



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 09:43 PM GMT

PDB ID : 1QCN
Title : CRYSTAL STRUCTURE OF FUMARYLACETOACETATE HYDROLASE
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Deposited on : 1999-05-14
Resolution : 1.90 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

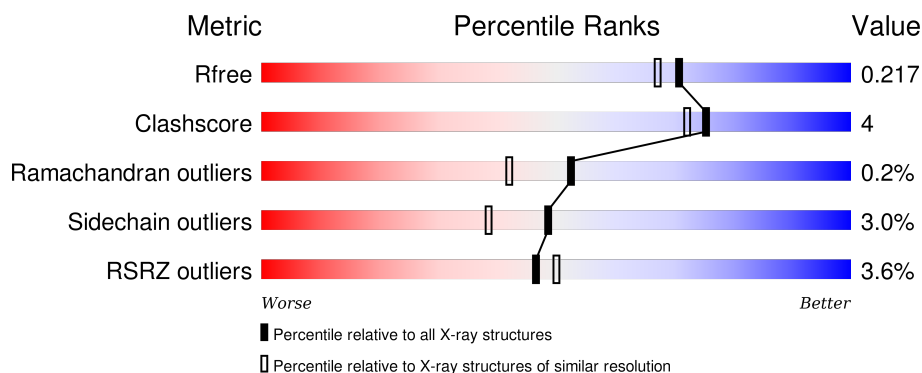
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.90 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	4755 (1.90-1.90)
Clashscore	102246	5398 (1.90-1.90)
Ramachandran outliers	100387	5338 (1.90-1.90)
Sidechain outliers	100360	5339 (1.90-1.90)
RSRZ outliers	91569	4766 (1.90-1.90)

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	421	<div> <div>3%</div> <div>88%</div> <div>10% ..</div> </div>
1	B	421	<div> <div>4%</div> <div>91%</div> <div>8%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ACT	A	1004	-	-	X	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7086 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 FUMARYLACETOACETATE HYDROLASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	417	Total	C	N	O	S	Se	0	0	1
			3222	2048	563	590	6	15			
1	B	420	Total	C	N	O	S	Se	0	0	1
			3241	2058	566	595	6	16			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION ARTIFACT	UNP P35505
A	0	SER	-	EXPRESSION ARTIFACT	UNP P35505
A	1	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	71	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	115	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	140	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	177	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	180	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	198	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	202	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	228	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	231	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	266	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	270	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	308	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	322	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	326	MSE	MET	MODIFIED RESIDUE	UNP P35505
A	362	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	499	GLY	-	EXPRESSION ARTIFACT	UNP P35505
B	500	SER	-	EXPRESSION ARTIFACT	UNP P35505
B	501	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	571	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	615	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	640	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	677	MSE	MET	MODIFIED RESIDUE	UNP P35505

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Chain	Residue	Modelled	Actual	Comment	Reference
B	680	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	698	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	702	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	728	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	731	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	766	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	770	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	808	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	822	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	826	MSE	MET	MODIFIED RESIDUE	UNP P35505
B	862	MSE	MET	MODIFIED RESIDUE	UNP P35505

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

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

- Molecule 3 is NICKEL (II) ION (three-letter code: NI) (formula: Ni).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Ni 1 1	0	0

- Molecule 4 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



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

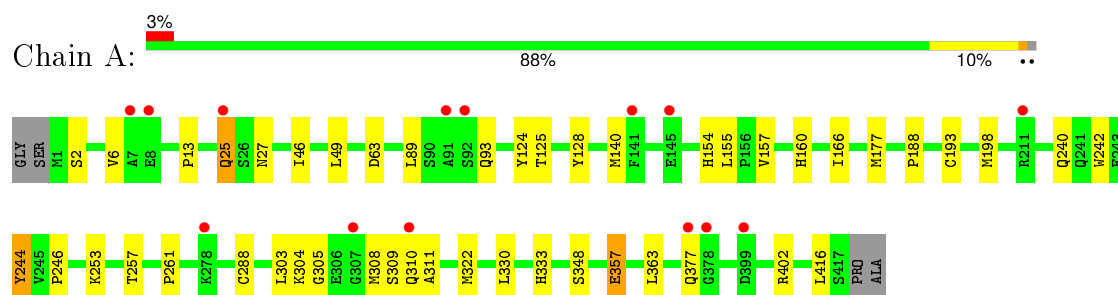
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	291	Total	O	0	0
			291	291		
5	B	313	Total	O	0	0
			313	313		

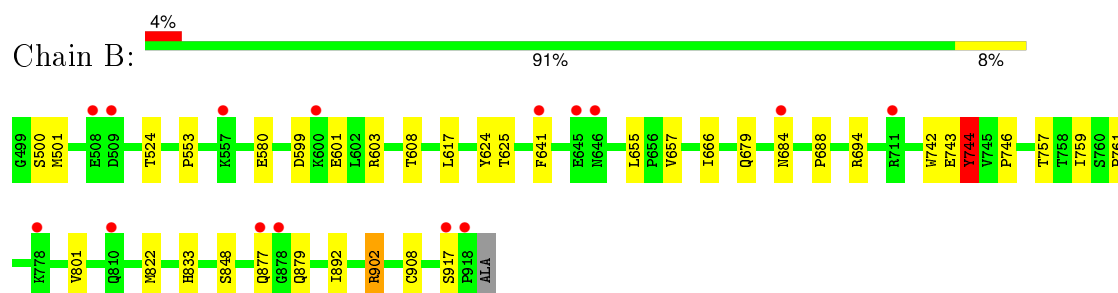
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: FUMARYLACETOACETATE HYDROLASE



• Molecule 1: FUMARYLACETOACETATE HYDROLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.32Å 110.34Å 67.53Å 90.00° 102.38° 90.00°	Depositor
Resolution (Å)	22.00 – 1.90 22.30 – 1.89	Depositor EDS
% Data completeness (in resolution range)	96.2 (22.00-1.90) 97.9 (22.30-1.89)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.90 (at 1.89Å)	Xtriage
Refinement program	X-PLOR 3.1	Depositor
R, R_{free}	0.191 , 0.220 0.189 , 0.217	Depositor DCC
R_{free} test set	3586 reflections (5.31%)	DCC
Wilson B-factor (Å ²)	11.1	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.0	EDS
Estimated twinning fraction	0.021 for l,-k,h	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 71600 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7086	wwPDB-VP
Average B, all atoms (Å ²)	12.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.48	0/3296	0.69	2/4453 (0.0%)
1	B	0.49	0/3314	0.70	2/4474 (0.0%)
All	All	0.49	0/6610	0.70	4/8927 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	694	ARG	NE-CZ-NH1	-6.20	117.20	120.30
1	A	93	GLN	N-CA-C	-5.60	95.88	111.00
1	A	244	TYR	N-CA-C	5.30	125.31	111.00
1	B	744	TYR	N-CA-C	5.30	125.30	111.00

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	3222	0	3160	33	0
1	B	3241	0	3177	18	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	8	0	6	4	0
4	B	8	0	6	0	0
5	A	291	0	0	7	0
5	B	313	0	0	4	0
All	All	7086	0	6349	50	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 4.

All (50) 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:240:GLN:HE22	4:A:1004:ACT:H3	1.37	0.87
1:A:253:LYS:HZ3	4:A:1004:ACT:H1	1.45	0.81
1:B:822:MSE:HE2	1:B:848:SER:HB2	1.64	0.77
1:B:761:PRO:HD2	5:B:1157:HOH:O	1.83	0.77
1:A:125:THR:OG1	1:A:333:HIS:HE1	1.69	0.76
1:B:625:THR:OG1	1:B:833:HIS:HE1	1.71	0.73
1:A:253:LYS:NZ	4:A:1004:ACT:H1	2.06	0.71
1:A:310:GLN:HA	1:A:310:GLN:OE1	1.91	0.70
1:A:140:MSE:HE1	1:A:363:LEU:HD11	1.76	0.65
1:A:288:CYS:HB2	5:A:1200:HOH:O	2.03	0.58
1:A:140:MSE:HE1	1:A:363:LEU:CD1	2.33	0.58
1:A:25:GLN:HG3	5:A:1199:HOH:O	2.05	0.56
1:A:310:GLN:H	1:A:377:GLN:HE22	1.53	0.55
1:A:154:HIS:HD2	5:A:1168:HOH:O	1.89	0.54
1:A:310:GLN:H	1:A:377:GLN:NE2	2.06	0.53
1:A:6:VAL:HG11	1:A:13:PRO:HA	1.90	0.52
1:A:160:HIS:HE1	5:B:1097:HOH:O	1.93	0.51
1:A:2:SER:HA	1:A:89:LEU:O	2.12	0.49
1:A:128:TYR:HB3	1:A:157:VAL:HG23	1.95	0.49
1:A:309:SER:H	1:A:377:GLN:HE22	1.62	0.48
1:B:688:PRO:HG3	1:B:742:TRP:CZ2	2.48	0.48
1:A:261:PRO:HD2	5:A:1158:HOH:O	2.14	0.47
1:A:309:SER:N	1:A:377:GLN:HE22	2.11	0.47
1:A:46:ILE:HB	1:A:49:LEU:HD12	1.96	0.47
1:A:322:MSE:HE2	1:A:348:SER:HB2	1.95	0.47
1:B:902:ARG:NH2	5:B:1165:HOH:O	2.49	0.46
1:B:553:PRO:HD2	1:B:580:GLU:OE2	2.16	0.46
1:A:177:MSE:HG3	5:A:1067:HOH:O	2.16	0.46
1:B:801:VAL:HG22	1:B:892:ILE:HG12	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:524:THR:HG21	1:B:608:THR:HG21	1.99	0.44
1:B:655:LEU:HD11	1:B:657:VAL:HG12	1.99	0.44
1:B:879:GLN:HA	5:B:1277:HOH:O	2.17	0.43
1:B:599:ASP:O	1:B:603:ARG:HB2	2.19	0.43
1:A:125:THR:OG1	1:A:333:HIS:CE1	2.61	0.43
1:A:310:GLN:CA	1:A:310:GLN:OE1	2.61	0.43
1:B:655:LEU:CD1	1:B:657:VAL:HG12	2.49	0.43
1:B:892:ILE:HB	1:B:908:CYS:HB3	2.00	0.43
1:B:617:LEU:HD22	1:B:759:ILE:HD11	2.00	0.42
1:A:166:ILE:HA	1:A:257:THR:O	2.18	0.42
1:A:188:PRO:HG3	1:A:242:TRP:CZ2	2.54	0.42
1:A:304:LYS:HB2	1:A:311:ALA:HB2	2.01	0.42
1:B:743:GLU:CG	1:B:744:TYR:N	2.82	0.41
1:B:666:ILE:HA	1:B:757:THR:O	2.21	0.41
1:A:155:LEU:HB3	1:B:679:GLN:NE2	2.36	0.41
1:A:357:GLU:HG2	5:A:1051:HOH:O	2.19	0.41
1:A:303:LEU:C	1:A:303:LEU:HD23	2.41	0.41
1:A:305:GLY:H	1:A:308:MSE:SE	2.54	0.41
1:A:240:GLN:NE2	5:A:1077:HOH:O	2.53	0.41
1:B:743:GLU:HG3	1:B:744:TYR:N	2.36	0.40
1:A:240:GLN:NE2	4:A:1004:ACT:H3	2.19	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	415/421 (99%)	403 (97%)	12 (3%)	0	100	100
1	B	418/421 (99%)	404 (97%)	12 (3%)	2 (0%)	34	21
All	All	833/842 (99%)	807 (97%)	24 (3%)	2 (0%)	52	42

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	877	GLN
1	B	917	SER

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	350/338 (104%)	338 (97%)	12 (3%)	44	33
1	B	353/338 (104%)	344 (98%)	9 (2%)	55	47
All	All	703/676 (104%)	682 (97%)	21 (3%)	48	38

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	GLN
1	A	27	ASN
1	A	63	ASP
1	A	124	TYR
1	A	193	CYS
1	A	198	MSE
1	A	244	TYR
1	A	246	PRO
1	A	330	LEU
1	A	357	GLU
1	A	402	ARG
1	A	416	LEU
1	B	500	SER
1	B	501	MSE
1	B	601	GLU
1	B	624	TYR
1	B	641	PHE
1	B	684	ASN
1	B	744	TYR
1	B	746	PRO
1	B	902	ARG

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

Mol	Chain	Res	Type
1	A	27	ASN
1	A	39	GLN
1	A	154	HIS
1	A	160	HIS
1	A	240	GLN
1	A	333	HIS
1	A	377	GLN
1	B	539	GLN
1	B	660	HIS
1	B	740	GLN
1	B	789	HIS
1	B	833	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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
4	ACT	A	1004	2	1,3,3	2.93	1 (100%)	0,3,3	0.00	-
4	ACT	A	1005	-	1,3,3	3.53	1 (100%)	0,3,3	0.00	-
4	ACT	B	1006	2	1,3,3	4.11	1 (100%)	0,3,3	0.00	-
4	ACT	B	1007	-	1,3,3	4.01	1 (100%)	0,3,3	0.00	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	ACT	A	1004	2	-	0/0/0/0	0/0/0/0
4	ACT	A	1005	-	-	0/0/0/0	0/0/0/0
4	ACT	B	1006	2	-	0/0/0/0	0/0/0/0
4	ACT	B	1007	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1004	ACT	CH3-C	2.93	1.52	1.48
4	A	1005	ACT	CH3-C	3.53	1.53	1.48
4	B	1007	ACT	CH3-C	4.01	1.54	1.48
4	B	1006	ACT	CH3-C	4.11	1.54	1.48

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 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1004	ACT	4	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	401/421 (95%)	-0.10	14 (3%) 48 51	4, 10, 23, 29	0
1	B	404/421 (95%)	-0.08	15 (3%) 45 49	4, 10, 22, 35	0
All	All	805/842 (95%)	-0.09	29 (3%) 46 50	4, 10, 23, 35	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	918	PRO	10.1
1	B	878	GLY	7.7
1	B	917	SER	5.3
1	B	646	ASN	4.6
1	B	877	GLN	4.6
1	B	641	PHE	3.9
1	A	91	ALA	3.6
1	A	307	GLY	3.5
1	B	645	GLU	3.3
1	A	310	GLN	3.1
1	A	378	GLY	3.1
1	A	145	GLU	2.9
1	A	25	GLN	2.7
1	A	399	ASP	2.7
1	A	92	SER	2.6
1	A	8	GLU	2.6
1	B	557	LYS	2.6
1	B	600	LYS	2.6
1	A	141	PHE	2.5
1	B	509	ASP	2.4
1	A	211	ARG	2.4
1	A	278	LYS	2.3
1	B	684	ASN	2.3
1	B	508	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	778	LYS	2.2
1	B	711	ARG	2.2
1	A	377	GLN	2.1
1	A	7	ALA	2.1
1	B	810	GLN	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 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
4	ACT	A	1004	4/4	0.87	0.15	3.35	11,12,12,13	0
4	ACT	B	1006	4/4	0.95	0.10	1.38	9,9,10,10	0
4	ACT	B	1007	4/4	0.86	0.16	0.97	23,23,23,23	0
4	ACT	A	1005	4/4	0.96	0.07	-0.94	12,13,13,13	0
2	CA	A	1001	1/1	0.99	0.05	-2.32	6,6,6,6	0
2	CA	B	1002	1/1	0.99	0.05	-2.65	8,8,8,8	0
3	NI	B	1003	1/1	0.98	0.05	-	13,13,13,13	0

6.5 Other polymers [i](#)

There are no such residues in this entry.