Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:03 AM GMT

PDB ID	:	2P82
Title	:	Cysteine protease ATG4A
Authors	:	Walker, J.R.; Davis, T.; Mujib, S.; Butler-Cole, C.; Finerty Jr., P.J.; Weigelt, J.; Sundstrom, M.; Arrowsmith, C.H.; Edwards, A.M.; Bochkarev, A.; Dhe-Paganon, S.; Structural Genomics Consortium (SGC)
Deposited on	:	2007-03-21
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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

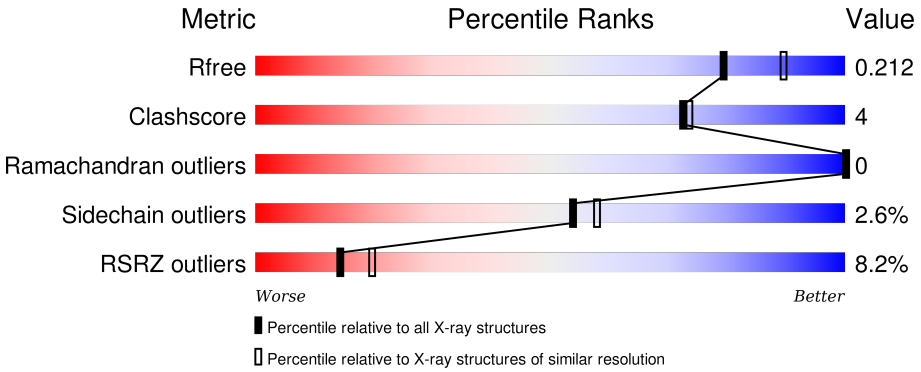
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance (i)

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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (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 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 <=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	355	9% 76% 10% • 12%
1	B	355	8% 76% 12% 12%
1	C	355	7% 80% 6% • 14%
1	D	355	5% 75% 9% 15%

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
3	EDO	B	3	-	-	-	X
3	EDO	C	361	-	-	-	X
3	EDO	C	362	-	-	-	X
3	EDO	D	361	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10944 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 Cysteine protease ATG4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	3	0
			2529	1625	428	452	24			
1	B	312	Total	C	N	O	S	0	3	0
			2524	1618	427	457	22			
1	C	307	Total	C	N	O	S	0	3	0
			2492	1600	423	448	21			
1	D	301	Total	C	N	O	S	0	3	0
			2437	1568	412	435	22			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	MET	-	CLONING ARTIFACT	UNP Q8WYN0
A	6	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
A	7	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
A	8	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
A	9	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
A	10	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
A	11	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
A	12	SER	-	CLONING ARTIFACT	UNP Q8WYN0
A	13	SER	-	CLONING ARTIFACT	UNP Q8WYN0
A	14	GLY	-	CLONING ARTIFACT	UNP Q8WYN0
A	15	ARG	-	CLONING ARTIFACT	UNP Q8WYN0
A	16	GLU	-	CLONING ARTIFACT	UNP Q8WYN0
A	17	ASN	-	CLONING ARTIFACT	UNP Q8WYN0
A	18	LEU	-	CLONING ARTIFACT	UNP Q8WYN0
A	19	TYR	-	CLONING ARTIFACT	UNP Q8WYN0
A	20	PHE	-	CLONING ARTIFACT	UNP Q8WYN0
A	21	GLN	-	CLONING ARTIFACT	UNP Q8WYN0
A	22	GLY	-	CLONING ARTIFACT	UNP Q8WYN0
B	5	MET	-	CLONING ARTIFACT	UNP Q8WYN0
B	6	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
B	7	HIS	-	CLONING ARTIFACT	UNP Q8WYN0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	8	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
B	9	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
B	10	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
B	11	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
B	12	SER	-	CLONING ARTIFACT	UNP Q8WYN0
B	13	SER	-	CLONING ARTIFACT	UNP Q8WYN0
B	14	GLY	-	CLONING ARTIFACT	UNP Q8WYN0
B	15	ARG	-	CLONING ARTIFACT	UNP Q8WYN0
B	16	GLU	-	CLONING ARTIFACT	UNP Q8WYN0
B	17	ASN	-	CLONING ARTIFACT	UNP Q8WYN0
B	18	LEU	-	CLONING ARTIFACT	UNP Q8WYN0
B	19	TYR	-	CLONING ARTIFACT	UNP Q8WYN0
B	20	PHE	-	CLONING ARTIFACT	UNP Q8WYN0
B	21	GLN	-	CLONING ARTIFACT	UNP Q8WYN0
B	22	GLY	-	CLONING ARTIFACT	UNP Q8WYN0
C	5	MET	-	CLONING ARTIFACT	UNP Q8WYN0
C	6	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
C	7	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
C	8	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
C	9	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
C	10	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
C	11	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
C	12	SER	-	CLONING ARTIFACT	UNP Q8WYN0
C	13	SER	-	CLONING ARTIFACT	UNP Q8WYN0
C	14	GLY	-	CLONING ARTIFACT	UNP Q8WYN0
C	15	ARG	-	CLONING ARTIFACT	UNP Q8WYN0
C	16	GLU	-	CLONING ARTIFACT	UNP Q8WYN0
C	17	ASN	-	CLONING ARTIFACT	UNP Q8WYN0
C	18	LEU	-	CLONING ARTIFACT	UNP Q8WYN0
C	19	TYR	-	CLONING ARTIFACT	UNP Q8WYN0
C	20	PHE	-	CLONING ARTIFACT	UNP Q8WYN0
C	21	GLN	-	CLONING ARTIFACT	UNP Q8WYN0
C	22	GLY	-	CLONING ARTIFACT	UNP Q8WYN0
D	5	MET	-	CLONING ARTIFACT	UNP Q8WYN0
D	6	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
D	7	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
D	8	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
D	9	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
D	10	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
D	11	HIS	-	CLONING ARTIFACT	UNP Q8WYN0
D	12	SER	-	CLONING ARTIFACT	UNP Q8WYN0
D	13	SER	-	CLONING ARTIFACT	UNP Q8WYN0

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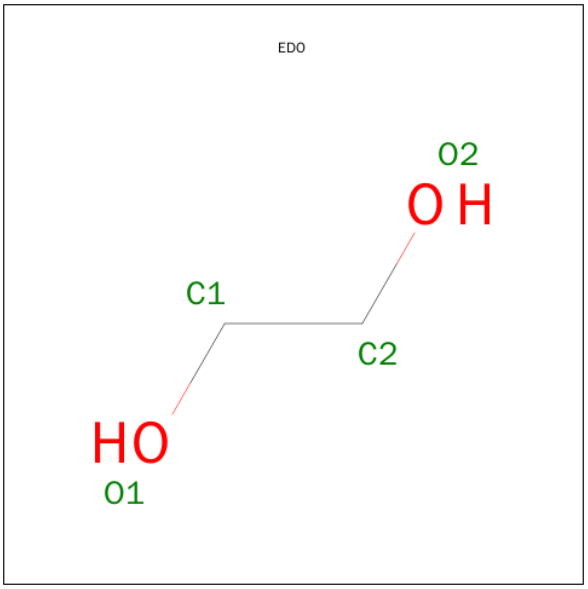
Chain	Residue	Modelled	Actual	Comment	Reference
D	14	GLY	-	CLONING ARTIFACT	UNP Q8WYN0
D	15	ARG	-	CLONING ARTIFACT	UNP Q8WYN0
D	16	GLU	-	CLONING ARTIFACT	UNP Q8WYN0
D	17	ASN	-	CLONING ARTIFACT	UNP Q8WYN0
D	18	LEU	-	CLONING ARTIFACT	UNP Q8WYN0
D	19	TYR	-	CLONING ARTIFACT	UNP Q8WYN0
D	20	PHE	-	CLONING ARTIFACT	UNP Q8WYN0
D	21	GLN	-	CLONING ARTIFACT	UNP Q8WYN0
D	22	GLY	-	CLONING ARTIFACT	UNP Q8WYN0

- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total Cl 1 1	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 4 is water.

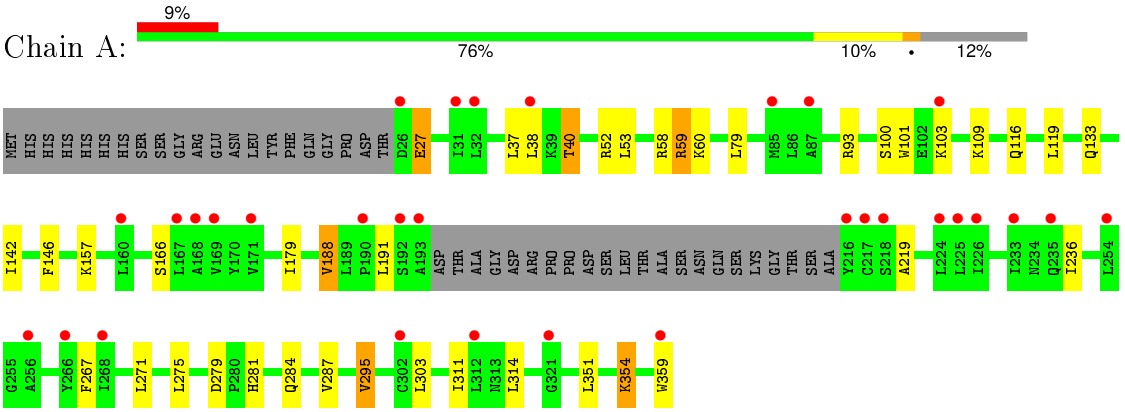
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	248	Total O 264 264	0	16
4	B	194	Total O 203 203	0	9
4	C	214	Total O 224 224	0	10
4	D	202	Total O 210 210	0	8

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.

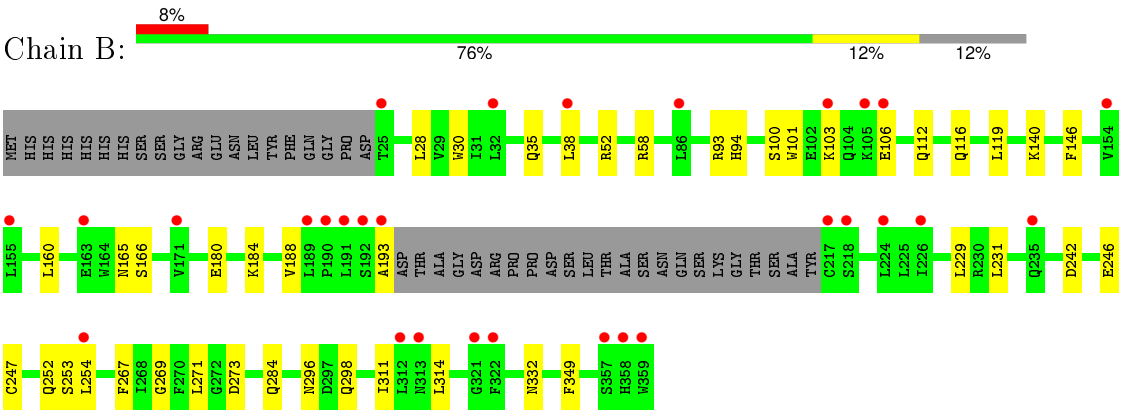
- Molecule 1: Cysteine protease ATG4A

Chain A:



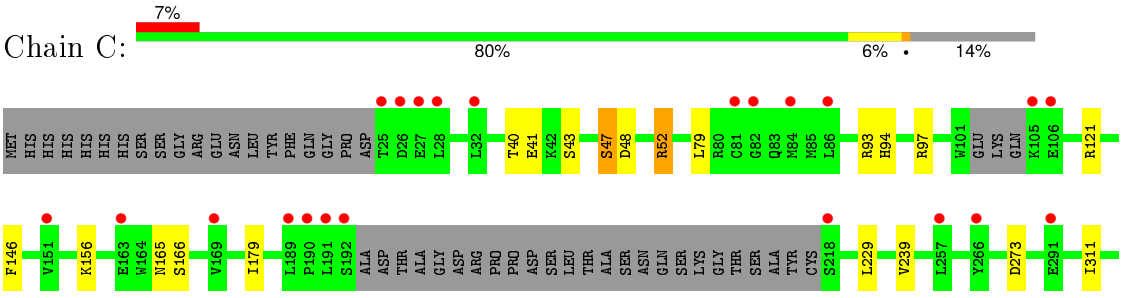
- Molecule 1: Cysteine protease ATG4A

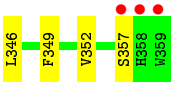
Chain B:



- Molecule 1: Cysteine protease ATG4A

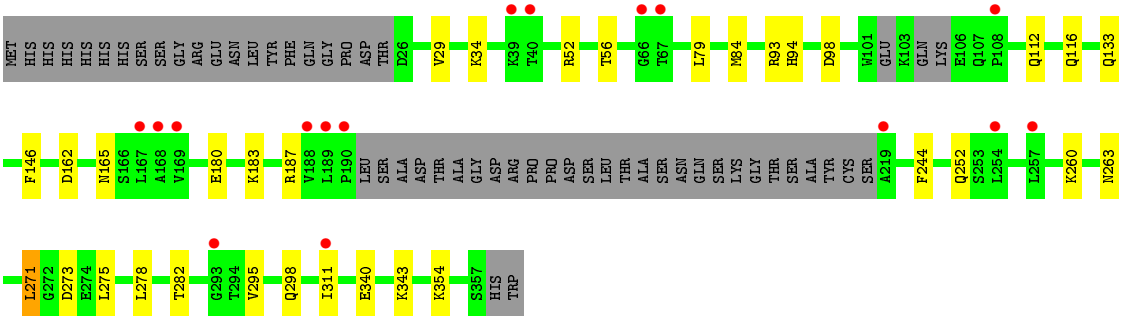
Chain C:





• Molecule 1: Cysteine protease ATG4A

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	94.41Å 94.41Å 337.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	38.69 – 2.10 38.68 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.2 (38.69-2.10) 95.2 (38.68-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$< I/\sigma(I) >$ [1]	3.13 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.175 , 0.213 0.175 , 0.212	Depositor DCC
R_{free} test set	4967 reflections (5.34%)	DCC
Wilson B-factor (Å^2)	35.7	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 59.0	EDS
Estimated twinning fraction	0.021 for -h,-k,l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 97969 reflections	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	10944	wwPDB-VP
Average B, all atoms (Å^2)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.94% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: EDO, CL

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	0.68	5/2593 (0.2%)	0.61	3/3505 (0.1%)
1	B	0.49	1/2586 (0.0%)	0.56	0/3496
1	C	0.53	1/2555 (0.0%)	0.57	0/3451
1	D	0.46	0/2494	0.58	0/3367
All	All	0.55	7/10228 (0.1%)	0.58	3/13819 (0.0%)

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	354	LYS	CG-CD	13.71	1.99	1.52
1	A	27	GLU	CD-OE1	13.19	1.40	1.25
1	A	27	GLU	CD-OE2	12.28	1.39	1.25
1	B	193	ALA	C-O	9.97	1.42	1.23
1	C	357	SER	CB-OG	9.81	1.55	1.42
1	A	354	LYS	CE-NZ	5.70	1.63	1.49
1	A	359	TRP	C-OXT	5.04	1.32	1.23

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	354	LYS	CG-CD-CE	-6.54	92.27	111.90
1	A	354	LYS	CB-CG-CD	-5.43	97.49	111.60
1	A	27	GLU	OE1-CD-OE2	5.42	129.81	123.30

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	2529	0	2487	27	0
1	B	2524	0	2484	22	0
1	C	2492	0	2464	11	0
1	D	2437	0	2419	23	0
2	D	1	0	0	0	0
3	A	16	0	24	0	0
3	B	12	0	18	1	0
3	C	16	0	24	3	0
3	D	16	0	24	2	0
4	A	264	0	0	1	0
4	B	203	0	0	2	0
4	C	224	0	0	1	0
4	D	210	0	0	2	0
All	All	10944	0	9944	83	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 (83) 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:354:LYS:CG	1:A:354:LYS:CD	1.99	1.39
1:A:179:ILE:HD11	1:A:351:LEU:HD11	1.51	0.90
1:A:354:LYS:CG	1:A:354:LYS:CE	2.57	0.82
1:D:260[B]:LYS:HG2	1:D:263:ASN:HB2	1.63	0.79
1:A:179:ILE:CD1	1:A:351:LEU:HD11	2.15	0.77
1:B:252:GLN:HE22	1:B:332[B]:ASN:HD22	1.32	0.75
1:A:236:ILE:HD11	1:A:314:LEU:HD23	1.68	0.73
1:D:84:MET:CE	1:D:278:LEU:HD13	2.19	0.73
1:A:354:LYS:CB	1:A:354:LYS:CD	2.70	0.70
1:D:84:MET:HE3	1:D:278:LEU:HD13	1.83	0.59
1:C:94:HIS:NE2	1:C:165:ASN:ND2	2.50	0.58
1:A:275:LEU:HG	1:A:311:ILE:HG12	1.86	0.57
1:C:97:ARG:HD3	3:C:360:EDO:H12	1.86	0.57
1:A:188:VAL:HG13	1:A:219:ALA:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:296:ASN:ND2	1:B:298:GLN:OE1	2.34	0.57
1:C:239:VAL:HG21	1:C:346:LEU:HD12	1.88	0.55
1:D:34:LYS:HE3	1:D:98:ASP:OD1	2.07	0.55
1:D:84:MET:CE	1:D:278:LEU:CD1	2.85	0.54
1:D:84:MET:HE1	1:D:278:LEU:CD1	2.37	0.54
1:B:267:PHE:CZ	1:B:314:LEU:HD13	2.42	0.54
1:A:133:GLN:HG3	4:A:525:HOH:O	2.07	0.54
1:A:287:VAL:HG12	1:A:295:VAL:HG22	1.90	0.53
1:D:273:ASP:O	1:D:311:ILE:HG13	2.08	0.53
1:B:100:SER:HB3	1:B:103:LYS:HE2	1.90	0.53
1:D:79:LEU:HD21	1:D:146:PHE:CZ	2.44	0.52
1:D:180:GLU:HG2	1:D:354:LYS:HA	1.91	0.52
1:A:267:PHE:CZ	1:A:314:LEU:CD1	2.93	0.51
1:A:38:LEU:HD22	1:A:271:LEU:HD21	1.92	0.51
1:D:29:VAL:HG22	1:D:271:LEU:HG	1.91	0.51
1:B:38:LEU:HD22	1:B:271:LEU:HD11	1.94	0.50
1:D:94:HIS:NE2	1:D:165:ASN:ND2	2.60	0.50
1:A:236:ILE:CD1	1:A:314:LEU:HD23	2.40	0.49
1:D:112:GLN:HG3	1:D:116:GLN:NE2	2.27	0.49
1:D:133:GLN:HG3	4:D:433:HOH:O	2.12	0.48
1:D:183:LYS:HB3	1:D:187:ARG:HD2	1.95	0.48
1:D:340:GLU:HA	1:D:343:LYS:HE3	1.94	0.48
1:A:27:GLU:HB2	1:A:271:LEU:HD11	1.95	0.48
1:C:48:ASP:O	1:C:52:ARG:HD2	2.13	0.47
1:D:56:THR:HB	1:D:282:THR:O	2.14	0.47
1:A:100:SER:HB3	1:A:103:LYS:HE2	1.97	0.47
1:B:140:LYS:HG2	1:B:146:PHE:CD2	2.49	0.47
1:B:58:ARG:HA	1:B:284:GLN:O	2.14	0.47
1:A:157:LYS:HD2	1:B:160:LEU:HD11	1.97	0.47
1:B:296:ASN:HB2	4:B:543:HOH:O	2.15	0.46
1:C:179:ILE:HG12	1:C:352:VAL:O	2.14	0.46
1:A:37:LEU:HB2	1:A:40:THR:HG23	1.96	0.46
1:B:229:LEU:HD21	1:B:349:PHE:HB3	1.96	0.46
1:B:332[A]:ASN:ND2	4:B:553:HOH:O	2.47	0.46
1:B:254:LEU:HD23	3:B:360:EDO:C2	2.46	0.46
1:C:273:ASP:O	1:C:311:ILE:HG13	2.15	0.46
1:D:275:LEU:HG	1:D:311:ILE:HG12	1.98	0.45
1:A:116:GLN:HA	1:A:119:LEU:HG	1.99	0.45
1:C:79:LEU:HD21	1:C:146:PHE:CZ	2.52	0.45
1:A:58:ARG:HA	1:A:284:GLN:O	2.17	0.45
1:A:133:GLN:NE2	1:A:142:ILE:HD11	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:279:ASP:OD1	1:A:281[B]:HIS:HD2	2.00	0.44
1:D:252:GLN:HG3	3:D:361:EDO:H11	1.99	0.44
1:D:112:GLN:HB2	4:D:564:HOH:O	2.18	0.44
1:B:112:GLN:HG3	1:B:116:GLN:NE2	2.33	0.44
1:A:59:ARG:NH2	1:A:60:LYS:HE2	2.32	0.44
1:D:112:GLN:OE1	1:D:295:VAL:HG12	2.18	0.43
1:C:229:LEU:HD21	1:C:349:PHE:HB3	2.00	0.43
1:D:162:ASP:OD2	1:D:165:ASN:HB2	2.18	0.43
1:A:37:LEU:CB	1:A:40:THR:HG23	2.47	0.43
1:C:156:LYS:HZ1	3:C:363:EDO:H22	1.83	0.43
1:D:84:MET:HE1	1:D:278:LEU:HD12	2.00	0.43
1:A:267:PHE:CZ	1:A:314:LEU:HD13	2.53	0.42
1:B:242:ASP:O	1:B:246:GLU:HG2	2.19	0.42
1:A:79:LEU:HD21	1:A:146:PHE:CZ	2.55	0.41
1:B:112:GLN:HG3	1:B:116:GLN:HE21	1.84	0.41
1:B:28:LEU:HD11	1:B:35:GLN:HB2	2.01	0.41
3:C:361:EDO:C2	4:C:462:HOH:O	2.69	0.41
1:A:354:LYS:NZ	1:A:354:LYS:CG	2.83	0.41
1:B:273:ASP:O	1:B:311:ILE:HG13	2.20	0.41
1:C:43:SER:O	1:C:47:SER:HB3	2.21	0.41
1:C:40:THR:HG22	1:C:41:GLU:HG3	2.02	0.41
1:B:94:HIS:NE2	1:B:165:ASN:ND2	2.69	0.41
1:B:30:TRP:O	1:B:269:GLY:HA3	2.20	0.41
1:B:247:CYS:O	1:B:253:SER:HB2	2.20	0.40
1:B:180:GLU:O	1:B:184:LYS:HG3	2.22	0.40
1:A:53:LEU:HA	1:A:53:LEU:HD23	1.94	0.40
1:B:116:GLN:HA	1:B:119:LEU:HG	2.04	0.40
1:D:252:GLN:HG3	3:D:361:EDO:C1	2.52	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	311/355 (88%)	308 (99%)	3 (1%)	0	100	100
1	B	311/355 (88%)	306 (98%)	5 (2%)	0	100	100
1	C	304/355 (86%)	300 (99%)	4 (1%)	0	100	100
1	D	297/355 (84%)	291 (98%)	6 (2%)	0	100	100
All	All	1223/1420 (86%)	1205 (98%)	18 (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	276/313 (88%)	265 (96%)	11 (4%)	38	38
1	B	277/313 (88%)	270 (98%)	7 (2%)	55	59
1	C	274/313 (88%)	269 (98%)	5 (2%)	66	72
1	D	267/313 (85%)	262 (98%)	5 (2%)	65	70
All	All	1094/1252 (87%)	1066 (97%)	28 (3%)	54	58

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	40	THR
1	A	52	ARG
1	A	59	ARG
1	A	93	ARG
1	A	101	TRP
1	A	109	LYS
1	A	166	SER
1	A	188	VAL
1	A	191	LEU
1	A	295	VAL
1	A	303	LEU
1	B	52	ARG
1	B	93	ARG

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Mol	Chain	Res	Type
1	B	101	TRP
1	B	106	GLU
1	B	166	SER
1	B	188	VAL
1	B	231	LEU
1	C	47	SER
1	C	52	ARG
1	C	93	ARG
1	C	121	ARG
1	C	166	SER
1	D	52	ARG
1	D	93	ARG
1	D	244	PHE
1	D	271	LEU
1	D	298	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	133	GLN
1	A	262	ASN
1	A	345	ASN
1	B	165	ASN
1	B	284	GLN
1	C	165	ASN
1	C	262	ASN
1	C	284	GLN
1	D	133	GLN
1	D	153	GLN
1	D	165	ASN
1	D	262	ASN
1	D	284	GLN

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 16 ligands modelled in this entry, 1 is monoatomic - leaving 15 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	EDO	A	2	-	3,3,3	0.45	0	2,2,2	0.61	0
3	EDO	A	360	-	3,3,3	0.46	0	2,2,2	0.54	0
3	EDO	A	361	-	3,3,3	0.42	0	2,2,2	0.63	0
3	EDO	A	362	-	3,3,3	0.56	0	2,2,2	0.29	0
3	EDO	B	3	-	3,3,3	0.48	0	2,2,2	0.59	0
3	EDO	B	360	-	3,3,3	0.33	0	2,2,2	0.60	0
3	EDO	B	361	-	3,3,3	0.50	0	2,2,2	0.48	0
3	EDO	C	360	-	3,3,3	0.55	0	2,2,2	0.34	0
3	EDO	C	361	-	3,3,3	0.42	0	2,2,2	0.52	0
3	EDO	C	362	-	3,3,3	0.37	0	2,2,2	0.79	0
3	EDO	C	363	-	3,3,3	0.63	0	2,2,2	0.29	0
3	EDO	D	360	-	3,3,3	0.40	0	2,2,2	0.48	0
3	EDO	D	361	-	3,3,3	0.43	0	2,2,2	0.55	0
3	EDO	D	362	-	3,3,3	0.50	0	2,2,2	0.37	0
3	EDO	D	4	-	3,3,3	0.42	0	2,2,2	0.67	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	EDO	A	2	-	-	0/1/1/1	0/0/0/0
3	EDO	A	360	-	-	0/1/1/1	0/0/0/0
3	EDO	A	361	-	-	0/1/1/1	0/0/0/0
3	EDO	A	362	-	-	0/1/1/1	0/0/0/0
3	EDO	B	3	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	360	-	-	0/1/1/1	0/0/0/0
3	EDO	B	361	-	-	0/1/1/1	0/0/0/0
3	EDO	C	360	-	-	0/1/1/1	0/0/0/0
3	EDO	C	361	-	-	0/1/1/1	0/0/0/0
3	EDO	C	362	-	-	0/1/1/1	0/0/0/0
3	EDO	C	363	-	-	0/1/1/1	0/0/0/0
3	EDO	D	360	-	-	0/1/1/1	0/0/0/0
3	EDO	D	361	-	-	0/1/1/1	0/0/0/0
3	EDO	D	362	-	-	0/1/1/1	0/0/0/0
3	EDO	D	4	-	-	0/1/1/1	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.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	360	EDO	1	0
3	C	360	EDO	1	0
3	C	361	EDO	1	0
3	C	363	EDO	1	0
3	D	361	EDO	2	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, 95^{th} 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	312/355 (87%)	0.37	31 (9%) 9 13	26, 35, 51, 62	0
1	B	312/355 (87%)	0.37	29 (9%) 11 15	30, 38, 62, 75	0
1	C	307/355 (86%)	0.29	25 (8%) 15 20	25, 34, 50, 67	0
1	D	301/355 (84%)	0.18	16 (5%) 30 39	23, 36, 53, 61	0
All	All	1232/1420 (86%)	0.30	101 (8%) 14 20	23, 36, 55, 75	0

All (101) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	216	TYR	7.8
1	C	25	THR	6.7
1	A	217	CYS	6.5
1	C	191	LEU	6.1
1	B	359	TRP	5.5
1	B	191	LEU	5.3
1	B	25	THR	5.3
1	C	192	SER	5.1
1	C	218	SER	5.0
1	B	193	ALA	4.9
1	C	26	ASP	4.7
1	C	190	PRO	4.5
1	A	32	LEU	4.4
1	A	167	LEU	4.4
1	C	359	TRP	4.4
1	B	105	LYS	4.3
1	B	192	SER	4.3
1	B	106	GLU	4.3
1	A	218	SER	4.3
1	B	217	CYS	4.1
1	C	357	SER	4.0

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Mol	Chain	Res	Type	RSRZ
1	B	103	LYS	4.0
1	D	189	LEU	3.9
1	A	26	ASP	3.9
1	D	67	THR	3.9
1	C	189	LEU	3.7
1	A	169	VAL	3.6
1	A	103	LYS	3.5
1	B	358	HIS	3.5
1	A	224	LEU	3.5
1	A	226	ILE	3.4
1	A	193	ALA	3.4
1	D	219	ALA	3.4
1	A	254	LEU	3.4
1	A	168	ALA	3.4
1	A	312	LEU	3.3
1	A	359	TRP	3.3
1	A	31	ILE	3.3
1	D	190	PRO	3.3
1	A	233	ILE	3.2
1	B	357	SER	3.1
1	C	106	GLU	3.1
1	C	169	VAL	3.1
1	B	226	ILE	3.1
1	D	169	VAL	3.0
1	B	32	LEU	2.9
1	C	27	GLU	2.9
1	B	224	LEU	2.9
1	C	358	HIS	2.8
1	C	105	LYS	2.8
1	A	190	PRO	2.8
1	A	302	CYS	2.7
1	B	171	VAL	2.7
1	C	82	GLY	2.7
1	B	254	LEU	2.6
1	C	266	TYR	2.6
1	B	218	SER	2.5
1	C	257	LEU	2.5
1	C	86	LEU	2.5
1	D	257	LEU	2.5
1	B	235	GLN	2.5
1	A	171	VAL	2.5
1	D	168	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	163	GLU	2.4
1	C	81	CYS	2.4
1	A	235	GLN	2.4
1	D	40	THR	2.4
1	B	312	LEU	2.4
1	C	84	MET	2.4
1	C	151	VAL	2.3
1	C	163	GLU	2.3
1	A	85	MET	2.3
1	A	160	LEU	2.3
1	B	322	PHE	2.3
1	A	192	SER	2.3
1	C	291	GLU	2.3
1	C	28	LEU	2.3
1	B	321	GLY	2.2
1	D	66	GLY	2.2
1	D	108	PRO	2.2
1	A	321	GLY	2.2
1	B	155	LEU	2.2
1	A	38	LEU	2.2
1	B	189	LEU	2.2
1	A	256	ALA	2.2
1	C	32	LEU	2.2
1	A	266	TYR	2.1
1	A	87	ALA	2.1
1	D	311	ILE	2.1
1	D	254	LEU	2.1
1	B	190	PRO	2.1
1	D	188	VAL	2.1
1	A	268	ILE	2.1
1	A	225	LEU	2.1
1	D	167	LEU	2.1
1	B	38	LEU	2.1
1	B	86	LEU	2.1
1	D	39	LYS	2.1
1	B	313	ASN	2.0
1	D	293	GLY	2.0
1	B	154	VAL	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, 95^{th} 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
3	EDO	D	361	4/4	0.94	0.32	8.63	51,56,57,59	0
3	EDO	B	3	4/4	0.96	0.23	4.52	55,59,60,62	0
3	EDO	C	362	4/4	0.94	0.25	4.06	57,57,58,59	0
3	EDO	C	361	4/4	0.92	0.17	3.01	48,56,56,58	0
3	EDO	A	362	4/4	0.92	0.15	0.76	53,53,55,57	0
3	EDO	D	4	4/4	0.96	0.10	0.52	53,55,56,59	0
3	EDO	B	361	4/4	0.83	0.16	0.45	54,58,60,63	0
3	EDO	A	361	4/4	0.93	0.17	0.32	39,40,42,44	0
3	EDO	A	2	4/4	0.93	0.12	0.13	67,69,70,72	0
3	EDO	C	363	4/4	0.87	0.15	-0.17	50,54,55,55	0
3	EDO	D	362	4/4	0.93	0.10	-0.65	54,60,61,64	0
3	EDO	C	360	4/4	0.94	0.10	-0.66	40,44,45,45	0
3	EDO	B	360	4/4	0.97	0.11	-0.98	46,49,49,50	0
3	EDO	A	360	4/4	0.92	0.11	-1.07	40,40,41,42	0
3	EDO	D	360	4/4	0.97	0.07	-1.12	41,44,46,46	0
2	CL	D	1	1/1	0.94	0.23	-	67,67,67,67	1

6.5 Other polymers (i)

There are no such residues in this entry.