



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:37 PM UTC

PDB ID : 4DFE / pdb_00004dfe
Title : Crystal structure of 3-oxoacyl-[acyl-carrier-protein] synthase III from *Burkholderia xenovorans*
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2012-01-23
Resolution : 2.35 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

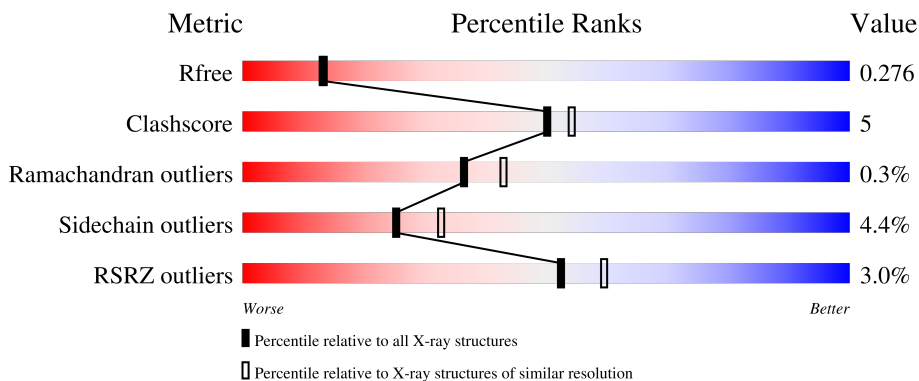
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	333	
1	B	333	
1	C	333	
1	D	333	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 9719 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 3-oxoacyl-[acyl-carrier-protein] synthase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	322	Total 2346	C 1473	N 419	O 446	S 8	0	0	0
1	B	324	Total 2352	C 1481	N 421	O 442	S 8	0	2	0
1	C	322	Total 2342	C 1471	N 416	O 447	S 8	0	0	0
1	D	323	Total 2385	C 1495	N 429	O 453	S 8	0	1	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP Q13VL5
A	-2	PRO	-	expression tag	UNP Q13VL5
A	-1	GLY	-	expression tag	UNP Q13VL5
A	0	SER	-	expression tag	UNP Q13VL5
B	-3	GLY	-	expression tag	UNP Q13VL5
B	-2	PRO	-	expression tag	UNP Q13VL5
B	-1	GLY	-	expression tag	UNP Q13VL5
B	0	SER	-	expression tag	UNP Q13VL5
C	-3	GLY	-	expression tag	UNP Q13VL5
C	-2	PRO	-	expression tag	UNP Q13VL5
C	-1	GLY	-	expression tag	UNP Q13VL5
C	0	SER	-	expression tag	UNP Q13VL5
D	-3	GLY	-	expression tag	UNP Q13VL5
D	-2	PRO	-	expression tag	UNP Q13VL5
D	-1	GLY	-	expression tag	UNP Q13VL5
D	0	SER	-	expression tag	UNP Q13VL5

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	C O	0	0
			4	2 2		

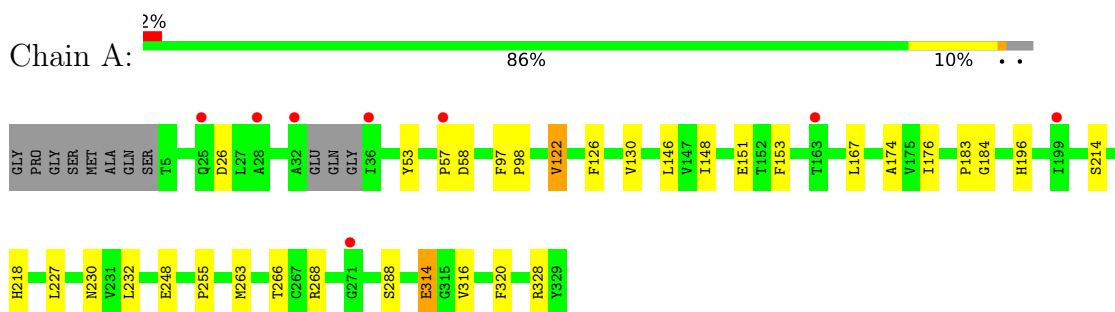
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	67	Total	O	0	0
			67	67		
3	B	75	Total	O	0	0
			75	75		
3	C	65	Total	O	0	0
			65	65		
3	D	83	Total	O	0	0
			83	83		

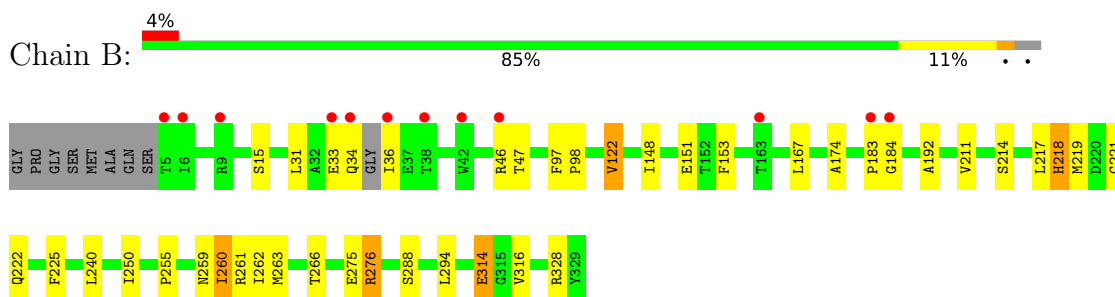
3 Residue-property plots [i](#)

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.

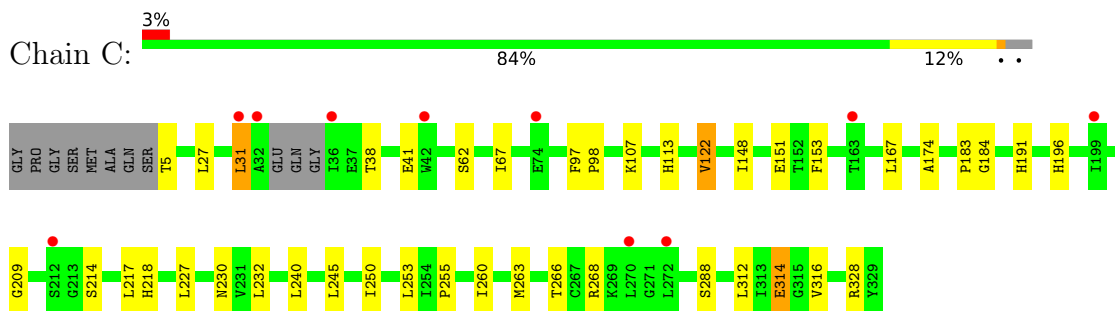
- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 3



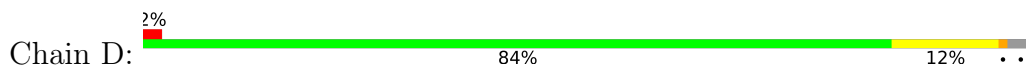
- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 3

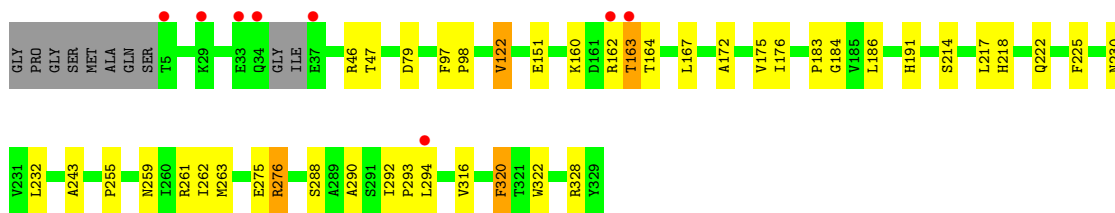


- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 3



- Molecule 1: 3-oxoacyl-[acyl-carrier-protein] synthase 3





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.99Å 67.03Å 89.20Å 113.72° 89.98° 100.25°	Depositor
Resolution (Å)	50.00 – 2.35 50.00 – 2.35	Depositor EDS
% Data completeness (in resolution range)	98.0 (50.00-2.35) 98.0 (50.00-2.35)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.45 (at 2.34Å)	Xtrriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.227 , 0.275 0.227 , 0.276	Depositor DCC
R_{free} test set	2548 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	29.7	Xtrriage
Anisotropy	0.083	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	9719	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 20.29 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 8.9826e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality i

5.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: CSO, EDO

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	0.94	0/2380	0.85	3/3241 (0.1%)
1	B	1.05	1/2391 (0.0%)	0.87	0/3256
1	C	0.95	0/2375	0.83	0/3235
1	D	1.04	2/2419 (0.1%)	0.87	0/3288
All	All	1.00	3/9565 (0.0%)	0.85	3/13020 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	4

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	218	HIS	CG-CD2	5.87	1.42	1.35
1	D	218	HIS	CG-CD2	5.86	1.42	1.35
1	D	191	HIS	CG-ND1	-5.08	1.32	1.38

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	57	PRO	CA-C-N	6.45	132.43	121.14
1	A	57	PRO	C-N-CA	6.45	132.43	121.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	58	ASP	N-CA-CB	-6.31	100.11	110.40

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	PRO	Peptide
1	B	183	PRO	Peptide
1	C	183	PRO	Peptide
1	D	183	PRO	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	2346	0	2277	14	0
1	B	2352	0	2298	32	0
1	C	2342	0	2260	24	0
1	D	2385	0	2354	30	0
2	B	4	0	6	0	0
3	A	67	0	0	2	0
3	B	75	0	0	0	0
3	C	65	0	0	2	0
3	D	83	0	0	2	0
All	All	9719	0	9195	98	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 5.

All (98) 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:31:LEU:O	1:B:36:ILE:CB	1.93	1.17
1:D:255:PRO:HG2	1:D:263:MET:HE3	1.50	0.94
1:B:261:ARG:HG3	1:B:261:ARG:HH21	1.35	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:259:ASN:HD21	1:D:262:ILE:HD12	1.37	0.89
1:B:46[B]:ARG:CG	1:B:47:THR:HG23	2.03	0.88
1:D:163:THR:HG22	1:D:164:THR:HG23	1.58	0.85
1:B:46[B]:ARG:HG2	1:B:47:THR:HG23	1.57	0.83
1:A:26:ASP:OD2	3:A:462:HOH:O	1.96	0.82
1:D:316:VAL:HG21	1:D:320:PHE:CE1	2.15	0.80
1:B:261:ARG:HG3	1:B:261:ARG:NH2	1.96	0.77
1:B:259:ASN:HD21	1:B:262:ILE:HD12	1.50	0.76
1:C:31:LEU:HD21	1:C:38:THR:HG22	1.65	0.76
1:B:255:PRO:HG2	1:B:263:MET:HE3	1.69	0.74
1:C:184:GLY:HA2	1:C:328:ARG:O	1.90	0.72
1:A:184:GLY:HA2	1:A:328:ARG:O	1.91	0.71
1:D:290:ALA:O	1:D:294:LEU:HD13	1.89	0.71
1:B:46[B]:ARG:HG3	1:B:47:THR:HG23	1.73	0.69
1:A:255:PRO:HG2	1:A:263:MET:HE3	1.77	0.67
1:D:184:GLY:HA2	1:D:328:ARG:O	1.93	0.67
1:B:46[B]:ARG:HG3	1:B:47:THR:CG2	2.24	0.67
1:D:259:ASN:HD21	1:D:262:ILE:CD1	2.07	0.67
1:D:255:PRO:HG2	1:D:263:MET:CE	2.22	0.67
1:B:184:GLY:HA2	1:B:328:ARG:O	1.94	0.66
1:D:259:ASN:ND2	1:D:262:ILE:HD12	2.11	0.64
1:D:316:VAL:HG23	1:D:322:TRP:HB3	1.80	0.63
1:B:259:ASN:ND2	1:B:262:ILE:HD12	2.15	0.59
1:B:259:ASN:HD21	1:B:262:ILE:CD1	2.14	0.59
1:C:266:THR:HG21	1:C:314:GLU:OE2	2.04	0.58
1:D:261:ARG:NH1	3:D:431:HOH:O	2.36	0.58
1:C:62:SER:OG	1:C:107:LYS:NZ	2.37	0.57
1:A:266:THR:HG21	1:A:314:GLU:OE2	2.05	0.57
1:D:172:ALA:C	1:D:294:LEU:HD11	2.31	0.56
1:A:53:TYR:HB2	3:A:441:HOH:O	2.05	0.56
1:C:31:LEU:HD21	1:C:38:THR:CG2	2.35	0.56
1:C:27:LEU:O	1:C:31:LEU:HD22	2.06	0.55
1:D:230:ASN:OD1	1:D:230:ASN:C	2.50	0.54
1:C:253:LEU:HD13	1:C:312:LEU:HD23	1.89	0.54
1:B:34:GLN:O	1:B:36:ILE:CB	2.57	0.53
1:D:316:VAL:CG2	1:D:320:PHE:CE1	2.89	0.53
1:A:230:ASN:C	1:A:230:ASN:OD1	2.52	0.53
1:B:219:MET:HE3	1:B:221:GLY:HA2	1.90	0.53
1:B:148:ILE:CD1	1:B:174:ALA:HB2	2.40	0.52
1:D:97:PHE:HB2	1:D:98:PRO:HA	1.93	0.50
1:B:97:PHE:HB2	1:B:98:PRO:HA	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:151:GLU:HG3	1:C:288:SER:HB3	1.94	0.50
1:C:232:LEU:HD21	1:C:316:VAL:HG13	1.93	0.50
1:A:146:LEU:HD13	1:A:176:ILE:HD11	1.93	0.50
1:B:148:ILE:HD12	1:B:174:ALA:HB2	1.93	0.50
1:C:217:LEU:HD23	1:C:217:LEU:C	2.37	0.50
1:B:240:LEU:HD11	1:B:250:ILE:HD11	1.93	0.50
1:C:230:ASN:OD1	1:C:230:ASN:C	2.55	0.50
1:C:255:PRO:HG2	1:C:263:MET:HE3	1.94	0.49
1:B:266:THR:HG21	1:B:314:GLU:OE2	2.13	0.49
1:B:225:PHE:CE1	1:B:262:ILE:HG13	2.48	0.49
1:C:191:HIS:CE1	3:C:410:HOH:O	2.65	0.49
1:A:151:GLU:HG3	1:A:288:SER:HB3	1.96	0.48
1:B:151:GLU:HG3	1:B:288:SER:HB3	1.94	0.48
1:C:148:ILE:CD1	1:C:174:ALA:HB2	2.42	0.48
1:A:232:LEU:HD21	1:A:316:VAL:HG13	1.95	0.48
1:B:148:ILE:CD1	1:B:174:ALA:CB	2.91	0.48
1:B:192:ALA:O	1:C:113:HIS:HA	2.13	0.48
1:D:163:THR:HG22	1:D:164:THR:CG2	2.38	0.47
1:C:240:LEU:HD21	1:C:250:ILE:HD11	1.96	0.47
1:A:196:HIS:CD2	1:A:227:LEU:HD11	2.49	0.47
1:D:225:PHE:CE1	1:D:262:ILE:HG13	2.50	0.47
1:C:196:HIS:CD2	1:C:227:LEU:HD11	2.49	0.47
1:D:151:GLU:HG3	1:D:288:SER:HB3	1.95	0.47
1:D:172:ALA:O	1:D:294:LEU:HD11	2.15	0.47
1:B:33:GLU:O	1:B:34:GLN:CB	2.64	0.46
1:C:97:PHE:HB2	1:C:98:PRO:HA	1.97	0.46
1:B:46[B]:ARG:CG	1:B:47:THR:CG2	2.81	0.46
1:D:276:ARG:HA	1:D:276:ARG:HD2	1.58	0.45
1:D:186:LEU:HB3	1:D:243:ALA:HB1	1.98	0.45
1:B:276:ARG:HA	1:B:276:ARG:HD2	1.58	0.45
1:D:186:LEU:HD11	1:D:328:ARG:NH2	2.31	0.45
1:D:222:GLN:HB3	3:D:473:HOH:O	2.17	0.45
1:D:79:ASP:C	1:D:79:ASP:OD2	2.60	0.45
1:A:97:PHE:HB2	1:A:98:PRO:HA	1.99	0.44
1:B:217:LEU:C	1:B:217:LEU:HD23	2.43	0.44
1:B:259:ASN:HD21	1:B:262:ILE:CG1	2.29	0.44
1:D:232:LEU:HD23	1:D:232:LEU:HA	1.66	0.44
1:A:148:ILE:CD1	1:A:174:ALA:HB2	2.48	0.44
1:C:196:HIS:CG	1:C:227:LEU:HD11	2.52	0.44
1:A:227:LEU:HD23	1:A:227:LEU:HA	1.79	0.44
1:C:148:ILE:CD1	1:C:174:ALA:CB	2.96	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:46:ARG:HB3	1:D:47:THR:HG23	2.00	0.44
1:D:292:ILE:N	1:D:293:PRO:HD2	2.33	0.43
1:B:46[A]:ARG:HB3	1:B:47:THR:HG23	2.00	0.43
1:B:15:SER:HB2	1:B:294:LEU:HD23	2.00	0.43
1:C:148:ILE:HD13	1:C:174:ALA:CB	2.49	0.42
1:D:175:VAL:HG12	1:D:176:ILE:N	2.34	0.42
1:A:126:PHE:O	1:A:130:VAL:HG23	2.19	0.42
1:B:211:VAL:HG21	1:C:209:GLY:O	2.20	0.42
1:C:148:ILE:HD12	1:C:174:ALA:HB2	2.02	0.41
1:D:217:LEU:C	1:D:217:LEU:HD23	2.45	0.41
1:D:175:VAL:CG1	1:D:176:ILE:N	2.83	0.41
1:B:260:ILE:HD12	1:B:260:ILE:HA	1.90	0.40
1:C:67:ILE:HD11	3:C:440:HOH:O	2.21	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	317/333 (95%)	310 (98%)	6 (2%)	1 (0%)	36	43
1	B	321/333 (96%)	316 (98%)	4 (1%)	1 (0%)	36	43
1	C	317/333 (95%)	310 (98%)	6 (2%)	1 (0%)	36	43
1	D	319/333 (96%)	312 (98%)	6 (2%)	1 (0%)	36	43
All	All	1274/1332 (96%)	1248 (98%)	22 (2%)	4 (0%)	36	43

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	122	VAL
1	B	122	VAL

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Mol	Chain	Res	Type
1	C	122	VAL
1	D	122	VAL

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	235/260 (90%)	226 (96%)	9 (4%)	29	39
1	B	234/260 (90%)	223 (95%)	11 (5%)	23	30
1	C	232/260 (89%)	220 (95%)	12 (5%)	21	25
1	D	244/260 (94%)	234 (96%)	10 (4%)	27	36
All	All	945/1040 (91%)	903 (96%)	42 (4%)	25	33

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	VAL
1	A	153	PHE
1	A	167	LEU
1	A	214	SER
1	A	218	HIS
1	A	248	GLU
1	A	268	ARG
1	A	314	GLU
1	A	320	PHE
1	B	122	VAL
1	B	153	PHE
1	B	167	LEU
1	B	214	SER
1	B	218	HIS
1	B	222	GLN
1	B	260	ILE
1	B	275	GLU
1	B	276	ARG
1	B	314	GLU

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Mol	Chain	Res	Type
1	B	316	VAL
1	C	5	THR
1	C	31	LEU
1	C	41	GLU
1	C	122	VAL
1	C	153	PHE
1	C	167	LEU
1	C	214	SER
1	C	218	HIS
1	C	245	LEU
1	C	260	ILE
1	C	268	ARG
1	C	314	GLU
1	D	122	VAL
1	D	160	LYS
1	D	162[A]	ARG
1	D	162[B]	ARG
1	D	163	THR
1	D	167	LEU
1	D	214	SER
1	D	275	GLU
1	D	276	ARG
1	D	320	PHE

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

Mol	Chain	Res	Type
1	A	106	ASN
1	A	196	HIS
1	B	178	GLN
1	B	196	HIS
1	B	222	GLN
1	B	259	ASN
1	C	50	HIS
1	C	70	GLN
1	C	178	GLN
1	C	196	HIS
1	D	259	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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
1	CSO	B	123	1	3,6,7	1.26	0	1,6,8	0.92	0
1	CSO	D	123	1	3,6,7	0.95	0	1,6,8	0.62	0
1	CSO	C	123	1	3,6,7	0.68	0	1,6,8	0.70	0
1	CSO	A	123	1	4,5,7	0.74	0	1,5,8	0.31	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
1	CSO	B	123	1	-	0/1/5/7	-
1	CSO	D	123	1	-	0/1/5/7	-
1	CSO	C	123	1	-	0/1/5/7	-
1	CSO	A	123	1	-	0/1/4/7	-

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.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	EDO	B	401	-	3,3,3	0.52	0	2,2,2	0.33	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
2	EDO	B	401	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

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 [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	321/333 (96%)	0.39	8 (2%) 58 64	16, 33, 52, 64	0
1	B	323/333 (96%)	0.26	12 (3%) 45 51	14, 25, 51, 73	2 (0%)
1	C	321/333 (96%)	0.37	10 (3%) 51 58	15, 34, 54, 65	0
1	D	322/333 (96%)	0.25	8 (2%) 58 64	15, 26, 42, 58	1 (0%)
All	All	1287/1332 (96%)	0.32	38 (2%) 52 59	14, 29, 51, 73	3 (0%)

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	36	ILE	4.4
1	B	5	THR	4.3
1	C	32	ALA	3.8
1	A	36	ILE	3.8
1	A	32	ALA	3.7
1	D	37	GLU	3.4
1	B	184	GLY	3.1
1	B	34	GLN	3.1
1	D	33	GLU	2.9
1	B	46[A]	ARG	2.8
1	C	199	ILE	2.8
1	A	163	THR	2.7
1	B	42	TRP	2.7
1	B	33	GLU	2.6
1	B	6	ILE	2.6
1	A	57	PRO	2.5
1	C	42	TRP	2.4
1	A	271	GLY	2.4
1	D	29	LYS	2.4
1	B	163	THR	2.4
1	B	9	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	D	34	GLN	2.4
1	D	163	THR	2.3
1	D	294	LEU	2.3
1	A	199	ILE	2.3
1	B	36	ILE	2.3
1	C	270	LEU	2.2
1	B	38	THR	2.2
1	C	163	THR	2.2
1	D	5	THR	2.2
1	A	25	GLN	2.1
1	D	162[A]	ARG	2.1
1	C	31	LEU	2.1
1	B	183	PRO	2.1
1	A	28	ALA	2.1
1	C	74	GLU	2.1
1	C	272	LEU	2.1
1	C	212	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q<0.9
1	CSO	D	123	7/8	0.90	0.09	20,21,24,25	0
1	CSO	C	123	7/8	0.91	0.10	26,27,31,31	0
1	CSO	A	123	6/8	0.91	0.10	29,30,33,37	0
1	CSO	B	123	7/8	0.93	0.09	17,17,22,23	0

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(\AA^2)	Q<0.9
2	EDO	B	401	4/4	0.96	0.07	24,24,25,25	0

6.5 Other polymers [i](#)

There are no such residues in this entry.