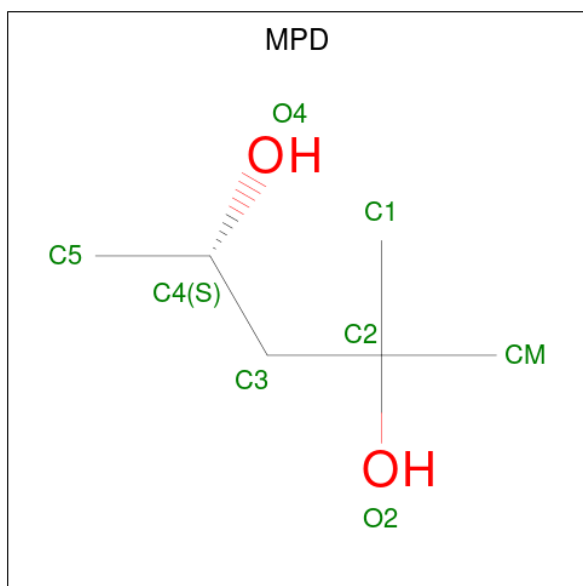
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

- Molecule 3 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		
3	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	196	Total	O	0	0
			196	196		

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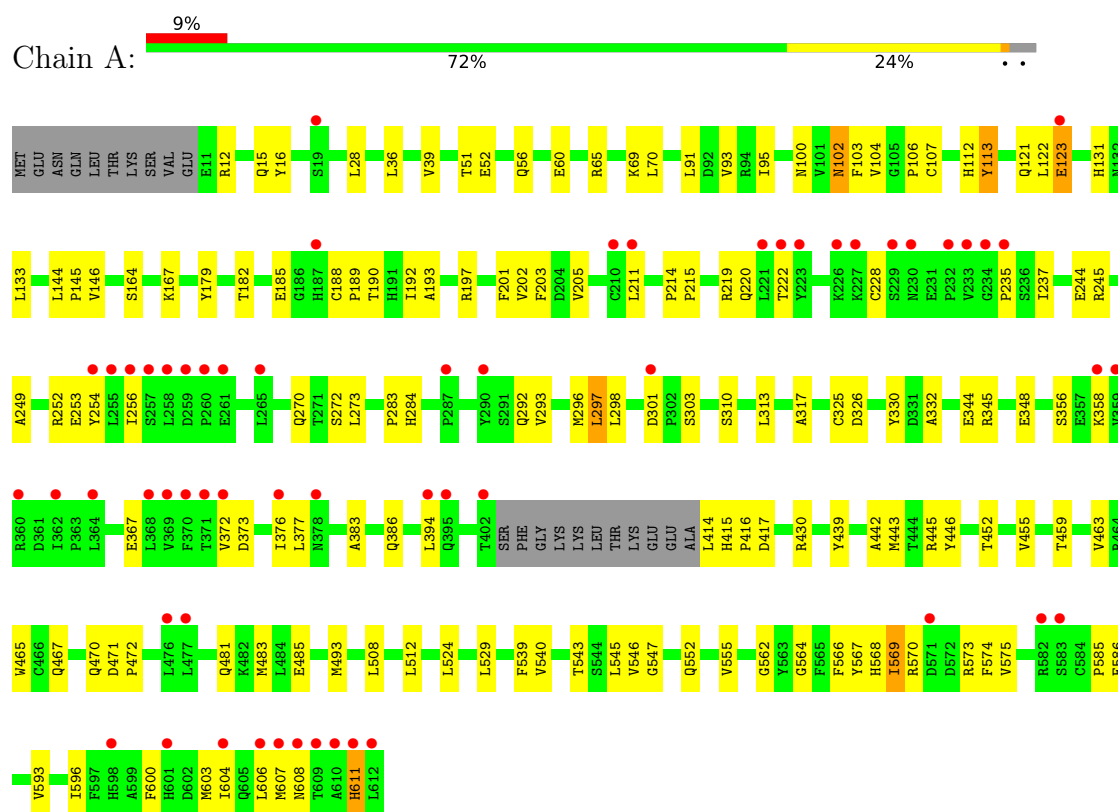
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	331	Total 331	O 331	0	0

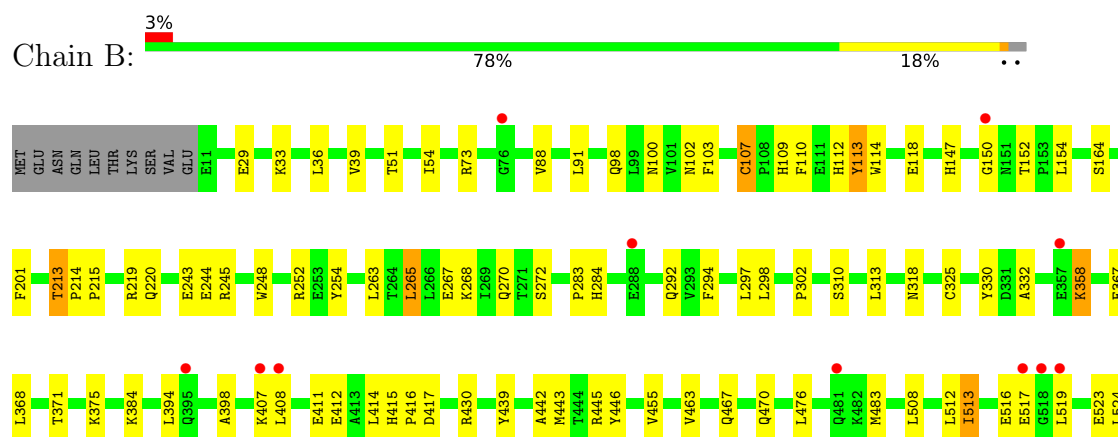
3 Residue-property plots

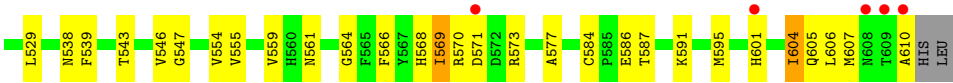
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Peroxisomal carnitine O-octanoyltransferase



- Molecule 1: Peroxisomal carnitine O-octanoyltransferase





4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	164.00Å 164.00Å 159.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	28.00 – 2.10 28.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.1 (28.00-2.10) 95.2 (28.00-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.67 (at 2.10Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.196 , 0.224 0.196 , 0.224	Depositor DCC
R_{free} test set	6635 reflections (7.18%)	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.068	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 56.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10230	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% 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: EPE, MPD

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	0.36	0/4900	0.85	14/6636 (0.2%)
1	B	0.43	0/4968	0.90	18/6727 (0.3%)
All	All	0.40	0/9868	0.88	32/13363 (0.2%)

There are no bond length outliers.

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	564	GLY	N-CA-C	-9.09	96.80	110.71
1	A	332	ALA	N-CA-C	7.80	120.68	111.71
1	B	107	CYS	N-CA-C	-7.66	100.00	109.65
1	B	332	ALA	N-CA-C	7.50	120.33	111.71
1	B	245	ARG	N-CA-C	6.62	119.06	111.11
1	B	91	LEU	N-CA-C	6.42	119.09	111.71
1	B	244	GLU	N-CA-C	-6.38	100.98	110.23
1	B	100	ASN	N-CA-C	6.30	120.80	113.18
1	A	91	LEU	N-CA-C	6.29	118.94	111.71
1	B	150	GLY	N-CA-C	-6.25	98.38	113.18
1	B	547	GLY	N-CA-C	6.07	119.47	111.52
1	B	586	GLU	N-CA-C	5.93	117.42	111.07
1	B	243	GLU	N-CA-C	5.92	118.17	110.53
1	B	113	TYR	N-CA-C	5.81	119.47	112.38
1	B	543	THR	N-CA-C	5.79	117.76	109.14
1	A	107	CYS	N-CA-C	-5.75	102.40	109.65
1	B	213	THR	N-CA-C	5.60	116.57	110.13
1	A	113	TYR	N-CA-C	5.45	119.19	112.54
1	A	543	THR	N-CA-C	5.43	117.23	109.14
1	A	569	ILE	N-CA-C	5.42	116.38	108.53
1	B	446	TYR	N-CA-C	-5.35	105.61	111.82
1	A	471	ASP	CA-C-N	5.32	125.64	119.47

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	471	ASP	C-N-CA	5.32	125.64	119.47
1	A	100	ASN	N-CA-C	5.26	119.70	113.28
1	A	564	GLY	N-CA-C	-5.24	100.75	113.18
1	A	244	GLU	N-CA-C	-5.22	102.66	110.23
1	B	569	ILE	N-CA-C	5.15	115.90	108.48
1	A	452	THR	N-CA-C	5.11	117.17	109.41
1	A	245	ARG	N-CA-C	5.11	117.51	111.33
1	B	513	ILE	N-CA-C	-5.05	105.47	110.62
1	B	587	THR	N-CA-C	5.04	117.94	110.48
1	A	446	TYR	N-CA-C	-5.01	106.01	111.82

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4775	0	4676	97	0
1	B	4842	0	4750	84	0
2	A	15	0	18	0	0
2	B	15	0	18	1	0
3	A	8	0	14	0	0
3	B	48	0	84	4	0
4	A	196	0	0	3	0
4	B	331	0	0	5	0
All	All	10230	0	9560	182	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 9.

All (182) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:483:MET:HE1	1:B:607:MET:HE1	1.19	1.14
1:A:604:ILE:HA	1:A:607:MET:HE2	1.38	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:483:MET:CE	1:B:607:MET:HE1	2.00	0.91
1:A:568:HIS:HE1	1:A:570:ARG:HE	1.16	0.90
1:A:546:VAL:HG23	1:A:568:HIS:HB3	1.59	0.84
1:B:252:ARG:HH21	1:B:270:GLN:HE22	1.27	0.82
1:B:298:LEU:HD13	1:B:394:LEU:HD21	1.63	0.81
1:B:371:THR:HG21	4:B:882:HOH:O	1.80	0.79
1:B:414:LEU:HD11	1:B:607:MET:HE3	1.62	0.79
1:B:430:ARG:HE	1:B:470:GLN:HE22	1.28	0.79
1:B:568:HIS:HE1	1:B:570:ARG:HE	1.29	0.78
1:B:430:ARG:HE	1:B:470:GLN:NE2	1.83	0.75
1:B:219:ARG:HH21	1:B:220:GLN:HE22	1.34	0.75
1:B:570:ARG:HD2	1:B:573:ARG:HH11	1.51	0.74
1:B:443:MET:HE2	1:B:445:ARG:HD3	1.67	0.74
1:A:219:ARG:HH21	1:A:220:GLN:HE22	1.36	0.73
1:A:430:ARG:HE	1:A:470:GLN:HE22	1.37	0.73
1:B:283:PRO:HA	1:B:292:GLN:HE21	1.53	0.73
1:B:284:HIS:H	1:B:292:GLN:NE2	1.86	0.73
1:A:416:PRO:HB2	1:A:569:ILE:HD13	1.70	0.71
1:B:407:LYS:O	1:B:411:GLU:HG3	1.90	0.71
1:A:283:PRO:HA	1:A:292:GLN:HE21	1.57	0.70
1:A:483:MET:HE3	1:A:606:LEU:HD23	1.75	0.69
1:A:298:LEU:HD13	1:A:394:LEU:HD21	1.75	0.68
1:B:463:VAL:O	1:B:467:GLN:HG3	1.94	0.67
1:B:416:PRO:HB2	1:B:569:ILE:HD13	1.75	0.67
1:A:570:ARG:HD2	1:A:573:ARG:HH11	1.58	0.67
1:A:546:VAL:HG22	1:A:567:TYR:O	1.95	0.67
1:A:430:ARG:HE	1:A:470:GLN:NE2	1.94	0.65
1:A:52:GLU:O	1:A:56:GLN:HG3	1.98	0.64
1:B:517:GLU:HB2	1:B:519:LEU:HG	1.79	0.64
1:A:123:GLU:CD	1:A:123:GLU:H	2.04	0.64
1:A:546:VAL:CG2	1:A:568:HIS:HB3	2.28	0.63
1:A:112:HIS:CD2	1:A:113:TYR:H	2.16	0.63
1:B:398:ALA:HB1	4:B:897:HOH:O	1.98	0.63
1:A:121:GLN:NE2	1:A:317:ALA:HA	2.13	0.63
1:A:252:ARG:HH21	1:A:270:GLN:HE22	1.44	0.63
1:A:603:MET:O	1:A:607:MET:HG3	1.99	0.62
1:B:371:THR:CG2	4:B:882:HOH:O	2.45	0.62
1:A:443:MET:HE2	1:A:445:ARG:HD3	1.82	0.61
1:A:568:HIS:CE1	1:A:570:ARG:HE	2.08	0.61
1:B:112:HIS:CD2	1:B:113:TYR:H	2.18	0.61
1:A:465:TRP:CZ2	1:A:483:MET:HE2	2.36	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:358:LYS:NZ	1:B:358:LYS:HB3	2.16	0.60
1:B:252:ARG:HH21	1:B:270:GLN:NE2	2.00	0.59
1:A:310:SER:O	1:A:325:CYS:HB3	2.02	0.59
1:A:483:MET:HE1	1:A:603:MET:HA	1.85	0.59
1:B:302:PRO:HG2	1:B:384:LYS:HG3	1.85	0.58
1:B:154:LEU:HD13	1:B:443:MET:HE1	1.85	0.58
1:A:345:ARG:HH21	1:A:348:GLU:CD	2.13	0.57
1:B:265:LEU:HG	1:B:368:LEU:HB3	1.86	0.56
1:A:144:LEU:HD12	1:A:145:PRO:HD2	1.87	0.56
1:A:570:ARG:HG2	4:A:674:HOH:O	2.05	0.56
1:B:407:LYS:HG3	1:B:571:ASP:HB2	1.88	0.56
1:A:192:ILE:HD11	1:A:203:PHE:CZ	2.40	0.56
1:B:147:HIS:CD2	1:B:445:ARG:HH22	2.24	0.55
1:B:298:LEU:HD13	1:B:394:LEU:CD2	2.36	0.55
1:A:235:PRO:HG2	4:A:722:HOH:O	2.06	0.55
1:A:373:ASP:O	1:A:377:LEU:HG	2.07	0.55
1:B:219:ARG:HH21	1:B:220:GLN:NE2	2.03	0.55
1:A:65:ARG:O	1:A:69:LYS:HG2	2.08	0.54
1:A:442:ALA:HB2	1:A:455:VAL:HG23	1.90	0.53
1:A:555:VAL:HG22	1:A:566:PHE:CZ	2.43	0.53
1:B:29:GLU:O	1:B:33:LYS:HG2	2.09	0.53
1:B:294:PHE:CE1	1:B:554:VAL:HG13	2.44	0.53
1:B:554:VAL:CG1	1:B:577:ALA:HB1	2.39	0.52
2:B:701:EPE:O8	2:B:701:EPE:H32	2.09	0.52
1:A:249:ALA:O	1:A:253:GLU:HG3	2.10	0.52
1:A:284:HIS:H	1:A:292:GLN:NE2	2.08	0.52
1:A:190:THR:O	1:A:205:VAL:HG22	2.10	0.51
1:B:36:LEU:HD21	3:B:705:MPD:HM2	1.91	0.51
1:A:51:THR:OG1	1:A:529:LEU:HD12	2.10	0.51
1:B:254:TYR:CZ	1:B:375:LYS:HD3	2.46	0.51
1:A:593:VAL:O	1:A:596:ILE:HG22	2.10	0.51
1:A:545:LEU:HG	1:A:547:GLY:H	1.76	0.50
1:A:439:TYR:CD1	1:A:439:TYR:C	2.89	0.50
1:B:98:GLN:O	1:B:102:ASN:HB2	2.11	0.50
1:B:439:TYR:C	1:B:439:TYR:CD1	2.89	0.50
1:A:164:SER:HB3	1:A:179:TYR:HB2	1.93	0.49
1:A:252:ARG:O	1:A:256:ILE:HG13	2.12	0.49
1:B:554:VAL:HG11	1:B:577:ALA:HB1	1.94	0.49
1:A:356:SER:OG	1:A:358:LYS:HG2	2.13	0.48
1:A:383:ALA:O	1:A:386:GLN:HG3	2.13	0.48
1:B:118:GLU:OE2	1:B:318:ASN:HB3	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:182:THR:OG1	1:A:185:GLU:HG3	2.13	0.48
1:B:476:LEU:HB3	1:B:610:ALA:HB2	1.96	0.48
1:B:554:VAL:HG12	1:B:577:ALA:HB3	1.95	0.48
1:A:344:GLU:O	1:A:348:GLU:HG3	2.14	0.48
1:B:252:ARG:NH2	1:B:270:GLN:HE22	2.03	0.48
1:B:201:PHE:CE2	1:B:367:GLU:HB2	2.47	0.48
1:B:513:ILE:O	1:B:517:GLU:HG2	2.12	0.48
1:A:214:PRO:HB2	1:A:215:PRO:HD3	1.95	0.48
1:A:481:GLN:O	1:A:485:GLU:HG3	2.14	0.47
1:B:36:LEU:O	1:B:39:VAL:HG22	2.13	0.47
1:A:459:THR:CG2	1:A:493:MET:HE1	2.45	0.47
1:A:193:ALA:HA	1:A:202:VAL:HG12	1.95	0.47
1:B:214:PRO:HB2	1:B:215:PRO:HD3	1.96	0.47
1:B:103:PHE:HA	1:B:555:VAL:HG12	1.96	0.46
1:B:442:ALA:HB2	1:B:455:VAL:HG23	1.97	0.46
1:A:555:VAL:HG22	1:A:566:PHE:CE2	2.51	0.46
1:B:54:ILE:HG23	1:B:523:GLU:HG3	1.96	0.46
1:A:508:LEU:O	1:A:512:LEU:HG	2.15	0.46
1:A:36:LEU:O	1:A:39:VAL:HG22	2.16	0.46
1:A:104:VAL:HG21	1:A:298:LEU:HG	1.96	0.46
1:A:197:ARG:HG3	1:A:228:CYS:HB3	1.97	0.46
1:A:167:LYS:HE3	1:A:326:ASP:OD2	2.15	0.46
1:B:546:VAL:HG12	1:B:546:VAL:O	2.15	0.46
1:B:110:PHE:HA	1:B:114:TRP:O	2.17	0.45
1:A:106:PRO:HB3	1:A:293:VAL:HG11	1.99	0.45
1:A:133:LEU:HD13	1:A:211:LEU:HD11	1.99	0.45
1:B:263:LEU:O	1:B:267:GLU:HG3	2.17	0.45
1:B:284:HIS:H	1:B:292:GLN:HE21	1.62	0.45
1:A:414:LEU:HD12	1:A:607:MET:SD	2.57	0.45
1:B:358:LYS:HB3	1:B:358:LYS:HZ2	1.82	0.45
1:A:600:PHE:O	1:A:604:ILE:HG12	2.16	0.45
1:B:268:LYS:HE3	3:B:703:MPD:O2	2.16	0.45
1:B:220:GLN:NE2	1:B:220:GLN:HA	2.33	0.44
1:A:93:VAL:HG12	1:A:95:ILE:HG12	1.99	0.44
1:B:538:ASN:HA	1:B:559:VAL:HG11	2.00	0.44
1:B:604:ILE:HD13	1:B:604:ILE:HA	1.89	0.44
1:B:561:ASN:HA	1:B:584:CYS:SG	2.57	0.44
1:B:524:LEU:C	1:B:524:LEU:HD23	2.42	0.44
1:A:540:VAL:HG23	1:A:562:GLY:HA2	2.00	0.44
1:B:554:VAL:CG1	1:B:577:ALA:CB	2.95	0.44
1:B:555:VAL:HG22	1:B:566:PHE:CE2	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:297:LEU:HD12	1:A:297:LEU:HA	1.86	0.43
1:B:51:THR:OG1	1:B:529:LEU:HD12	2.17	0.43
1:A:585:PRO:HG2	1:A:586:GLU:OE2	2.19	0.43
1:B:591:LYS:O	1:B:595:MET:HG2	2.19	0.43
1:B:601:HIS:O	1:B:605:GLN:HG3	2.18	0.43
1:A:65:ARG:CZ	1:A:69:LYS:HD3	2.48	0.43
1:A:254:TYR:HD1	1:A:376:ILE:HD11	1.83	0.43
1:A:415:HIS:CD2	1:A:417:ASP:H	2.36	0.43
1:A:301:ASP:CG	1:A:303:SER:HG	2.25	0.43
1:B:213:THR:HB	1:B:214:PRO:HD2	2.00	0.43
1:A:439:TYR:HB2	1:A:539:PHE:CG	2.53	0.43
1:A:608:ASN:O	1:A:611:HIS:HB2	2.19	0.43
1:A:103:PHE:HA	1:A:555:VAL:HG12	2.00	0.43
1:B:73:ARG:HB2	4:B:964:HOH:O	2.18	0.43
1:A:463:VAL:O	1:A:467:GLN:HG3	2.19	0.43
1:B:220:GLN:HA	1:B:220:GLN:HE21	1.83	0.43
1:A:16:TYR:HD2	1:A:146:VAL:HG11	1.82	0.43
1:A:205:VAL:O	1:A:211:LEU:HD12	2.19	0.43
1:A:465:TRP:HZ2	1:A:483:MET:HE2	1.83	0.42
1:A:56:GLN:O	1:A:60:GLU:HG3	2.19	0.42
1:A:292:GLN:HG2	1:A:296:MET:HE3	2.01	0.42
1:A:483:MET:HE2	1:A:603:MET:HG2	2.01	0.42
1:A:144:LEU:HD12	1:A:145:PRO:CD	2.48	0.42
1:A:298:LEU:HD13	1:A:394:LEU:CD2	2.47	0.42
1:B:107:CYS:HB3	1:B:109:HIS:CE1	2.55	0.42
1:A:102:ASN:HD22	1:A:102:ASN:N	2.17	0.42
1:B:412:GLU:HB3	1:B:607:MET:HG2	2.01	0.42
1:B:512:LEU:O	1:B:516:GLU:HG3	2.20	0.42
1:A:201:PHE:CE2	1:A:367:GLU:HB2	2.54	0.42
1:B:164:SER:HA	1:B:272:SER:O	2.20	0.42
1:A:188:CYS:O	1:A:189:PRO:C	2.63	0.42
1:B:415:HIS:CD2	1:B:417:ASP:H	2.37	0.42
1:B:554:VAL:HG12	1:B:577:ALA:CB	2.49	0.41
1:A:524:LEU:C	1:A:524:LEU:HD23	2.45	0.41
1:A:416:PRO:CB	1:A:569:ILE:HD13	2.46	0.41
1:A:283:PRO:HA	1:A:292:GLN:NE2	2.32	0.41
1:A:12:ARG:O	1:A:15:GLN:HG2	2.21	0.41
1:A:569:ILE:HG23	1:A:574:PHE:HE1	1.85	0.41
1:B:439:TYR:HB2	1:B:539:PHE:CG	2.56	0.41
1:A:546:VAL:HG22	1:A:567:TYR:C	2.45	0.41
1:A:552:GLN:OE1	1:A:568:HIS:HD2	2.04	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:131:HIS:HE1	4:A:715:HOH:O	2.04	0.41
1:A:197:ARG:HG3	1:A:228:CYS:CB	2.51	0.41
1:B:408:LEU:O	1:B:408:LEU:HD23	2.21	0.41
1:A:272:SER:O	1:A:273:LEU:C	2.64	0.41
1:B:112:HIS:HD2	1:B:113:TYR:H	1.65	0.40
1:B:310:SER:O	1:B:325:CYS:HB3	2.21	0.40
1:B:88:VAL:HG12	3:B:707:MPD:H13	2.01	0.40
1:A:237:ILE:HD11	1:A:372:VAL:HG11	2.03	0.40
1:A:470:GLN:O	1:A:472:PRO:HD3	2.22	0.40
1:B:292:GLN:NE2	4:B:932:HOH:O	2.53	0.40
1:B:508:LEU:O	1:B:512:LEU:HG	2.21	0.40
1:A:122:LEU:HD23	1:A:222:THR:OG1	2.22	0.40
1:B:213:THR:HB	1:B:214:PRO:CD	2.51	0.40
1:A:568:HIS:CD2	1:A:575:VAL:HB	2.56	0.40
1:B:152:THR:HG23	3:B:704:MPD:H11	2.04	0.40
1:B:414:LEU:HD11	1:B:607:MET:CE	2.41	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	587/612 (96%)	566 (96%)	21 (4%)	0	100	100
1	B	598/612 (98%)	584 (98%)	14 (2%)	0	100	100
All	All	1185/1224 (97%)	1150 (97%)	35 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	522/541 (96%)	514 (98%)	8 (2%)	57	65
1	B	529/541 (98%)	521 (98%)	8 (2%)	57	65
All	All	1051/1082 (97%)	1035 (98%)	16 (2%)	57	65

All (16) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	70	LEU
1	A	102	ASN
1	A	123	GLU
1	A	297	LEU
1	A	313	LEU
1	A	330	TYR
1	A	611	HIS
1	B	248	TRP
1	B	265	LEU
1	B	297	LEU
1	B	313	LEU
1	B	330	TYR
1	B	358	LYS
1	B	604	ILE
1	B	606	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	102	ASN
1	A	109	HIS
1	A	112	HIS
1	A	121	GLN
1	A	131	HIS

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Mol	Chain	Res	Type
1	A	137	GLN
1	A	220	GLN
1	A	270	GLN
1	A	292	GLN
1	A	340	HIS
1	A	378	ASN
1	A	382	GLN
1	A	415	HIS
1	A	470	GLN
1	A	490	HIS
1	A	560	HIS
1	A	568	HIS
1	A	594	GLN
1	B	87	ASN
1	B	109	HIS
1	B	112	HIS
1	B	121	GLN
1	B	131	HIS
1	B	147	HIS
1	B	151	ASN
1	B	157	ASN
1	B	220	GLN
1	B	225	HIS
1	B	270	GLN
1	B	284	HIS
1	B	292	GLN
1	B	382	GLN
1	B	395	GLN
1	B	415	HIS
1	B	470	GLN
1	B	538	ASN
1	B	568	HIS
1	B	594	GLN
1	B	608	ASN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

9 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
3	MPD	B	706	-	7,7,7	0.47	0	9,10,10	0.52	0
2	EPE	A	613	-	15,15,15	1.39	1 (6%)	19,20,20	0.59	0
3	MPD	B	704	-	7,7,7	0.47	0	9,10,10	0.43	0
3	MPD	B	703	-	7,7,7	0.48	0	9,10,10	0.51	0
2	EPE	B	701	-	15,15,15	1.39	1 (6%)	19,20,20	0.61	0
3	MPD	A	614	-	7,7,7	1.05	1 (14%)	9,10,10	0.51	0
3	MPD	B	708	-	7,7,7	0.51	0	9,10,10	0.44	0
3	MPD	B	707	-	7,7,7	0.48	0	9,10,10	0.43	0
3	MPD	B	705	-	7,7,7	0.44	0	9,10,10	0.44	0

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
3	MPD	B	706	-	-	0/5/5/5	-
2	EPE	A	613	-	-	0/9/19/19	0/1/1/1
3	MPD	B	704	-	-	3/5/5/5	-
3	MPD	B	703	-	-	0/5/5/5	-
2	EPE	B	701	-	-	0/9/19/19	0/1/1/1
3	MPD	A	614	-	-	2/5/5/5	-
3	MPD	B	708	-	-	2/5/5/5	-
3	MPD	B	707	-	-	3/5/5/5	-
3	MPD	B	705	-	-	4/5/5/5	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	613	EPE	C10-S	4.32	1.83	1.77
2	B	701	EPE	C10-S	4.23	1.83	1.77
3	A	614	MPD	C3-C2	2.23	1.60	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (14) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	614	MPD	C2-C3-C4-C5
3	B	705	MPD	C2-C3-C4-O4
3	B	705	MPD	C2-C3-C4-C5
3	B	707	MPD	O2-C2-C3-C4
3	A	614	MPD	C2-C3-C4-O4
3	B	704	MPD	C1-C2-C3-C4
3	B	704	MPD	CM-C2-C3-C4
3	B	707	MPD	C1-C2-C3-C4
3	B	707	MPD	CM-C2-C3-C4
3	B	704	MPD	O2-C2-C3-C4
3	B	705	MPD	O2-C2-C3-C4
3	B	705	MPD	CM-C2-C3-C4
3	B	708	MPD	C1-C2-C3-C4
3	B	708	MPD	CM-C2-C3-C4

There are no ring outliers.

5 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	704	MPD	1	0
3	B	703	MPD	1	0
2	B	701	EPE	1	0
3	B	707	MPD	1	0
3	B	705	MPD	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

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	591/612 (96%)	0.64	58 (9%) 13 13	13, 28, 48, 86	0
1	B	600/612 (98%)	-0.23	16 (2%) 56 59	7, 15, 33, 73	0
All	All	1191/1224 (97%)	0.20	74 (6%) 26 28	7, 22, 44, 86	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	607	MET	6.3
1	A	612	LEU	6.2
1	B	610	ALA	5.0
1	B	609	THR	5.0
1	A	359	VAL	4.6
1	A	258	LEU	4.5
1	A	609	THR	4.3
1	A	611	HIS	4.2
1	B	150	GLY	4.0
1	A	372	VAL	4.0
1	A	369	VAL	3.8
1	A	370	PHE	3.8
1	A	606	LEU	3.5
1	A	402	THR	3.5
1	A	230	ASN	3.5
1	B	571	ASP	3.4
1	A	608	ASN	3.4
1	A	123	GLU	3.4
1	A	222	THR	3.3
1	A	601	HIS	3.3
1	B	395	GLN	3.3
1	A	476	LEU	3.3
1	A	260	PRO	3.3
1	A	229	SER	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	223	TYR	3.1
1	A	583	SER	3.0
1	A	232	PRO	3.0
1	A	604	ILE	2.9
1	A	210	CYS	2.9
1	A	582	ARG	2.9
1	A	610	ALA	2.9
1	A	255	LEU	2.8
1	A	221	LEU	2.8
1	A	233	VAL	2.8
1	A	371	THR	2.7
1	A	254	TYR	2.7
1	B	601	HIS	2.6
1	A	257	SER	2.6
1	B	517	GLU	2.6
1	A	265	LEU	2.6
1	A	290	TYR	2.5
1	B	519	LEU	2.5
1	A	301	ASP	2.4
1	A	226	LYS	2.4
1	A	358	LYS	2.4
1	A	234	GLY	2.4
1	A	261	GLU	2.4
1	A	227	LYS	2.4
1	A	287	PRO	2.4
1	A	19	SER	2.4
1	A	364	LEU	2.3
1	A	394	LEU	2.3
1	A	211	LEU	2.3
1	B	76	GLY	2.3
1	B	407	LYS	2.3
1	A	376	ILE	2.2
1	B	408	LEU	2.2
1	A	235	PRO	2.2
1	A	362	ILE	2.2
1	A	368	LEU	2.2
1	A	187	HIS	2.2
1	B	481	GLN	2.2
1	B	608	ASN	2.2
1	A	256	ILE	2.2
1	A	395	GLN	2.2
1	A	360	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	357	GLU	2.1
1	B	518	GLY	2.1
1	B	288	GLU	2.1
1	A	259	ASP	2.1
1	A	598	HIS	2.1
1	A	477	LEU	2.0
1	A	378	ASN	2.0
1	A	571	ASP	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 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	EPE	B	701	15/15	0.60	0.30	50,54,56,56	0
3	MPD	A	614	8/8	0.60	0.27	44,46,49,49	0
3	MPD	B	707	8/8	0.65	0.27	56,57,58,58	0
3	MPD	B	706	8/8	0.71	0.26	55,55,56,56	0
3	MPD	B	704	8/8	0.72	0.26	64,65,67,67	0
3	MPD	B	705	8/8	0.72	0.24	49,50,52,54	0
3	MPD	B	708	8/8	0.77	0.28	66,67,68,68	0
2	EPE	A	613	15/15	0.80	0.20	43,46,48,49	0
3	MPD	B	703	8/8	0.83	0.17	38,39,40,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.