



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 15, 2017 – 01:05 am GMT

PDB ID : 4O5M
Title : X-ray Crystal Structure of Isovaleryl-CoA Dehydrogenase from Brucella suis
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2013-12-19
Resolution : 2.20 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

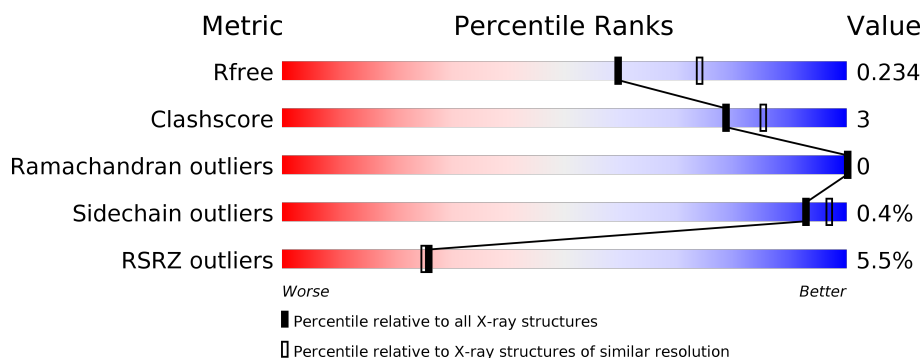
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	390	<div> <div>2%</div> <div> <div></div> <div>83%</div> <div>7%</div> <div>10%</div> </div> </div>
1	B	390	<div> <div>7%</div> <div> <div></div> <div>80%</div> <div>8%</div> <div>12%</div> </div> </div>
1	C	390	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>8%</div> <div>7%</div> </div> </div>
1	D	390	<div> <div>4%</div> <div> <div></div> <div>84%</div> <div>7%</div> <div>8%</div> </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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	CA	A	401	-	-	-	X
3	PG5	B	401	-	-	-	X
3	PG5	C	401	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10541 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 Isovaleryl-CoA dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	0	0
			2523	1586	445	474	18			
1	B	342	Total	C	N	O	S	0	0	0
			2457	1546	431	462	18			
1	C	362	Total	C	N	O	S	0	0	0
			2650	1665	461	505	19			
1	D	358	Total	C	N	O	S	0	1	0
			2625	1651	458	496	20			

There are 32 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	EXPRESSION TAG	UNP Q8G3C9
A	-6	ALA	-	EXPRESSION TAG	UNP Q8G3C9
A	-5	HIS	-	EXPRESSION TAG	UNP Q8G3C9
A	-4	HIS	-	EXPRESSION TAG	UNP Q8G3C9
A	-3	HIS	-	EXPRESSION TAG	UNP Q8G3C9
A	-2	HIS	-	EXPRESSION TAG	UNP Q8G3C9
A	-1	HIS	-	EXPRESSION TAG	UNP Q8G3C9
A	0	HIS	-	EXPRESSION TAG	UNP Q8G3C9
B	-7	MET	-	EXPRESSION TAG	UNP Q8G3C9
B	-6	ALA	-	EXPRESSION TAG	UNP Q8G3C9
B	-5	HIS	-	EXPRESSION TAG	UNP Q8G3C9
B	-4	HIS	-	EXPRESSION TAG	UNP Q8G3C9
B	-3	HIS	-	EXPRESSION TAG	UNP Q8G3C9
B	-2	HIS	-	EXPRESSION TAG	UNP Q8G3C9
B	-1	HIS	-	EXPRESSION TAG	UNP Q8G3C9
B	0	HIS	-	EXPRESSION TAG	UNP Q8G3C9
C	-7	MET	-	EXPRESSION TAG	UNP Q8G3C9
C	-6	ALA	-	EXPRESSION TAG	UNP Q8G3C9
C	-5	HIS	-	EXPRESSION TAG	UNP Q8G3C9
C	-4	HIS	-	EXPRESSION TAG	UNP Q8G3C9
C	-3	HIS	-	EXPRESSION TAG	UNP Q8G3C9

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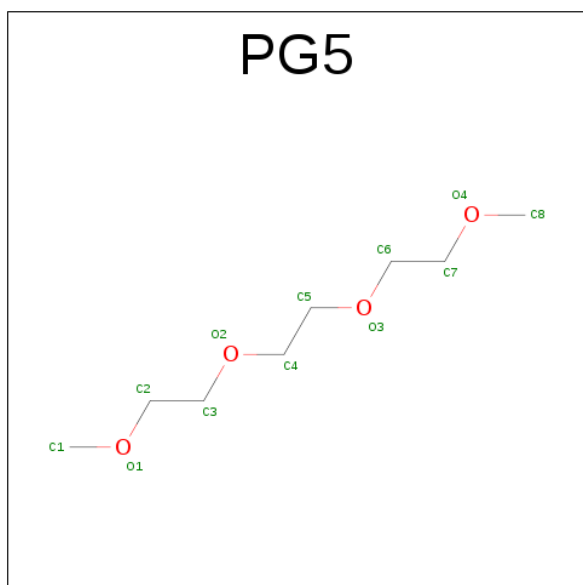
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Chain	Residue	Modelled	Actual	Comment	Reference
C	-2	HIS	-	EXPRESSION TAG	UNP Q8G3C9
C	-1	HIS	-	EXPRESSION TAG	UNP Q8G3C9
C	0	HIS	-	EXPRESSION TAG	UNP Q8G3C9
D	-7	MET	-	EXPRESSION TAG	UNP Q8G3C9
D	-6	ALA	-	EXPRESSION TAG	UNP Q8G3C9
D	-5	HIS	-	EXPRESSION TAG	UNP Q8G3C9
D	-4	HIS	-	EXPRESSION TAG	UNP Q8G3C9
D	-3	HIS	-	EXPRESSION TAG	UNP Q8G3C9
D	-2	HIS	-	EXPRESSION TAG	UNP Q8G3C9
D	-1	HIS	-	EXPRESSION TAG	UNP Q8G3C9
D	0	HIS	-	EXPRESSION TAG	UNP Q8G3C9

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Ca 1 1	0	0

- Molecule 3 is 1-METHOXY-2-[2-(2-METHOXY-ETHOXY)]-ETHANE (three-letter code: PG5) (formula: C₈H₁₈O₄).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total C O 12 8 4	0	0
3	C	1	Total C O 12 8 4	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	D	1	Total	C	O	0	0
			12	8	4		

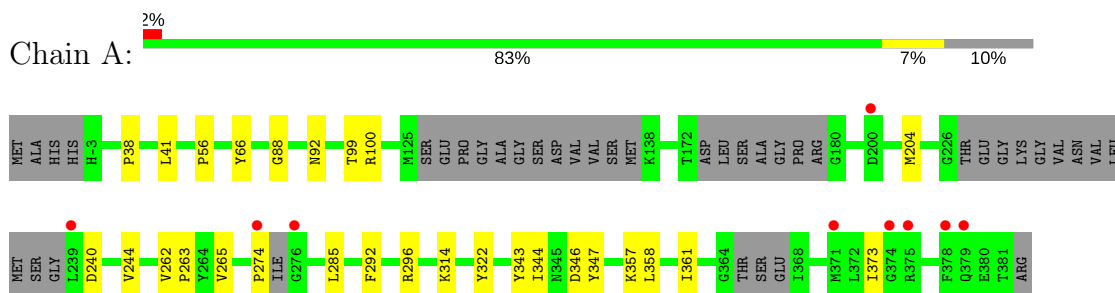
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	69	Total	O	0	0
			69	69		
4	B	37	Total	O	0	0
			37	37		
4	C	68	Total	O	0	0
			68	68		
4	D	75	Total	O	0	0
			75	75		

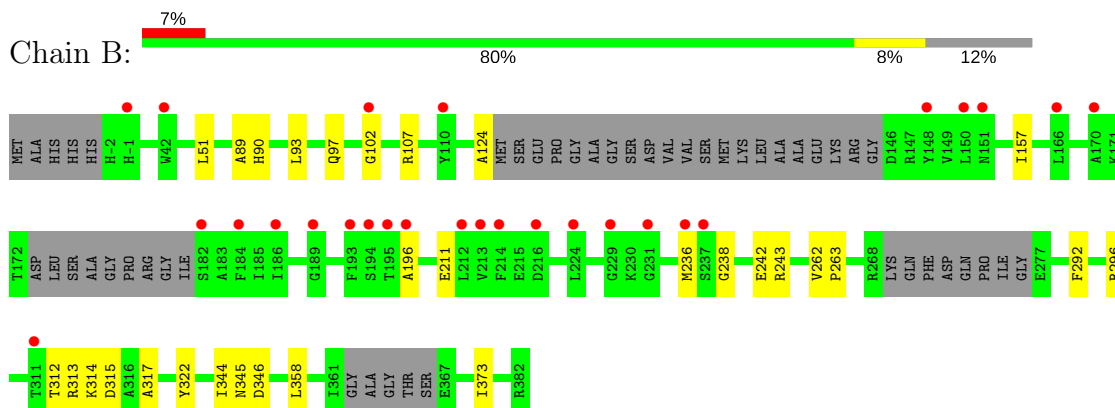
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

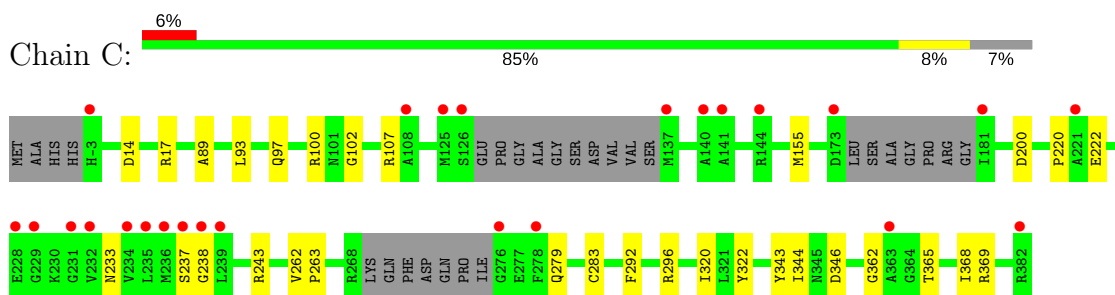
- Molecule 1: Isovaleryl-CoA dehydrogenase



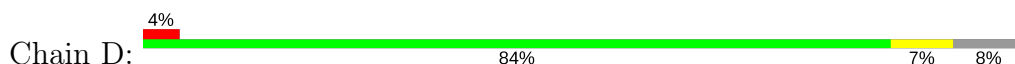
- Molecule 1: Isovaleryl-CoA dehydrogenase

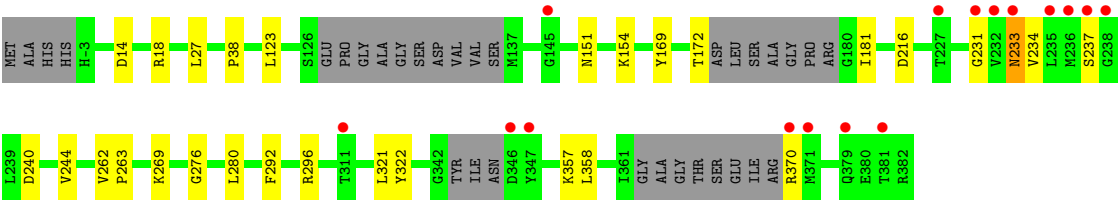


- Molecule 1: Isovaleryl-CoA dehydrogenase



- Molecule 1: Isovaleryl-CoA dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.21Å 91.07Å 102.14Å 90.00° 99.25° 90.00°	Depositor
Resolution (Å)	46.28 – 2.20 46.28 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.28-2.20) 98.8 (46.28-2.20)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.4_1496)	Depositor
R, R_{free}	0.200 , 0.234 0.200 , 0.234	Depositor DCC
R_{free} test set	3755 reflections (5.03%)	DCC
Wilson B-factor (Å ²)	40.0	Xtriage
Anisotropy	0.350	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 51.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10541	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.85% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, PG5

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	0.22	0/2565	0.42	1/3477 (0.0%)
1	B	0.21	0/2498	0.40	0/3390
1	C	0.22	0/2694	0.40	0/3649
1	D	0.22	0/2672	0.41	0/3617
All	All	0.22	0/10429	0.41	1/14133 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	274	PRO	N-CA-CB	6.14	110.67	103.30

There are no chirality outliers.

There are no planarity outliers.

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	2523	0	2345	17	0
1	B	2457	0	2279	19	0
1	C	2650	0	2510	19	0
1	D	2625	0	2489	20	0
2	A	1	0	0	0	0
3	B	12	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	12	0	18	0	0
3	D	12	0	18	1	0
4	A	69	0	0	0	0
4	B	37	0	0	0	0
4	C	68	0	0	0	0
4	D	75	0	0	0	0
All	All	10541	0	9677	66	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 3.

All (66) 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:D:14:ASP:OD2	1:D:18:ARG:NH2	2.20	0.74
1:B:322:TYR:HH	1:D:322:TYR:HH	1.37	0.70
1:C:279:GLN:HG2	1:D:276:GLY:HA3	1.73	0.69
1:B:93:LEU:HD21	1:B:242:GLU:HG3	1.76	0.67
1:B:344:ILE:HG22	1:B:346:ASP:H	1.61	0.65
1:D:321:LEU:HD21	1:D:370:ARG:HE	1.61	0.64
1:C:365:THR:H	1:C:368:ILE:HD12	1.63	0.63
1:D:233:ASN:O	1:D:237:SER:OG	2.10	0.62
1:A:322:TYR:HH	1:C:322:TYR:HH	1.50	0.60
1:C:362:GLY:O	1:C:369:ARG:NH2	2.36	0.58
1:C:100:ARG:HH22	1:C:237:SER:HB3	1.69	0.58
1:B:102:GLY:O	1:B:107:ARG:NH1	2.36	0.57
1:B:322:TYR:OH	1:D:322:TYR:OH	2.14	0.57
1:C:344:ILE:HG22	1:C:346:ASP:H	1.70	0.57
1:C:233:ASN:O	1:C:237:SER:OG	2.16	0.56
1:A:344:ILE:HB	1:A:347:TYR:CD2	2.42	0.54
1:B:97:GLN:HE21	1:B:238:GLY:HA3	1.72	0.54
1:B:236:MET:HB3	1:B:313:ARG:NH2	2.25	0.52
1:B:292:PHE:CZ	1:B:296:ARG:HD2	2.45	0.51
1:A:344:ILE:HB	1:A:347:TYR:HD2	1.76	0.51
1:D:151:ASN:OD1	1:D:216:ASP:N	2.32	0.50
1:C:292:PHE:CZ	1:C:296:ARG:HD2	2.46	0.50
1:A:322:TYR:OH	1:C:322:TYR:OH	2.23	0.50
1:C:243:ARG:HD3	1:C:320:ILE:HG21	1.94	0.50
1:D:292:PHE:CZ	1:D:296:ARG:HD2	2.47	0.49
1:B:89:ALA:O	1:B:93:LEU:HB2	2.12	0.49
1:A:204:MET:HG3	1:A:358:LEU:HD23	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:14:ASP:OD1	1:C:17:ARG:NH2	2.46	0.48
1:D:276:GLY:O	1:D:280:LEU:HD13	2.13	0.48
1:A:292:PHE:CZ	1:A:296:ARG:HD2	2.48	0.48
1:C:102:GLY:O	1:C:107:ARG:NH1	2.47	0.47
1:B:196:ALA:HB3	1:B:211:GLU:HB3	1.96	0.47
1:A:265:VAL:HG21	1:A:285:LEU:HD11	1.95	0.47
1:B:314:LYS:HB2	1:B:373:ILE:HG23	1.97	0.46
1:B:358:LEU:HB2	1:C:343:TYR:CZ	2.50	0.46
1:C:97:GLN:HE21	1:C:238:GLY:HA3	1.80	0.46
1:B:93:LEU:HD21	1:B:242:GLU:CG	2.45	0.46
1:A:344:ILE:HG22	1:A:346:ASP:H	1.80	0.46
1:B:243:ARG:HD2	1:B:317:ALA:HA	1.97	0.46
1:A:314:LYS:HB2	1:A:373:ILE:HG23	1.97	0.46
1:B:345:ASN:ND2	1:C:200:ASP:OD1	2.47	0.45
1:D:233:ASN:OD1	1:D:233:ASN:N	2.41	0.45
1:C:262:VAL:HB	1:C:263:PRO:HD3	2.00	0.44
1:D:262:VAL:HB	1:D:263:PRO:HD3	2.00	0.44
1:D:240:ASP:O	1:D:244:VAL:HG23	2.17	0.44
1:C:283:CYS:SG	1:D:280:LEU:HD21	2.58	0.44
1:C:220:PRO:HB2	1:C:222:GLU:HG2	1.99	0.44
1:A:38:PRO:HG2	1:A:41:LEU:HD12	2.00	0.43
1:A:88:GLY:O	1:A:92:ASN:HB3	2.18	0.43
1:B:312:THR:HG23	1:B:315:ASP:HB2	2.00	0.42
1:D:269:LYS:HZ2	3:D:401:PG5:C7	2.32	0.42
1:A:240:ASP:O	1:A:244:VAL:HG23	2.18	0.42
1:A:343:TYR:CZ	1:D:358:LEU:HB2	2.54	0.42
1:B:124:ALA:HA	1:B:157:ILE:HD12	2.00	0.42
1:D:181:ILE:O	1:D:231:GLY:N	2.51	0.42
1:A:357:LYS:O	1:A:361:ILE:HG12	2.20	0.42
1:D:154:LYS:HA	1:D:154:LYS:HD3	1.89	0.42
1:A:66:TYR:OH	1:A:100:ARG:HD2	2.19	0.42
1:D:27[B]:LEU:HD13	1:D:38:PRO:HG3	2.02	0.42
1:A:262:VAL:HB	1:A:263:PRO:HD3	2.02	0.42
1:B:262:VAL:HB	1:B:263:PRO:HD3	2.01	0.41
1:C:89:ALA:HA	1:C:93:LEU:HG	2.03	0.41
1:D:123:LEU:HD11	1:D:169:TYR:HE1	1.85	0.41
1:A:56:PRO:HD3	1:A:99:THR:HG23	2.03	0.41
1:D:357:LYS:HA	1:D:357:LYS:HD2	1.87	0.40
1:B:51:LEU:HD22	1:B:90:HIS:CD2	2.55	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	338/390 (87%)	331 (98%)	7 (2%)	0	100	100
1	B	332/390 (85%)	324 (98%)	8 (2%)	0	100	100
1	C	354/390 (91%)	345 (98%)	9 (2%)	0	100	100
1	D	349/390 (90%)	339 (97%)	10 (3%)	0	100	100
All	All	1373/1560 (88%)	1339 (98%)	34 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	233/305 (76%)	233 (100%)	0	100	100
1	B	226/305 (74%)	226 (100%)	0	100	100
1	C	254/305 (83%)	253 (100%)	1 (0%)	93	97
1	D	252/305 (83%)	249 (99%)	3 (1%)	75	86
All	All	965/1220 (79%)	961 (100%)	4 (0%)	93	97

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	155	MET
1	D	172	THR

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Mol	Chain	Res	Type
1	D	233	ASN
1	D	234	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	101	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](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 for Mogul analysis.

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	PG5	B	401	-	11,11,11	0.69	0	10,10,10	0.24	0
3	PG5	C	401	-	11,11,11	0.69	0	10,10,10	0.20	0
3	PG5	D	401	-	11,11,11	0.68	0	10,10,10	0.23	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	PG5	B	401	-	-	0/9/9/9	0/0/0/0
3	PG5	C	401	-	-	0/9/9/9	0/0/0/0
3	PG5	D	401	-	-	0/9/9/9	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	401	PG5	1	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	350/390 (89%)	0.09	9 (2%) 56 54	30, 53, 99, 127	0
1	B	342/390 (87%)	0.48	27 (7%) 13 12	35, 66, 106, 133	0
1	C	362/390 (92%)	0.35	25 (6%) 18 16	33, 53, 101, 134	0
1	D	358/390 (91%)	0.14	16 (4%) 34 32	27, 50, 104, 144	0
All	All	1412/1560 (90%)	0.26	77 (5%) 26 25	27, 55, 104, 144	0

All (77) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	231	GLY	5.6
1	A	276	GLY	5.6
1	C	231	GLY	5.6
1	A	378	PHE	4.9
1	B	150	LEU	4.8
1	D	237	SER	4.4
1	D	235	LEU	4.4
1	B	236	MET	4.2
1	C	236	MET	4.1
1	B	213	VAL	3.8
1	B	193	PHE	3.8
1	C	235	LEU	3.8
1	C	239	LEU	3.7
1	B	186	ILE	3.7
1	C	140	ALA	3.6
1	B	212	LEU	3.6
1	D	232	VAL	3.6
1	C	278	PHE	3.5
1	B	182	SER	3.5
1	B	-1	HIS	3.5
1	D	145	GLY	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	311	THR	3.4
1	C	181	ILE	3.4
1	B	229	GLY	3.3
1	B	184	PHE	3.3
1	B	148	TYR	3.3
1	C	229	GLY	3.3
1	C	363	ALA	3.2
1	C	125	MET	3.2
1	A	371	MET	3.1
1	C	232	VAL	3.1
1	C	137	MET	3.1
1	D	370	ARG	3.1
1	C	221	ALA	3.1
1	A	374	GLY	2.9
1	B	216	ASP	2.9
1	C	234	VAL	2.9
1	C	276	GLY	2.9
1	D	381	THR	2.9
1	C	126	SER	2.8
1	B	195	THR	2.8
1	B	196	ALA	2.7
1	A	375	ARG	2.7
1	C	-3	HIS	2.7
1	D	236	MET	2.7
1	D	233	ASN	2.7
1	D	347	TYR	2.6
1	B	231	GLY	2.6
1	D	371	MET	2.6
1	A	274	PRO	2.5
1	B	166	LEU	2.5
1	B	214	PHE	2.5
1	C	228	GLU	2.4
1	B	194	SER	2.4
1	B	224	LEU	2.4
1	D	346	ASP	2.3
1	D	227	THR	2.3
1	C	382	ARG	2.3
1	B	102	GLY	2.3
1	B	151	ASN	2.3
1	A	200	ASP	2.2
1	B	110	TYR	2.2
1	B	237	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	238	GLY	2.2
1	C	141	ALA	2.2
1	B	189	GLY	2.2
1	A	379	GLN	2.2
1	C	108	ALA	2.1
1	D	311	THR	2.1
1	A	239	LEU	2.1
1	B	42	TRP	2.1
1	C	173	ASP	2.1
1	C	144	ARG	2.1
1	D	379	GLN	2.0
1	C	238	GLY	2.0
1	C	237	SER	2.0
1	B	170	ALA	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	CA	A	401	1/1	0.90	0.23	4.30	91,91,91,91	0
3	PG5	C	401	12/12	0.90	0.16	2.30	46,53,65,65	0
3	PG5	B	401	12/12	0.90	0.18	2.12	49,57,75,75	0
3	PG5	D	401	12/12	0.85	0.17	0.66	50,62,71,74	0

6.5 Other polymers [i](#)

There are no such residues in this entry.