Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 07:50 AM GMT

PDB ID	:	3C8V
Title	:	Crystal structure of putative acetyltransferase (YP_390128.1) from Desulfovibrio desulfuricans G20 at 2.28 A resolution
Authors	:	Joint Center for Structural Genomics (JCSG)
Deposited on	:	2008-02-13
Resolution	:	2.28 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 (i) symbol.

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

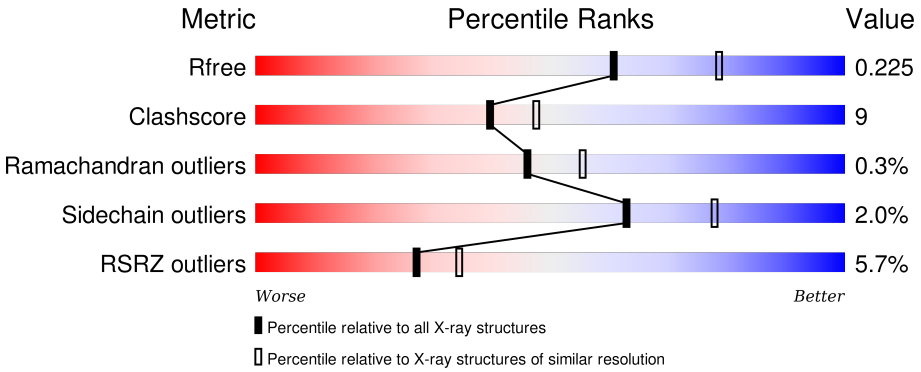
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	5193 (2.30-2.26)
Clashscore	102246	5929 (2.30-2.26)
Ramachandran outliers	100387	5851 (2.30-2.26)
Sidechain outliers	100360	5850 (2.30-2.26)
RSRZ outliers	91569	5204 (2.30-2.26)

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	496	2% 76% 15% 9%
1	B	496	4% 77% 15% • 7%
1	C	496	9% 75% 18% • 6%
1	D	496	5% 74% 19% 6%

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
2	CL	C	479	-	-	-	X
4	EDO	A	481	-	-	-	X
4	EDO	A	483	-	-	-	X
4	EDO	A	485	-	-	-	X
4	EDO	A	486	-	-	-	X
4	EDO	A	489	-	-	-	X
4	EDO	A	490	-	-	-	X
4	EDO	B	485	-	-	-	X
4	EDO	B	486	-	-	-	X
4	EDO	B	487	-	-	-	X
4	EDO	C	481	-	-	-	X
4	EDO	C	482	-	-	-	X
4	EDO	D	482	-	-	-	X
4	EDO	D	484	-	-	-	X
4	EDO	D	486	-	-	-	X
4	EDO	D	487	-	-	-	X
4	EDO	D	490	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 14949 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 Putative acetyltransferase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	453	Total	C	N	O	S	Se	0	2	0
			3533	2249	606	662	6	10			
1	B	461	Total	C	N	O	S	Se	0	1	0
			3594	2281	615	683	5	10			
1	C	465	Total	C	N	O	S	Se	0	1	0
			3567	2269	611	672	5	10			
1	D	464	Total	C	N	O	S	Se	0	1	0
			3590	2287	616	671	6	10			

There are 76 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-18	MSE	-	LEADER SEQUENCE	UNP Q30V63
A	-17	GLY	-	LEADER SEQUENCE	UNP Q30V63
A	-16	SER	-	LEADER SEQUENCE	UNP Q30V63
A	-15	ASP	-	LEADER SEQUENCE	UNP Q30V63
A	-14	LYS	-	LEADER SEQUENCE	UNP Q30V63
A	-13	ILE	-	LEADER SEQUENCE	UNP Q30V63
A	-12	HIS	-	LEADER SEQUENCE	UNP Q30V63
A	-11	HIS	-	LEADER SEQUENCE	UNP Q30V63
A	-10	HIS	-	LEADER SEQUENCE	UNP Q30V63
A	-9	HIS	-	LEADER SEQUENCE	UNP Q30V63
A	-8	HIS	-	LEADER SEQUENCE	UNP Q30V63
A	-7	HIS	-	LEADER SEQUENCE	UNP Q30V63
A	-6	GLU	-	LEADER SEQUENCE	UNP Q30V63
A	-5	ASN	-	LEADER SEQUENCE	UNP Q30V63
A	-4	LEU	-	LEADER SEQUENCE	UNP Q30V63
A	-3	TYR	-	LEADER SEQUENCE	UNP Q30V63
A	-2	PHE	-	LEADER SEQUENCE	UNP Q30V63
A	-1	GLN	-	LEADER SEQUENCE	UNP Q30V63
A	0	GLY	-	LEADER SEQUENCE	UNP Q30V63
B	-18	MSE	-	LEADER SEQUENCE	UNP Q30V63
B	-17	GLY	-	LEADER SEQUENCE	UNP Q30V63

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-16	SER	-	LEADER SEQUENCE	UNP Q30V63
B	-15	ASP	-	LEADER SEQUENCE	UNP Q30V63
B	-14	LYS	-	LEADER SEQUENCE	UNP Q30V63
B	-13	ILE	-	LEADER SEQUENCE	UNP Q30V63
B	-12	HIS	-	LEADER SEQUENCE	UNP Q30V63
B	-11	HIS	-	LEADER SEQUENCE	UNP Q30V63
B	-10	HIS	-	LEADER SEQUENCE	UNP Q30V63
B	-9	HIS	-	LEADER SEQUENCE	UNP Q30V63
B	-8	HIS	-	LEADER SEQUENCE	UNP Q30V63
B	-7	HIS	-	LEADER SEQUENCE	UNP Q30V63
B	-6	GLU	-	LEADER SEQUENCE	UNP Q30V63
B	-5	ASN	-	LEADER SEQUENCE	UNP Q30V63
B	-4	LEU	-	LEADER SEQUENCE	UNP Q30V63
B	-3	TYR	-	LEADER SEQUENCE	UNP Q30V63
B	-2	PHE	-	LEADER SEQUENCE	UNP Q30V63
B	-1	GLN	-	LEADER SEQUENCE	UNP Q30V63
B	0	GLY	-	LEADER SEQUENCE	UNP Q30V63
C	-18	MSE	-	LEADER SEQUENCE	UNP Q30V63
C	-17	GLY	-	LEADER SEQUENCE	UNP Q30V63
C	-16	SER	-	LEADER SEQUENCE	UNP Q30V63
C	-15	ASP	-	LEADER SEQUENCE	UNP Q30V63
C	-14	LYS	-	LEADER SEQUENCE	UNP Q30V63
C	-13	ILE	-	LEADER SEQUENCE	UNP Q30V63
C	-12	HIS	-	LEADER SEQUENCE	UNP Q30V63
C	-11	HIS	-	LEADER SEQUENCE	UNP Q30V63
C	-10	HIS	-	LEADER SEQUENCE	UNP Q30V63
C	-9	HIS	-	LEADER SEQUENCE	UNP Q30V63
C	-8	HIS	-	LEADER SEQUENCE	UNP Q30V63
C	-7	HIS	-	LEADER SEQUENCE	UNP Q30V63
C	-6	GLU	-	LEADER SEQUENCE	UNP Q30V63
C	-5	ASN	-	LEADER SEQUENCE	UNP Q30V63
C	-4	LEU	-	LEADER SEQUENCE	UNP Q30V63
C	-3	TYR	-	LEADER SEQUENCE	UNP Q30V63
C	-2	PHE	-	LEADER SEQUENCE	UNP Q30V63
C	-1	GLN	-	LEADER SEQUENCE	UNP Q30V63
C	0	GLY	-	LEADER SEQUENCE	UNP Q30V63
D	-18	MSE	-	LEADER SEQUENCE	UNP Q30V63
D	-17	GLY	-	LEADER SEQUENCE	UNP Q30V63
D	-16	SER	-	LEADER SEQUENCE	UNP Q30V63
D	-15	ASP	-	LEADER SEQUENCE	UNP Q30V63
D	-14	LYS	-	LEADER SEQUENCE	UNP Q30V63
D	-13	ILE	-	LEADER SEQUENCE	UNP Q30V63

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-12	HIS	-	LEADER SEQUENCE	UNP Q30V63
D	-11	HIS	-	LEADER SEQUENCE	UNP Q30V63
D	-10	HIS	-	LEADER SEQUENCE	UNP Q30V63
D	-9	HIS	-	LEADER SEQUENCE	UNP Q30V63
D	-8	HIS	-	LEADER SEQUENCE	UNP Q30V63
D	-7	HIS	-	LEADER SEQUENCE	UNP Q30V63
D	-6	GLU	-	LEADER SEQUENCE	UNP Q30V63
D	-5	ASN	-	LEADER SEQUENCE	UNP Q30V63
D	-4	LEU	-	LEADER SEQUENCE	UNP Q30V63
D	-3	TYR	-	LEADER SEQUENCE	UNP Q30V63
D	-2	PHE	-	LEADER SEQUENCE	UNP Q30V63
D	-1	GLN	-	LEADER SEQUENCE	UNP Q30V63
D	0	GLY	-	LEADER SEQUENCE	UNP Q30V63

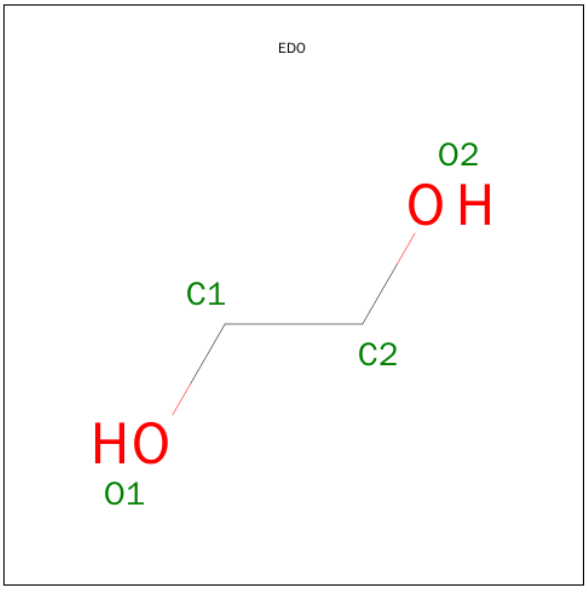
- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

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

- Molecule 5 is water.

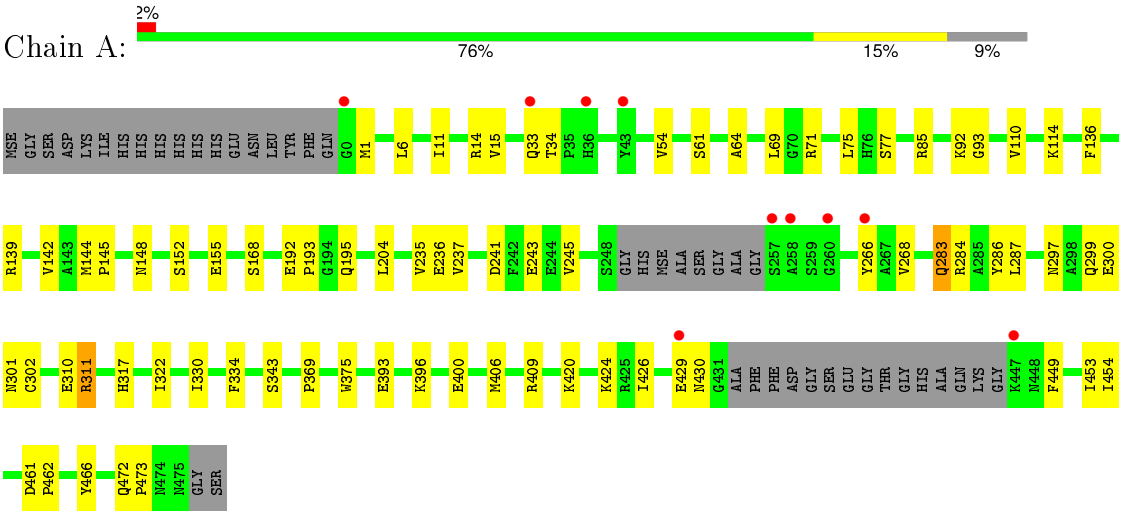
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	183	Total O 183 183	0	0
5	B	132	Total O 132 132	0	0
5	C	93	Total O 93 93	0	0
5	D	132	Total O 132 132	0	0

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.

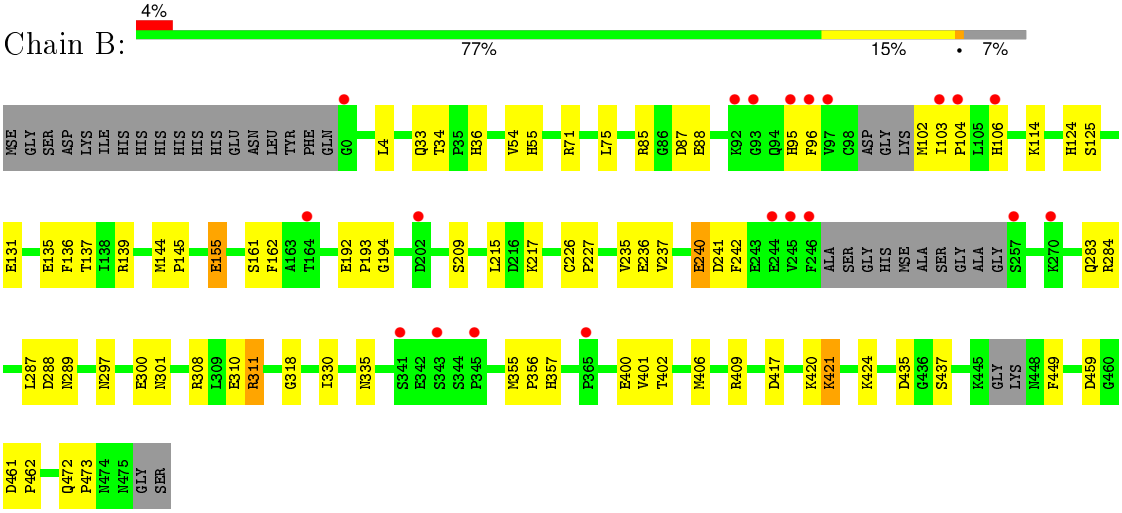
- Molecule 1: Putative acetyltransferase

Chain A:



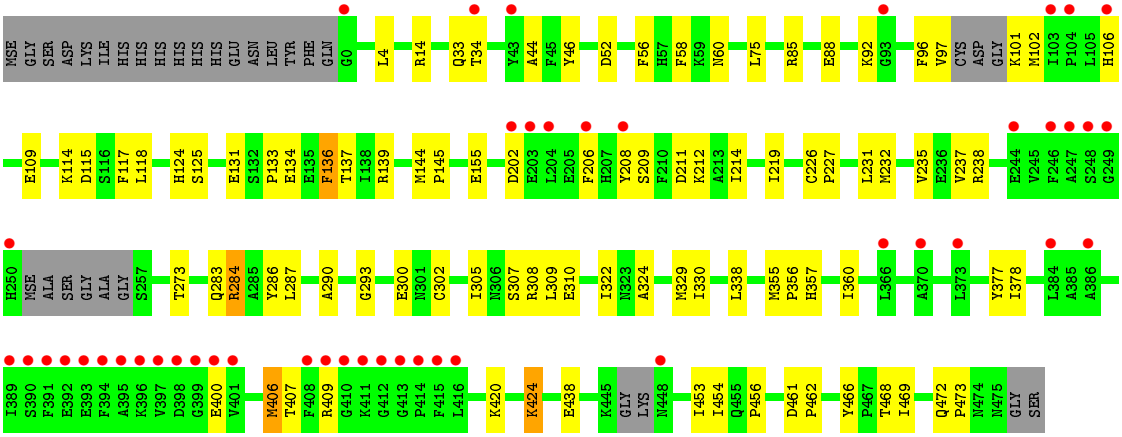
- Molecule 1: Putative acetyltransferase

Chain B:



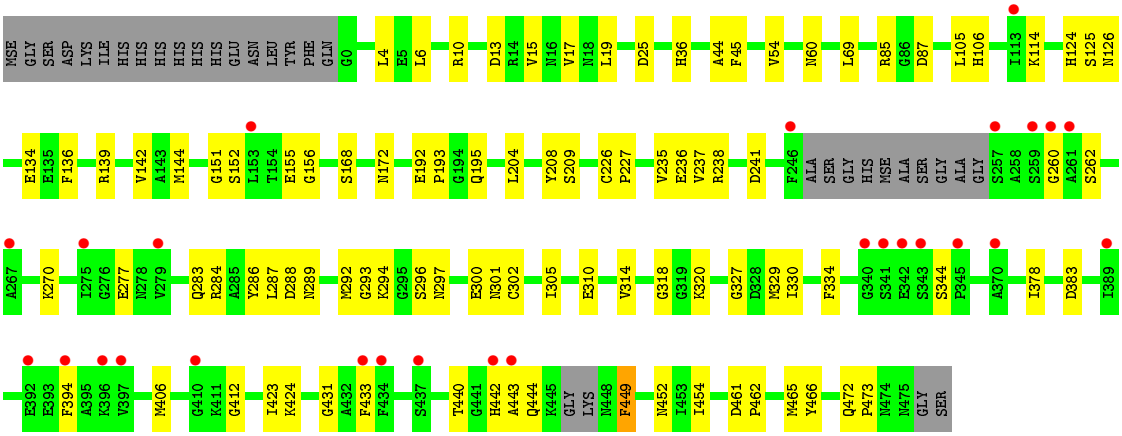
- Molecule 1: Putative acetyltransferase

Chain C:



- Molecule 1: Putative acetyltransferase

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α, β, γ	249.62Å 249.62Å 104.90Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.06 – 2.28 48.04 – 2.28	Depositor EDS
% Data completeness (in resolution range)	95.1 (48.06-2.28) 95.1 (48.04-2.28)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.05 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.4.0067	Depositor
R, R_{free}	0.180 , 0.223 0.185 , 0.225	Depositor DCC
R_{free} test set	5271 reflections (5.28%)	DCC
Wilson B-factor (Å^2)	40.0	Xtriage
Anisotropy	0.263	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 52.1	EDS
Estimated twinning fraction	0.015 for h,-h-k,-l	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Outliers	0 of 105055 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	14949	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% 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: MG, 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	0/3609	0.82	1/4865 (0.0%)
1	B	0.60	0/3670	0.80	0/4947
1	C	0.52	0/3640	0.80	0/4910
1	D	0.60	0/3667	0.81	2/4945 (0.0%)
All	All	0.60	0/14586	0.81	3/19667 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	D	25	ASP	CB-CG-OD1	5.40	123.16	118.30
1	A	14	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	D	449	PHE	CB-CG-CD1	5.16	124.41	120.80

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3533	0	3415	56	0
1	B	3594	0	3437	56	0
1	C	3567	0	3400	71	0
1	D	3590	0	3435	65	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	3	0	0	0	0
2	B	3	0	0	0	0
2	C	2	0	0	0	0
2	D	4	0	0	0	0
3	C	1	0	0	0	0
4	A	40	0	60	3	0
4	B	28	0	42	0	0
4	C	8	0	12	0	0
4	D	36	0	54	3	0
5	A	183	0	0	3	0
5	B	132	0	0	2	0
5	C	93	0	0	3	0
5	D	132	0	0	1	0
All	All	14949	0	13855	249	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 9.

All (249) 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)
5:A:564:HOH:O	4:D:490:EDO:H11	1.59	1.01
1:B:240:GLU:HG3	1:B:241:ASP:N	1.75	0.99
1:B:283:GLN:O	1:B:300:GLU:HG2	1.61	0.98
1:B:85:ARG:NH1	1:B:87:ASP:OD2	2.00	0.95
1:B:310:GLU:O	1:B:311:ARG:HB2	1.71	0.89
1:C:238:ARG:HG3	1:C:238:ARG:HH11	1.40	0.84
1:D:85:ARG:CZ	1:D:300:GLU:HG2	2.11	0.81
1:B:240:GLU:CG	1:B:241:ASP:N	2.48	0.75
1:C:284:ARG:HH11	1:C:284:ARG:HG3	1.53	0.71
1:C:92:LYS:HG3	1:C:106:HIS:O	1.91	0.71
1:D:237:VAL:CG1	1:D:237:VAL:O	2.41	0.69
1:C:238:ARG:HG3	1:C:238:ARG:NH1	2.07	0.68
1:A:449:PHE:CD1	1:A:449:PHE:C	2.66	0.68
1:A:472:GLN:HB2	1:A:473:PRO:HD2	1.76	0.68
1:C:44:ALA:HB3	1:C:454:ILE:HG22	1.76	0.67
1:C:472:GLN:HB2	1:C:473:PRO:CD	2.25	0.67
1:B:85:ARG:HH21	1:B:300:GLU:HG3	1.59	0.66
1:A:472:GLN:HB2	1:A:473:PRO:CD	2.25	0.66
1:D:286:TYR:C	1:D:287:LEU:HD23	2.16	0.65
1:A:1:MSE:HE3	1:A:6:LEU:HD13	1.78	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:472:GLN:HB2	1:B:473:PRO:CD	2.26	0.64
1:A:139:ARG:O	1:A:155:GLU:HA	1.96	0.64
1:B:472:GLN:HB2	1:B:473:PRO:HD2	1.79	0.64
1:D:237:VAL:HG12	1:D:237:VAL:O	1.96	0.64
1:D:283:GLN:O	1:D:284:ARG:HB2	1.96	0.63
1:B:237:VAL:O	1:B:237:VAL:CG1	2.47	0.62
1:D:472:GLN:HB2	1:D:473:PRO:CD	2.30	0.62
1:D:54:VAL:O	1:D:473:PRO:HD3	2.00	0.62
1:D:85:ARG:NH2	1:D:300:GLU:HG2	2.15	0.61
1:B:85:ARG:NH2	1:B:300:GLU:HG3	2.15	0.61
1:C:85:ARG:CZ	1:C:300:GLU:HG2	2.30	0.61
1:C:226:CYS:HB2	1:C:227:PRO:CD	2.29	0.61
1:D:260:GLY:O	1:D:444:GLN:NE2	2.32	0.61
1:D:238:ARG:HH21	1:D:305:ILE:HD13	1.66	0.60
1:D:235:VAL:HG23	1:D:236:GLU:N	2.17	0.60
1:B:237:VAL:HG12	1:B:237:VAL:O	2.01	0.60
1:C:329:MSE:HE1	1:C:424:LYS:HZ3	1.67	0.60
1:D:262:SER:HB2	1:D:443:ALA:O	2.02	0.60
1:D:472:GLN:HB2	1:D:473:PRO:HD2	1.83	0.59
1:D:431:GLY:C	1:D:433:PHE:H	2.04	0.59
1:B:435:ASP:OD1	1:B:437:SER:N	2.36	0.59
1:C:226:CYS:HB2	1:C:227:PRO:HD2	1.85	0.58
1:A:237:VAL:CG1	1:A:237:VAL:O	2.51	0.58
1:C:284:ARG:NH1	1:C:284:ARG:HG3	2.19	0.58
1:A:426:ILE:HD11	4:A:490:EDO:H11	1.84	0.58
1:B:400:GLU:HG2	1:B:409:ARG:HG3	1.84	0.58
1:D:454:ILE:HG23	1:D:466:TYR:CE2	2.38	0.58
1:A:237:VAL:HG12	1:A:237:VAL:O	2.03	0.58
1:C:139:ARG:O	1:C:155:GLU:HA	2.04	0.57
1:C:44:ALA:HB3	1:C:454:ILE:CG2	2.33	0.57
1:D:330:ILE:N	1:D:330:ILE:HD12	2.19	0.57
1:A:69:LEU:HD11	1:A:449:PHE:CE2	2.40	0.56
1:D:204:LEU:HD23	1:D:204:LEU:C	2.25	0.56
1:C:202:ASP:O	1:C:409:ARG:NH2	2.36	0.56
1:C:400:GLU:HG2	1:C:409:ARG:HG3	1.87	0.56
1:D:287:LEU:HD23	1:D:287:LEU:N	2.20	0.56
1:D:13:ASP:O	1:D:17[B]:VAL:HG22	2.06	0.55
1:B:144:MSE:HB3	1:B:145:PRO:HD2	1.88	0.55
1:D:105:LEU:HG	1:D:134:GLU:HG3	1.89	0.55
1:B:4:LEU:HD23	1:B:36:HIS:HA	1.88	0.55
1:A:54:VAL:O	1:A:473:PRO:HD3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:242:PHE:CE1	1:B:284:ARG:HA	2.42	0.54
1:C:101:LYS:C	1:C:102:MSE:HG3	2.26	0.54
1:C:338:LEU:HD22	1:C:360:ILE:HD12	1.89	0.54
1:C:237:VAL:CG1	1:C:237:VAL:O	2.56	0.54
1:A:310:GLU:O	1:A:311:ARG:HB2	2.08	0.54
1:D:44:ALA:HB3	1:D:454:ILE:HG22	1.88	0.54
1:D:292:MSE:HE3	1:D:296:SER:HB3	1.89	0.54
1:C:308:ARG:HD3	1:C:310:GLU:OE2	2.09	0.53
1:D:156:GLY:O	1:D:172:ASN:HA	2.08	0.53
1:C:238:ARG:HD3	1:C:286:TYR:CZ	2.44	0.53
1:B:144:MSE:HB3	1:B:145:PRO:CD	2.39	0.53
1:B:308:ARG:HD3	1:B:310:GLU:OE2	2.09	0.52
1:B:288:ASP:O	1:B:289:ASN:HB2	2.10	0.52
1:B:96:PHE:CZ	1:B:103:ILE:CB	2.93	0.52
1:D:235:VAL:CG2	1:D:236:GLU:N	2.73	0.52
1:A:461:ASP:N	1:A:462:PRO:CD	2.73	0.52
1:D:423:ILE:HG23	1:D:424:LYS:N	2.25	0.51
1:A:1:MSE:CE	1:A:6:LEU:HD13	2.39	0.51
1:C:438:GLU:CA	5:C:549:HOH:O	2.58	0.51
1:D:139:ARG:O	1:D:155:GLU:HA	2.09	0.51
1:C:284:ARG:HH11	1:C:284:ARG:CG	2.21	0.51
1:C:453:ILE:CG2	1:C:454:ILE:N	2.74	0.50
1:A:400:GLU:HG2	1:A:409:ARG:HG3	1.94	0.50
1:B:283:GLN:O	1:B:284:ARG:HB2	2.11	0.50
1:A:85:ARG:CZ	1:A:300:GLU:HG2	2.41	0.50
1:C:237:VAL:HG12	1:C:237:VAL:O	2.10	0.50
1:C:293:GLY:HA3	1:C:310:GLU:O	2.10	0.50
1:A:142:VAL:CG1	1:A:144:MSE:HE3	2.42	0.50
1:A:11:ILE:O	1:A:15:VAL:HG23	2.11	0.50
1:D:69:LEU:HD21	1:D:87:ASP:HB3	1.92	0.50
1:D:114:LYS:HD3	4:D:490:EDO:H21	1.94	0.50
1:D:241:ASP:OD2	1:D:270:LYS:NZ	2.45	0.50
1:A:322:ILE:HD12	1:A:322:ILE:N	2.27	0.49
1:B:96:PHE:CE1	1:B:103:ILE:CB	2.95	0.49
1:D:461:ASP:N	1:D:462:PRO:CD	2.75	0.49
1:B:300:GLU:O	1:B:301:ASN:HB2	2.12	0.49
1:A:449:PHE:C	1:A:449:PHE:HD1	2.14	0.48
1:C:14:ARG:NH1	1:C:115:ASP:OD2	2.46	0.48
1:C:137[A]:THR:CG2	1:C:139:ARG:HD3	2.44	0.48
1:D:310:GLU:HB2	1:D:327:GLY:O	2.13	0.48
1:A:144:MSE:HB3	1:A:145:PRO:CD	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:322:ILE:HD12	1:C:322:ILE:N	2.28	0.48
1:A:61:SER:HB3	1:A:77:SER:O	2.12	0.48
1:C:211:ASP:OD2	1:C:214:ILE:HG13	2.12	0.48
1:B:75:LEU:O	1:B:114:LYS:HA	2.14	0.48
1:B:54:VAL:O	1:B:473:PRO:HD3	2.14	0.48
1:C:85:ARG:NH2	1:C:300:GLU:HG2	2.27	0.48
1:A:235:VAL:HG23	1:A:236:GLU:N	2.29	0.48
1:D:300:GLU:O	1:D:301:ASN:HB2	2.12	0.48
1:A:192:GLU:HB3	1:A:193:PRO:CD	2.43	0.48
1:A:148:ASN:HB3	5:A:565:HOH:O	2.13	0.47
1:A:454:ILE:HG23	1:A:466:TYR:CE2	2.49	0.47
1:C:137[A]:THR:HG21	1:C:139:ARG:HD3	1.94	0.47
1:C:355:MSE:HB3	1:C:356:PRO:HD2	1.96	0.47
1:C:85:ARG:NH1	1:C:283:GLN:OE1	2.47	0.47
1:C:453:ILE:HG22	1:C:454:ILE:N	2.28	0.47
1:C:117:PHE:O	1:C:118:LEU:HD23	2.14	0.47
1:C:88:GLU:OE2	1:C:124:HIS:CE1	2.68	0.47
1:B:139:ARG:O	1:B:155:GLU:HA	2.15	0.47
1:A:375:TRP:CH2	1:A:406:MSE:HE3	2.49	0.47
1:B:161:SER:O	1:B:162:PHE:HB2	2.15	0.47
1:A:33:GLN:O	1:A:34:THR:C	2.53	0.47
1:C:472:GLN:HB2	1:C:473:PRO:HD2	1.96	0.47
1:C:286:TYR:C	1:C:287:LEU:HD23	2.35	0.47
1:C:356:PRO:O	1:C:357:HIS:HB2	2.15	0.47
1:C:330:ILE:HD12	1:C:330:ILE:N	2.30	0.46
1:D:394:PHE:O	1:D:412:GLY:HA3	2.15	0.46
1:B:417:ASP:O	1:B:421:LYS:HB2	2.15	0.46
1:D:262:SER:CB	1:D:443:ALA:O	2.63	0.46
1:B:461:ASP:HB3	1:B:462:PRO:HD3	1.97	0.46
1:C:461:ASP:N	1:C:462:PRO:CD	2.79	0.46
1:B:355:MSE:HB3	1:B:356:PRO:HD2	1.97	0.46
1:D:4:LEU:HD23	1:D:36:HIS:HA	1.97	0.46
1:C:208:TYR:CG	1:C:209:SER:N	2.83	0.46
1:A:204:LEU:C	1:A:204:LEU:HD23	2.36	0.46
1:B:209:SER:HB3	5:B:577:HOH:O	2.16	0.46
1:A:92:LYS:HG2	1:A:93:GLY:N	2.30	0.46
1:B:88:GLU:OE1	1:B:125:SER:HA	2.16	0.45
1:C:456:PRO:HB3	1:C:466:TYR:CE1	2.51	0.45
1:C:101:LYS:O	1:C:102:MSE:HG3	2.17	0.45
1:B:124:HIS:CD2	1:B:125:SER:H	2.35	0.45
1:D:288:ASP:O	1:D:289:ASN:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:318:GLY:HA3	1:B:335:ASN:OD1	2.17	0.45
1:B:449:PHE:C	1:B:449:PHE:CD1	2.89	0.45
1:B:194:GLY:HA3	1:B:215:LEU:HD22	1.98	0.45
1:D:6:LEU:O	1:D:10:ARG:HG2	2.17	0.45
1:D:152:SER:HB3	1:D:168:SER:O	2.17	0.45
1:C:96:PHE:CB	5:C:541:HOH:O	2.65	0.45
1:D:431:GLY:C	1:D:433:PHE:N	2.69	0.45
1:A:300:GLU:HB2	1:A:317:HIS:CE1	2.51	0.45
1:C:124:HIS:CG	1:C:125:SER:H	2.33	0.45
1:A:241:ASP:O	1:A:245:VAL:HG23	2.17	0.45
1:D:106:HIS:ND1	4:D:488:EDO:H12	2.32	0.45
1:D:292:MSE:HE3	1:D:296:SER:CB	2.47	0.44
1:A:85:ARG:NE	1:A:300:GLU:HG2	2.32	0.44
1:B:114:LYS:O	1:B:139:ARG:HA	2.16	0.44
1:A:393:GLU:OE1	1:A:396:LYS:NZ	2.39	0.44
1:C:454:ILE:HG23	1:C:466:TYR:CE2	2.52	0.44
1:D:15:VAL:HG21	1:D:142:VAL:HG23	1.99	0.44
1:C:307:SER:HB3	1:C:324:ALA:O	2.18	0.44
1:A:461:ASP:N	1:A:462:PRO:HD2	2.32	0.44
1:B:461:ASP:N	1:B:462:PRO:HD2	2.32	0.44
1:A:152:SER:HB3	1:A:168:SER:O	2.17	0.44
1:C:4:LEU:HD12	1:C:4:LEU:O	2.18	0.44
1:C:109:GLU:HA	1:C:134:GLU:O	2.17	0.44
1:C:232:MSE:O	1:C:235:VAL:HG22	2.18	0.44
1:C:420:LYS:O	1:C:424:LYS:HB2	2.18	0.44
1:D:208:TYR:CG	1:D:209:SER:N	2.86	0.44
1:C:284:ARG:HD2	1:C:284:ARG:HA	1.80	0.44
1:A:75:LEU:O	1:A:114:LYS:HA	2.18	0.44
1:B:135:GLU:HG2	1:B:137:THR:HG23	1.99	0.44
1:C:206:PHE:CE2	1:C:406:MSE:HE2	2.53	0.43
1:D:124:HIS:CG	1:D:125:SER:H	2.36	0.43
1:D:318:GLY:O	1:D:320:LYS:NZ	2.44	0.43
1:B:330:ILE:N	1:B:330:ILE:HD12	2.32	0.43
1:C:231:LEU:HD23	1:C:231:LEU:HA	1.83	0.43
1:D:114:LYS:O	1:D:139:ARG:HA	2.17	0.43
1:A:204:LEU:HD12	5:A:606:HOH:O	2.18	0.43
1:C:33:GLN:O	1:C:34:THR:C	2.56	0.43
1:B:85:ARG:NE	1:B:300:GLU:OE2	2.51	0.43
1:D:192:GLU:O	1:D:195:GLN:HG2	2.19	0.43
1:B:226:CYS:HB2	1:B:227:PRO:HD2	2.01	0.43
1:D:126:ASN:O	1:D:151:GLY:HA2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:69:LEU:HD11	1:A:449:PHE:CZ	2.54	0.43
1:A:426:ILE:HD11	4:A:490:EDO:C1	2.47	0.43
1:A:286:TYR:C	1:A:287:LEU:HD23	2.39	0.43
1:D:330:ILE:N	1:D:330:ILE:CD1	2.82	0.42
1:D:192:GLU:HB3	1:D:193:PRO:CD	2.49	0.42
1:C:273:THR:HG23	1:C:290:ALA:O	2.19	0.42
1:B:235:VAL:HG23	1:B:236:GLU:N	2.35	0.42
1:A:144:MSE:HB3	1:A:145:PRO:HD2	2.00	0.42
1:A:192:GLU:O	1:A:195:GLN:HG2	2.19	0.42
1:D:297:ASN:HB3	1:D:314:VAL:HG22	2.00	0.42
1:A:299:GLN:O	1:A:300:GLU:C	2.58	0.42
1:A:454:ILE:HG23	1:A:466:TYR:HE2	1.85	0.42
1:A:420:LYS:O	1:A:424:LYS:HB2	2.19	0.42
1:A:71:ARG:HB3	1:A:110:VAL:HG12	2.01	0.42
1:B:297:ASN:ND2	1:B:297:ASN:C	2.72	0.42
1:D:293:GLY:HA3	1:D:310:GLU:O	2.20	0.42
1:B:33:GLN:O	1:B:34:THR:C	2.57	0.42
1:A:330:ILE:HD12	1:A:330:ILE:N	2.35	0.42
1:A:283:GLN:O	1:A:284:ARG:HB2	2.19	0.42
1:C:454:ILE:HD11	1:C:469:ILE:HD13	2.01	0.42
1:A:245:VAL:HG12	1:A:245:VAL:O	2.18	0.42
1:B:217:LYS:NZ	5:B:617:HOH:O	2.52	0.42
1:D:378:ILE:HA	1:D:383:ASP:HB3	2.02	0.42
1:D:442:HIS:C	1:D:444:GLN:H	2.23	0.41
1:B:401:VAL:HG12	1:B:402:THR:N	2.35	0.41
1:B:95:HIS:HB3	1:B:102:MSE:HG3	2.01	0.41
1:D:226:CYS:HB2	1:D:227:PRO:CD	2.49	0.41
1:A:266:TYR:HB2	1:A:283:GLN:HB3	2.01	0.41
1:C:136:PHE:C	1:C:136:PHE:CD1	2.93	0.41
1:A:297:ASN:OD1	1:A:297:ASN:C	2.59	0.41
1:C:75:LEU:O	1:C:114:LYS:HA	2.20	0.41
1:D:454:ILE:HG23	1:D:466:TYR:HE2	1.84	0.41
1:B:435:ASP:C	1:B:435:ASP:OD1	2.58	0.41
1:A:426:ILE:O	1:A:430:ASN:CB	2.69	0.41
1:B:356:PRO:O	1:B:357:HIS:HB2	2.20	0.41
1:D:440:THR:HG22	1:D:440:THR:O	2.20	0.41
1:B:420:LYS:O	1:B:424:LYS:HB2	2.20	0.41
1:C:97:VAL:HG22	1:C:102:MSE:HG2	2.02	0.41
1:B:104:PRO:HG2	1:B:106:HIS:CE1	2.55	0.41
1:C:226:CYS:CB	1:C:227:PRO:CD	2.96	0.41
1:C:46:TYR:HB2	1:C:56:PHE:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:45:PHE:HA	1:D:452:ASN:O	2.21	0.41
1:B:192:GLU:HB3	1:B:193:PRO:CD	2.51	0.41
1:A:334:PHE:CZ	4:A:490:EDO:H21	2.56	0.41
1:C:308:ARG:C	1:C:309:LEU:HD12	2.41	0.41
1:C:117:PHE:C	1:C:118:LEU:HD23	2.42	0.41
1:D:277:GLU:O	1:D:294:LYS:HA	2.21	0.41
1:C:144:MSE:HB3	1:C:145:PRO:CD	2.51	0.41
1:D:284:ARG:NH2	5:D:613:HOH:O	2.53	0.40
1:C:58:PHE:O	1:C:468:THR:HA	2.21	0.40
1:B:55:HIS:HB3	1:B:71:ARG:HG2	2.02	0.40
1:D:423:ILE:CG2	1:D:424:LYS:N	2.83	0.40
1:A:300:GLU:O	1:A:301:ASN:HB2	2.21	0.40
1:D:461:ASP:N	1:D:462:PRO:HD2	2.35	0.40
1:A:453:ILE:HG22	1:A:454:ILE:N	2.36	0.40
1:B:355:MSE:HE2	1:B:355:MSE:HB3	1.99	0.40
1:A:245:VAL:HG21	1:A:268:VAL:HG22	2.02	0.40
1:D:142:VAL:CG1	1:D:144:MSE:HE3	2.51	0.40
1:C:305:ILE:C	1:C:307:SER:N	2.73	0.40
1:D:465:MSE:HB3	1:D:465:MSE:HE3	2.00	0.40
1:C:377:TYR:C	1:C:378:ILE:HG13	2.42	0.40
1:C:206:PHE:C	1:C:206:PHE:CD1	2.95	0.40
1:B:287:LEU:N	1:B:287:LEU:HD23	2.37	0.40
1:D:19:LEU:HD23	1:D:19:LEU:HA	1.88	0.40
1:C:133:PRO:HD2	5:C:503:HOH:O	2.20	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	449/496 (90%)	433 (96%)	13 (3%)	3 (1%)	26 30

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	454/496 (92%)	436 (96%)	17 (4%)	1 (0%)	52 63
1	C	458/496 (92%)	437 (95%)	20 (4%)	1 (0%)	52 63
1	D	459/496 (92%)	440 (96%)	18 (4%)	1 (0%)	52 63
All	All	1820/1984 (92%)	1746 (96%)	68 (4%)	6 (0%)	46 55

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	311	ARG
1	A	311	ARG
1	A	429	GLU
1	C	219	ILE
1	A	64	ALA
1	D	334	PHE

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	376/408 (92%)	370 (98%)	6 (2%)	70 83
1	B	382/408 (94%)	375 (98%)	7 (2%)	66 80
1	C	372/408 (91%)	362 (97%)	10 (3%)	52 68
1	D	377/408 (92%)	370 (98%)	7 (2%)	65 79
All	All	1507/1632 (92%)	1477 (98%)	30 (2%)	63 78

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	136	PHE
1	A	243	GLU
1	A	283	GLN
1	A	302	CYS
1	A	343	SER

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Mol	Chain	Res	Type
1	A	369	PRO
1	B	131	GLU
1	B	136	PHE
1	B	155	GLU
1	B	240	GLU
1	B	406	MSE
1	B	421	LYS
1	B	459	ASP
1	C	52	ASP
1	C	60	ASN
1	C	131	GLU
1	C	136	PHE
1	C	212	LYS
1	C	284	ARG
1	C	302	CYS
1	C	406	MSE
1	C	407	THR
1	C	424	LYS
1	D	60	ASN
1	D	136	PHE
1	D	302	CYS
1	D	329	MSE
1	D	344	SER
1	D	406	MSE
1	D	449	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	475	ASN
1	B	106	HIS
1	C	22	GLN
1	D	458	GLN

5.3.3 RNA

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 41 ligands modelled in this entry, 13 are monoatomic - leaving 28 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	EDO	A	481	-	3,3,3	0.59	0	2,2,2	0.23	0
4	EDO	A	482	-	3,3,3	0.47	0	2,2,2	0.29	0
4	EDO	A	483	-	3,3,3	0.55	0	2,2,2	0.05	0
4	EDO	A	484	-	3,3,3	0.52	0	2,2,2	0.65	0
4	EDO	A	485	-	3,3,3	0.58	0	2,2,2	0.25	0
4	EDO	A	486	-	3,3,3	0.55	0	2,2,2	0.27	0
4	EDO	A	487	-	3,3,3	0.68	0	2,2,2	0.37	0
4	EDO	A	488	-	3,3,3	0.41	0	2,2,2	0.62	0
4	EDO	A	489	-	3,3,3	0.42	0	2,2,2	0.47	0
4	EDO	A	490	-	3,3,3	0.49	0	2,2,2	0.22	0
4	EDO	B	481	-	3,3,3	0.51	0	2,2,2	0.29	0
4	EDO	B	482	-	3,3,3	0.84	0	2,2,2	0.22	0
4	EDO	B	483	-	3,3,3	0.50	0	2,2,2	0.22	0
4	EDO	B	484	-	3,3,3	0.47	0	2,2,2	0.48	0
4	EDO	B	485	-	3,3,3	0.52	0	2,2,2	0.31	0
4	EDO	B	486	-	3,3,3	0.48	0	2,2,2	0.38	0
4	EDO	B	487	-	3,3,3	0.56	0	2,2,2	0.28	0
4	EDO	C	481	-	3,3,3	0.47	0	2,2,2	0.24	0
4	EDO	C	482	-	3,3,3	0.52	0	2,2,2	0.41	0
4	EDO	D	482	-	3,3,3	0.64	0	2,2,2	0.08	0
4	EDO	D	483	-	3,3,3	0.53	0	2,2,2	0.35	0
4	EDO	D	484	-	3,3,3	0.66	0	2,2,2	0.04	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
4	EDO	D	485	-	3,3,3	0.57	0	2,2,2	0.29	0
4	EDO	D	486	-	3,3,3	0.55	0	2,2,2	0.12	0
4	EDO	D	487	-	3,3,3	0.46	0	2,2,2	0.41	0
4	EDO	D	488	-	3,3,3	0.56	0	2,2,2	0.44	0
4	EDO	D	489	-	3,3,3	0.52	0	2,2,2	0.14	0
4	EDO	D	490	-	3,3,3	0.53	0	2,2,2	0.34	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
4	EDO	A	481	-	-	0/1/1/1	0/0/0/0
4	EDO	A	482	-	-	0/1/1/1	0/0/0/0
4	EDO	A	483	-	-	0/1/1/1	0/0/0/0
4	EDO	A	484	-	-	0/1/1/1	0/0/0/0
4	EDO	A	485	-	-	0/1/1/1	0/0/0/0
4	EDO	A	486	-	-	0/1/1/1	0/0/0/0
4	EDO	A	487	-	-	0/1/1/1	0/0/0/0
4	EDO	A	488	-	-	0/1/1/1	0/0/0/0
4	EDO	A	489	-	-	0/1/1/1	0/0/0/0
4	EDO	A	490	-	-	0/1/1/1	0/0/0/0
4	EDO	B	481	-	-	0/1/1/1	0/0/0/0
4	EDO	B	482	-	-	0/1/1/1	0/0/0/0
4	EDO	B	483	-	-	0/1/1/1	0/0/0/0
4	EDO	B	484	-	-	0/1/1/1	0/0/0/0
4	EDO	B	485	-	-	0/1/1/1	0/0/0/0
4	EDO	B	486	-	-	0/1/1/1	0/0/0/0
4	EDO	B	487	-	-	0/1/1/1	0/0/0/0
4	EDO	C	481	-	-	0/1/1/1	0/0/0/0
4	EDO	C	482	-	-	0/1/1/1	0/0/0/0
4	EDO	D	482	-	-	0/1/1/1	0/0/0/0
4	EDO	D	483	-	-	0/1/1/1	0/0/0/0
4	EDO	D	484	-	-	0/1/1/1	0/0/0/0
4	EDO	D	485	-	-	0/1/1/1	0/0/0/0
4	EDO	D	486	-	-	0/1/1/1	0/0/0/0
4	EDO	D	487	-	-	0/1/1/1	0/0/0/0
4	EDO	D	488	-	-	0/1/1/1	0/0/0/0
4	EDO	D	489	-	-	0/1/1/1	0/0/0/0
4	EDO	D	490	-	-	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.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	490	EDO	3	0
4	D	488	EDO	1	0
4	D	490	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	443/496 (89%)	0.14	10 (2%) 64 71	36, 46, 68, 94	0
1	B	451/496 (90%)	0.34	20 (4%) 38 46	34, 47, 68, 91	0
1	C	455/496 (91%)	0.47	46 (10%) 9 12	34, 47, 66, 96	0
1	D	454/496 (91%)	0.41	27 (5%) 26 33	36, 47, 74, 94	0
All	All	1803/1984 (90%)	0.34	103 (5%) 27 34	34, 47, 69, 96	0

All (103) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	257	SER	9.8
1	A	257	SER	7.1
1	B	257	SER	7.1
1	C	104	PRO	5.6
1	C	248	SER	5.1
1	C	391	PHE	5.0
1	B	97	VAL	4.8
1	C	412	GLY	4.8
1	C	249	GLY	4.5
1	B	96	PHE	4.5
1	C	247	ALA	4.4
1	C	394	PHE	4.3
1	C	448	ASN	4.3
1	B	245	VAL	4.2
1	C	250	HIS	4.1
1	C	373	LEU	4.0
1	C	401	VAL	4.0
1	C	399	GLY	4.0
1	C	43	TYR	4.0
1	A	447	LYS	4.0
1	C	413	GLY	4.0

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Mol	Chain	Res	Type	RSRZ
1	C	202	ASP	3.9
1	C	396	LYS	3.9
1	C	370	ALA	3.9
1	D	394	PHE	3.9
1	D	261	ALA	3.9
1	C	411	LYS	3.8
1	D	246	PHE	3.7
1	A	260	GLY	3.7
1	D	259	SER	3.6
1	C	103	ILE	3.6
1	D	443	ALA	3.5
1	B	93	GLY	3.5
1	C	414	PRO	3.4
1	C	389	ILE	3.4
1	A	258	ALA	3.4
1	D	260	GLY	3.4
1	B	95	HIS	3.1
1	B	104	PRO	3.1
1	A	36	HIS	3.1
1	A	266	TYR	3.1
1	D	397	VAL	3.1
1	C	410	GLY	3.0
1	A	0	GLY	3.0
1	C	366	LEU	3.0
1	D	341	SER	3.0
1	C	397	VAL	3.0
1	B	341	SER	3.0
1	B	246	PHE	2.9
1	D	279	VAL	2.9
1	D	442	HIS	2.9
1	C	395	ALA	2.9
1	C	416	LEU	2.9
1	C	409	ARG	2.8
1	C	204	LEU	2.8
1	C	392	GLU	2.8
1	D	392	GLU	2.8
1	D	340	GLY	2.8
1	D	389	ILE	2.8
1	B	103	ILE	2.7
1	D	267	ALA	2.7
1	A	33	GLN	2.7
1	D	343	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	34	THR	2.6
1	C	398	ASP	2.6
1	A	429	GLU	2.6
1	A	43	TYR	2.6
1	D	410	GLY	2.6
1	B	202	ASP	2.5
1	B	92	LYS	2.5
1	B	106	HIS	2.5
1	C	244	GLU	2.5
1	B	244	GLU	2.4
1	C	246	PHE	2.4
1	C	386	ALA	2.4
1	C	93	GLY	2.4
1	C	408	PHE	2.3
1	C	106	HIS	2.3
1	D	275	ILE	2.3
1	C	390	SER	2.3
1	D	437	SER	2.3
1	D	345	PRO	2.3
1	C	0	GLY	2.3
1	D	433	PHE	2.3
1	D	434	PHE	2.3
1	B	343	SER	2.2
1	D	342	GLU	2.2
1	C	384	LEU	2.2
1	D	396	LYS	2.2
1	B	365	PRO	2.2
1	D	113	ILE	2.2
1	C	203	GLU	2.2
1	D	370	ALA	2.2
1	C	393	GLU	2.1
1	B	0	GLY	2.1
1	C	400	GLU	2.1
1	C	206	PHE	2.1
1	D	153	LEU	2.1
1	B	164	THR	2.1
1	B	345	PRO	2.1
1	B	270	LYS	2.1
1	C	415	PHE	2.0
1	C	208	TYR	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
4	EDO	C	481	4/4	0.94	0.40	18.79	49,50,51,51	0
4	EDO	A	486	4/4	0.88	0.31	12.71	65,67,72,73	0
2	CL	C	479	1/1	0.67	0.25	11.50	94,94,94,94	0
4	EDO	B	486	4/4	0.85	0.56	10.91	80,82,87,87	0
4	EDO	D	482	4/4	0.81	0.22	9.79	50,51,53,61	0
4	EDO	A	485	4/4	0.96	0.27	8.57	45,56,59,61	0
4	EDO	A	490	4/4	0.90	0.20	7.80	55,58,59,63	0
4	EDO	D	487	4/4	0.89	0.36	6.78	77,78,79,79	0
4	EDO	A	481	4/4	0.88	0.23	5.09	66,74,75,77	0
4	EDO	C	482	4/4	0.95	0.24	4.88	58,59,61,61	0
4	EDO	B	485	4/4	0.83	0.24	4.44	64,65,67,68	0
4	EDO	A	483	4/4	0.94	0.22	4.12	40,43,44,49	0
4	EDO	A	489	4/4	0.89	0.21	3.98	66,71,72,72	0
4	EDO	B	487	4/4	0.92	0.17	3.36	65,71,74,78	0
4	EDO	D	490	4/4	0.90	0.24	2.94	37,46,49,55	0
4	EDO	D	484	4/4	0.84	0.23	2.44	71,76,76,77	0
4	EDO	D	486	4/4	0.95	0.27	2.24	52,54,54,55	0
4	EDO	B	481	4/4	0.92	0.18	1.86	44,46,46,49	0
4	EDO	D	485	4/4	0.93	0.15	1.62	60,60,63,64	0
4	EDO	A	487	4/4	0.91	0.18	1.50	58,58,60,62	0
4	EDO	D	488	4/4	0.89	0.18	1.46	47,52,52,54	0
4	EDO	A	484	4/4	0.97	0.17	1.03	33,34,42,44	0
4	EDO	B	482	4/4	0.88	0.16	0.26	45,51,52,58	0
4	EDO	D	489	4/4	0.92	0.15	-0.30	68,69,69,73	0
3	MG	C	480	1/1	0.97	0.10	-1.16	44,44,44,44	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
4	EDO	B	484	4/4	0.95	0.11	-1.32	58,58,58,62	0
4	EDO	A	488	4/4	0.95	0.11	-2.15	42,46,50,51	0
2	CL	A	478	1/1	0.96	0.11	-2.25	71,71,71,71	0
2	CL	D	478	1/1	0.91	0.08	-2.38	61,61,61,61	0
4	EDO	A	482	4/4	0.96	0.10	-2.62	43,45,46,54	0
2	CL	B	478	1/1	0.98	0.06	-2.86	43,43,43,43	0
2	CL	B	479	1/1	0.93	0.11	-2.95	67,67,67,67	0
4	EDO	D	483	4/4	0.97	0.07	-3.26	44,49,51,56	0
4	EDO	B	483	4/4	0.97	0.07	-3.91	41,47,51,56	0
2	CL	C	478	1/1	0.93	0.06	-3.98	76,76,76,76	0
2	CL	D	481	1/1	0.93	0.07	-4.01	72,72,72,72	0
2	CL	D	479	1/1	0.98	0.06	-4.13	40,40,40,40	0
2	CL	A	479	1/1	1.00	0.05	-4.16	33,33,33,33	0
2	CL	D	480	1/1	0.97	0.07	-4.17	59,59,59,59	0
2	CL	A	480	1/1	0.94	0.07	-4.20	67,67,67,67	0
2	CL	B	480	1/1	0.89	0.06	-	74,74,74,74	0

6.5 Other polymers (i)

There are no such residues in this entry.