



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:24 PM GMT

PDB ID : 4I5D
Title : Crystal structure of Ralstonia sp. alcohol dehydrogenase in its apo form
Authors : Jarasch, A.; Lerchner, A.; Meining, W.; Schiefner, A.; Skerra, A.
Deposited on : 2012-11-28
Resolution : 2.40 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

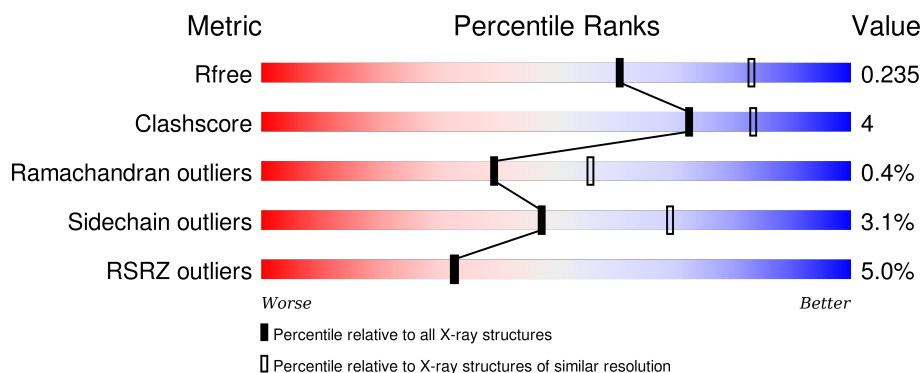
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	262	<div> <div>3%</div> <div>80% 7% • 11%</div> </div>
1	B	262	<div> <div>8%</div> <div>80% 9% 11%</div> </div>
1	C	262	<div> <div>4%</div> <div>79% 10% 11%</div> </div>
1	D	262	<div> <div>5%</div> <div>79% 9% • 11%</div> </div>
1	E	262	<div> <div>3%</div> <div>80% 8% • 11%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	262	<div><div></div><div>5%</div><div></div><div>80%</div><div></div><div>9%</div><div></div><div>11%</div></div>
1	G	262	<div><div></div><div>3%</div><div></div><div>80%</div><div></div><div>8%</div><div></div><div>11%</div></div>
1	H	262	<div><div></div><div>5%</div><div></div><div>79%</div><div></div><div>9%</div><div></div><div>11%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14524 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 Alcohol dehydrogenase/short-chain dehydrogenase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	H	233	Total	C	N	O	0	0	0
			1752	1104	314	334			
1	A	233	Total	C	N	O	0	0	0
			1752	1104	314	334			
1	B	233	Total	C	N	O	0	0	0
			1752	1104	314	334			
1	C	233	Total	C	N	O	0	0	0
			1752	1104	314	334			
1	D	233	Total	C	N	O	0	0	0
			1752	1104	314	334			
1	E	233	Total	C	N	O	0	0	0
			1752	1104	314	334			
1	F	233	Total	C	N	O	0	0	0
			1752	1104	314	334			
1	G	233	Total	C	N	O	0	0	0
			1752	1104	314	334			

There are 112 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-12	MET	-	EXPRESSION TAG	UNP C0IR58
H	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
H	-10	SER	-	EXPRESSION TAG	UNP C0IR58
H	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
H	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
H	-7	SER	-	EXPRESSION TAG	UNP C0IR58
H	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
H	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
H	0	GLY	-	EXPRESSION TAG	UNP C0IR58

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Chain	Residue	Modelled	Actual	Comment	Reference
H	1	ALA	-	EXPRESSION TAG	UNP C0IR58
A	-12	MET	-	EXPRESSION TAG	UNP C0IR58
A	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
A	-10	SER	-	EXPRESSION TAG	UNP C0IR58
A	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
A	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
A	-7	SER	-	EXPRESSION TAG	UNP C0IR58
A	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
A	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
A	0	GLY	-	EXPRESSION TAG	UNP C0IR58
A	1	ALA	-	EXPRESSION TAG	UNP C0IR58
B	-12	MET	-	EXPRESSION TAG	UNP C0IR58
B	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
B	-10	SER	-	EXPRESSION TAG	UNP C0IR58
B	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
B	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
B	-7	SER	-	EXPRESSION TAG	UNP C0IR58
B	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
B	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
B	0	GLY	-	EXPRESSION TAG	UNP C0IR58
B	1	ALA	-	EXPRESSION TAG	UNP C0IR58
C	-12	MET	-	EXPRESSION TAG	UNP C0IR58
C	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
C	-10	SER	-	EXPRESSION TAG	UNP C0IR58
C	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
C	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
C	-7	SER	-	EXPRESSION TAG	UNP C0IR58
C	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
C	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
C	0	GLY	-	EXPRESSION TAG	UNP C0IR58

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1	ALA	-	EXPRESSION TAG	UNP C0IR58
D	-12	MET	-	EXPRESSION TAG	UNP C0IR58
D	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
D	-10	SER	-	EXPRESSION TAG	UNP C0IR58
D	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
D	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
D	-7	SER	-	EXPRESSION TAG	UNP C0IR58
D	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
D	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
D	0	GLY	-	EXPRESSION TAG	UNP C0IR58
D	1	ALA	-	EXPRESSION TAG	UNP C0IR58
E	-12	MET	-	EXPRESSION TAG	UNP C0IR58
E	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
E	-10	SER	-	EXPRESSION TAG	UNP C0IR58
E	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
E	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
E	-7	SER	-	EXPRESSION TAG	UNP C0IR58
E	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
E	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
E	0	GLY	-	EXPRESSION TAG	UNP C0IR58
E	1	ALA	-	EXPRESSION TAG	UNP C0IR58
F	-12	MET	-	EXPRESSION TAG	UNP C0IR58
F	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
F	-10	SER	-	EXPRESSION TAG	UNP C0IR58
F	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
F	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
F	-7	SER	-	EXPRESSION TAG	UNP C0IR58
F	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
F	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
F	0	GLY	-	EXPRESSION TAG	UNP C0IR58

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Chain	Residue	Modelled	Actual	Comment	Reference
F	1	ALA	-	EXPRESSION TAG	UNP C0IR58
G	-12	MET	-	EXPRESSION TAG	UNP C0IR58
G	-11	ALA	-	EXPRESSION TAG	UNP C0IR58
G	-10	SER	-	EXPRESSION TAG	UNP C0IR58
G	-9	ARG	-	EXPRESSION TAG	UNP C0IR58
G	-8	GLY	-	EXPRESSION TAG	UNP C0IR58
G	-7	SER	-	EXPRESSION TAG	UNP C0IR58
G	-6	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-5	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-4	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-3	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-2	HIS	-	EXPRESSION TAG	UNP C0IR58
G	-1	HIS	-	EXPRESSION TAG	UNP C0IR58
G	0	GLY	-	EXPRESSION TAG	UNP C0IR58
G	1	ALA	-	EXPRESSION TAG	UNP C0IR58

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	G	1	Total	O	S	0	0
			5	4	1		
2	H	1	Total	O	S	0	0
			5	4	1		

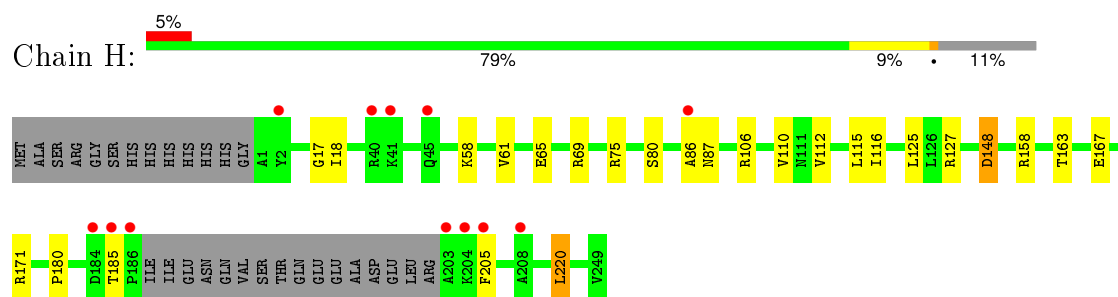
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	64	Total	O	0	0
			64	64		
3	B	43	Total	O	0	0
			43	43		
3	C	37	Total	O	0	0
			37	37		
3	D	80	Total	O	0	0
			80	80		
3	E	65	Total	O	0	0
			65	65		
3	F	52	Total	O	0	0
			52	52		
3	G	57	Total	O	0	0
			57	57		
3	H	70	Total	O	0	0
			70	70		

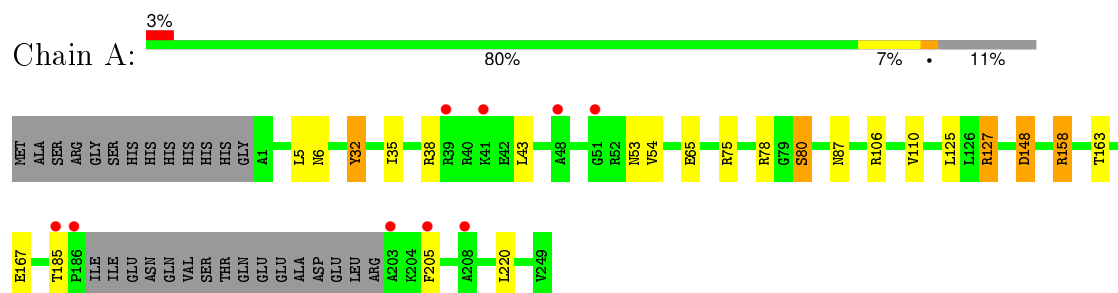
3 Residue-property plots [i](#)

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.

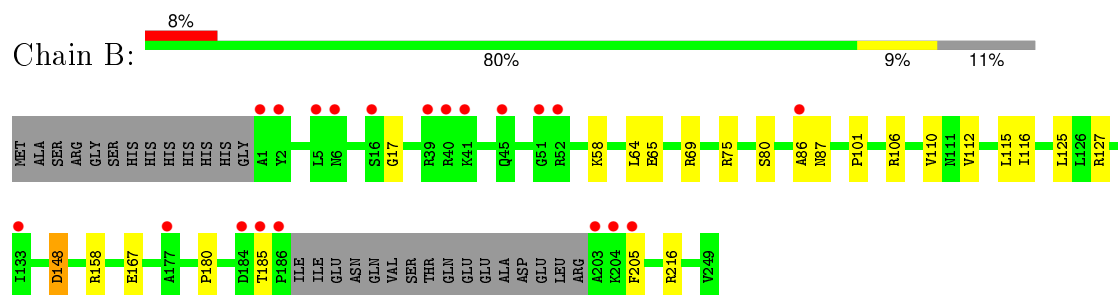
- Molecule 1: Alccohol dehydrogenase/short-chain dehydrogenase



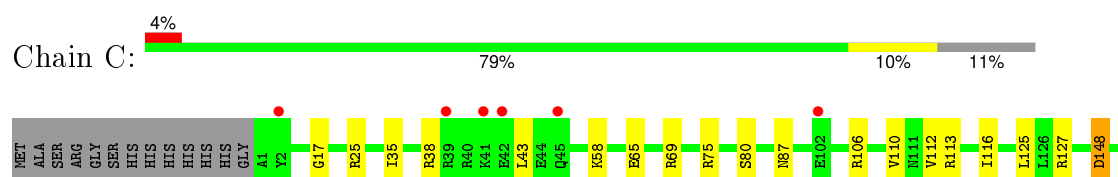
- Molecule 1: Alccohol dehydrogenase/short-chain dehydrogenase

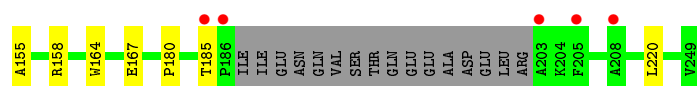


- Molecule 1: Alccohol dehydrogenase/short-chain dehydrogenase

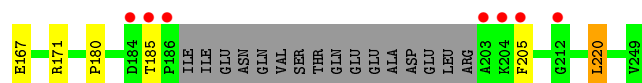
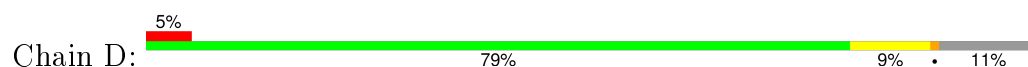


- Molecule 1: Alccohol dehydrogenase/short-chain dehydrogenase

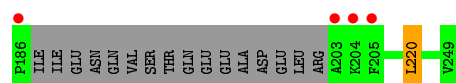




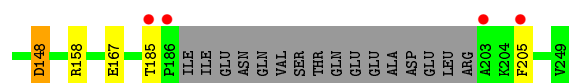
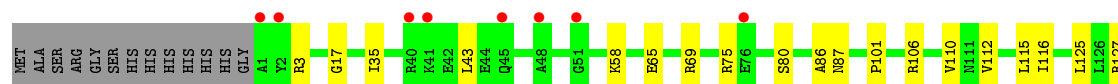
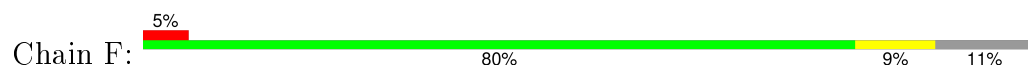
- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase



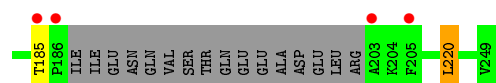
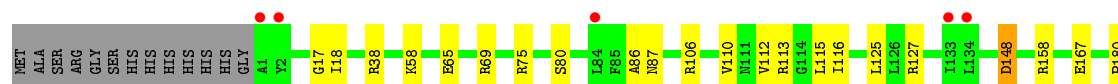
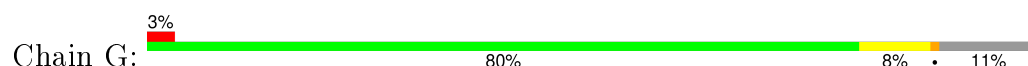
- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase



- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase



- Molecule 1: Alcohol dehydrogenase/short-chain dehydrogenase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	73.07Å 73.52Å 132.68Å 80.61° 86.80° 63.10°	Depositor
Resolution (Å)	30.00 – 2.40 29.50 – 2.40	Depositor EDS
% Data completeness (in resolution range)	96.7 (30.00-2.40) 91.4 (29.50-2.40)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.60 (at 2.39Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.195 , 0.231 0.198 , 0.235	Depositor DCC
R_{free} test set	4591 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 44.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 91854 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14524	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 5.04% 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 ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: SO4

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	0.98	4/1774 (0.2%)	0.90	4/2402 (0.2%)
1	B	0.72	0/1774	0.78	0/2402
1	C	0.70	1/1774 (0.1%)	0.77	1/2402 (0.0%)
1	D	0.79	0/1774	0.81	2/2402 (0.1%)
1	E	0.76	0/1774	0.78	1/2402 (0.0%)
1	F	0.71	0/1774	0.77	0/2402
1	G	0.71	0/1774	0.77	1/2402 (0.0%)
1	H	0.73	0/1774	0.78	2/2402 (0.1%)
All	All	0.77	5/14192 (0.0%)	0.80	11/19216 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	32	TYR	CE1-CZ	-13.20	1.21	1.38
1	A	32	TYR	CG-CD1	-11.13	1.24	1.39
1	A	32	TYR	CG-CD2	-9.46	1.26	1.39
1	A	32	TYR	CE2-CZ	-6.38	1.30	1.38
1	C	164	TRP	CD2-CE2	5.08	1.47	1.41

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	32	TYR	CD1-CE1-CZ	6.38	125.54	119.80
1	A	220	LEU	CA-CB-CG	-6.35	100.69	115.30
1	A	32	TYR	CB-CG-CD2	5.59	124.35	121.00
1	D	171	ARG	NE-CZ-NH2	-5.48	117.56	120.30
1	A	32	TYR	CE1-CZ-CE2	-5.29	111.33	119.80
1	E	220	LEU	CA-CB-CG	-5.23	103.27	115.30
1	D	220	LEU	CA-CB-CG	-5.16	103.44	115.30
1	H	220	LEU	CA-CB-CG	-5.12	103.52	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	220	LEU	CA-CB-CG	-5.10	103.56	115.30
1	H	171	ARG	NE-CZ-NH2	-5.06	117.77	120.30
1	C	25	ARG	NE-CZ-NH1	-5.04	117.78	120.30

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	1752	0	1799	26	0
1	B	1752	0	1799	14	0
1	C	1752	0	1799	15	0
1	D	1752	0	1799	16	0
1	E	1752	0	1799	18	0
1	F	1752	0	1799	13	0
1	G	1752	0	1799	15	0
1	H	1752	0	1799	18	0
2	A	5	0	0	1	0
2	B	5	0	0	0	0
2	C	5	0	0	1	0
2	D	5	0	0	0	0
2	E	5	0	0	0	0
2	F	5	0	0	0	0
2	G	5	0	0	1	0
2	H	5	0	0	0	0
3	A	64	0	0	1	0
3	B	43	0	0	3	0
3	C	37	0	0	1	0
3	D	80	0	0	2	0
3	E	65	0	0	1	0
3	F	52	0	0	1	0
3	G	57	0	0	0	0
3	H	70	0	0	2	0
All	All	14524	0	14392	118	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 (118) 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:H:61:VAL:HG23	3:H:425:HOH:O	1.77	0.84
1:D:115:LEU:HD13	3:D:440:HOH:O	1.81	0.80
1:B:112:VAL:O	1:B:116:ILE:HG13	1.85	0.76
1:A:32:TYR:HD2	1:A:78:ARG:HD3	1.53	0.72
1:A:87:ASN:CG	1:A:87:ASN:O	2.33	0.68
1:A:75:ARG:HE	1:A:125:LEU:HD21	1.61	0.66
1:C:75:ARG:HE	1:C:125:LEU:HD21	1.61	0.66
1:F:112:VAL:O	1:F:116:ILE:HG13	1.96	0.66
1:D:75:ARG:HE	1:D:125:LEU:HD21	1.61	0.66
1:A:32:TYR:CD2	1:A:78:ARG:HD3	2.30	0.65
1:H:75:ARG:HE	1:H:125:LEU:HD21	1.61	0.65
1:G:75:ARG:HE	1:G:125:LEU:HD21	1.62	0.65
1:H:112:VAL:O	1:H:116:ILE:HG13	1.97	0.65
1:A:6:ASN:HD21	1:E:75:ARG:CZ	2.10	0.64
1:F:75:ARG:HE	1:F:125:LEU:HD21	1.62	0.63
1:E:112:VAL:O	1:E:116:ILE:HG13	1.99	0.62
1:D:106:ARG:O	1:D:110:VAL:HG12	1.99	0.62
1:C:106:ARG:O	1:C:110:VAL:HG12	1.99	0.62
1:F:106:ARG:O	1:F:110:VAL:HG12	2.00	0.61
1:B:75:ARG:HE	1:B:125:LEU:HD21	1.64	0.61
1:E:106:ARG:O	1:E:110:VAL:HG12	2.01	0.61
1:E:75:ARG:HE	1:E:125:LEU:HD21	1.65	0.61
1:A:32:TYR:HD2	1:A:78:ARG:CD	2.14	0.60
1:D:75:ARG:HH21	1:D:125:LEU:HD23	1.67	0.60
1:G:106:ARG:O	1:G:110:VAL:HG12	2.03	0.59
1:G:112:VAL:O	1:G:116:ILE:HG13	2.03	0.59
1:C:112:VAL:O	1:C:116:ILE:HG13	2.03	0.59
1:H:75:ARG:HH21	1:H:125:LEU:HD23	1.69	0.58
1:H:106:ARG:O	1:H:110:VAL:HG12	2.02	0.58
1:D:112:VAL:O	1:D:116:ILE:HG13	2.04	0.57
1:A:158:ARG:HD3	1:A:158:ARG:C	2.26	0.56
1:C:38:ARG:HB2	2:C:301:SO4:O3	2.08	0.54
1:B:106:ARG:O	1:B:110:VAL:HG12	2.06	0.54
1:A:158:ARG:O	1:A:158:ARG:HD3	2.08	0.54
1:A:106:ARG:O	1:A:110:VAL:HG12	2.08	0.54
1:B:87:ASN:CG	1:B:87:ASN:O	2.45	0.54
1:F:87:ASN:O	1:F:87:ASN:CG	2.46	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:ASN:CG	1:C:87:ASN:O	2.46	0.53
1:B:216:ARG:HD3	3:B:428:HOH:O	2.08	0.53
1:A:32:TYR:CE1	1:A:53:ASN:C	2.83	0.52
1:G:38:ARG:HB2	2:G:301:SO4:O2	2.10	0.52
1:A:32:TYR:HE1	1:A:54:VAL:N	2.08	0.52
1:A:5:LEU:HD11	1:E:75:ARG:HH12	1.75	0.52
1:A:38:ARG:HB2	2:A:301:SO4:O4	2.09	0.52
1:D:87:ASN:CG	1:D:87:ASN:O	2.47	0.52
1:H:87:ASN:O	1:H:87:ASN:CG	2.47	0.52
1:E:87:ASN:CG	1:E:87:ASN:O	2.47	0.52
1:G:87:ASN:O	1:G:87:ASN:CG	2.48	0.51
1:C:75:ARG:HH21	1:C:125:LEU:HD23	1.76	0.51
1:G:75:ARG:HH21	1:G:125:LEU:HD23	1.75	0.51
1:A:32:TYR:HE1	1:A:53:ASN:C	2.14	0.50
1:E:75:ARG:HH21	1:E:125:LEU:HD23	1.77	0.49
1:B:75:ARG:HH21	1:B:125:LEU:HD23	1.77	0.49
1:F:75:ARG:HH21	1:F:125:LEU:HD23	1.77	0.49
1:A:75:ARG:HH21	1:A:125:LEU:HD23	1.78	0.49
1:A:75:ARG:CZ	1:E:6:ASN:HD21	2.26	0.48
1:B:167:GLU:OE2	1:C:148:ASP:OD1	2.31	0.48
1:D:163:THR:HG21	1:E:148:ASP:HA	1.95	0.48
1:D:65:GLU:CD	1:D:65:GLU:H	2.17	0.48
1:A:35:ILE:HG13	1:A:43:LEU:HD22	1.96	0.48
1:H:65:GLU:CD	1:H:65:GLU:H	2.18	0.47
1:D:180:PRO:HB3	1:D:220:LEU:HD13	1.97	0.47
1:D:148:ASP:OD1	1:E:167:GLU:OE2	2.33	0.47
1:B:180:PRO:HG2	3:B:430:HOH:O	2.15	0.46
1:D:167:GLU:OE2	1:E:148:ASP:OD1	2.33	0.46
1:C:155:ALA:HA	3:C:408:HOH:O	2.15	0.46
1:G:65:GLU:H	1:G:65:GLU:CD	2.19	0.46
1:G:180:PRO:HB3	1:G:220:LEU:HD13	1.97	0.46
1:C:65:GLU:CD	1:C:65:GLU:H	2.19	0.46
1:H:75:ARG:HE	1:H:125:LEU:CD2	2.28	0.46
1:E:65:GLU:H	1:E:65:GLU:CD	2.19	0.46
1:E:80:SER:HB2	3:E:425:HOH:O	2.15	0.45
1:D:75:ARG:HE	1:D:125:LEU:CD2	2.28	0.45
1:B:86:ALA:HB1	1:B:115:LEU:HD12	1.99	0.45
1:B:58:LYS:O	1:B:69:ARG:NH1	2.50	0.44
1:F:148:ASP:OD1	1:G:167:GLU:OE2	2.36	0.44
1:F:65:GLU:CD	1:F:65:GLU:H	2.21	0.44
1:H:180:PRO:HB3	1:H:220:LEU:HD13	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:86:ALA:HB1	1:H:115:LEU:HD12	2.00	0.44
1:D:3:ARG:HD3	3:D:458:HOH:O	2.17	0.44
1:C:35:ILE:HG13	1:C:43:LEU:HD22	2.00	0.43
1:D:86:ALA:HB1	1:D:115:LEU:HD12	2.00	0.43
1:D:18:ILE:HG23	1:D:220:LEU:HD23	2.00	0.43
1:E:180:PRO:HB3	1:E:220:LEU:HD13	2.01	0.43
1:A:32:TYR:HD1	1:A:53:ASN:O	2.00	0.43
1:H:148:ASP:OD1	1:A:167:GLU:OE2	2.36	0.43
1:H:18:ILE:HG23	1:H:220:LEU:HD23	2.01	0.43
1:H:61:VAL:CG2	3:H:425:HOH:O	2.51	0.43
1:H:163:THR:HG21	1:A:148:ASP:HA	2.00	0.43
1:B:65:GLU:CD	1:B:65:GLU:H	2.22	0.43
1:C:180:PRO:HB3	1:C:220:LEU:HD13	2.00	0.43
1:F:58:LYS:O	1:F:69:ARG:NH1	2.52	0.42
1:E:35:ILE:HG13	1:E:43:LEU:HD22	2.00	0.42
1:F:35:ILE:HG13	1:F:43:LEU:HD22	2.01	0.42
1:H:148:ASP:HA	1:A:163:THR:HG21	2.02	0.42
1:G:86:ALA:HB1	1:G:115:LEU:HD12	2.01	0.42
1:A:65:GLU:CD	1:A:65:GLU:H	2.22	0.42
1:E:58:LYS:O	1:E:69:ARG:NH1	2.53	0.42
1:E:86:ALA:HB1	1:E:115:LEU:HD12	2.02	0.42
1:A:32:TYR:CD1	1:A:53:ASN:O	2.73	0.42
1:C:75:ARG:HE	1:C:125:LEU:CD2	2.32	0.42
1:H:167:GLU:OE2	1:A:148:ASP:OD1	2.38	0.41
1:F:101:PRO:HB3	1:G:113:ARG:NH2	2.35	0.41
1:F:86:ALA:HB1	1:F:115:LEU:HD12	2.01	0.41
1:B:101:PRO:HB3	1:C:113:ARG:NH2	2.34	0.41
1:C:58:LYS:O	1:C:69:ARG:NH1	2.54	0.41
1:D:58:LYS:O	1:D:69:ARG:NH1	2.53	0.41
1:A:127:ARG:NH2	1:E:127:ARG:NH2	2.68	0.41
1:F:167:GLU:OE2	1:G:148:ASP:OD1	2.38	0.41
1:G:75:ARG:HE	1:G:125:LEU:CD2	2.31	0.41
1:G:58:LYS:O	1:G:69:ARG:NH1	2.54	0.41
1:B:64:LEU:HG	3:B:441:HOH:O	2.20	0.41
1:G:18:ILE:HG23	1:G:220:LEU:HD23	2.02	0.41
1:A:80:SER:HB2	3:A:429:HOH:O	2.20	0.40
1:F:3:ARG:HD3	3:F:434:HOH:O	2.21	0.40
1:H:18:ILE:CG2	1:H:220:LEU:HD23	2.51	0.40
1:B:148:ASP:OD1	1:C:167:GLU:OE2	2.39	0.40
1:H:58:LYS:O	1:H:69:ARG:NH1	2.54	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	229/262 (87%)	219 (96%)	10 (4%)	0	100	100
1	B	229/262 (87%)	219 (96%)	9 (4%)	1 (0%)	39	56
1	C	229/262 (87%)	222 (97%)	6 (3%)	1 (0%)	39	56
1	D	229/262 (87%)	222 (97%)	6 (3%)	1 (0%)	39	56
1	E	229/262 (87%)	222 (97%)	6 (3%)	1 (0%)	39	56
1	F	229/262 (87%)	222 (97%)	6 (3%)	1 (0%)	39	56
1	G	229/262 (87%)	222 (97%)	6 (3%)	1 (0%)	39	56
1	H	229/262 (87%)	221 (96%)	7 (3%)	1 (0%)	39	56
All	All	1832/2096 (87%)	1769 (97%)	56 (3%)	7 (0%)	39	56

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	17	GLY
1	C	17	GLY
1	F	17	GLY
1	H	17	GLY
1	D	17	GLY
1	E	17	GLY
1	G	17	GLY

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	179/204 (88%)	173 (97%)	6 (3%)	44	65
1	B	179/204 (88%)	173 (97%)	6 (3%)	44	65
1	C	179/204 (88%)	174 (97%)	5 (3%)	51	72
1	D	179/204 (88%)	173 (97%)	6 (3%)	44	65
1	E	179/204 (88%)	174 (97%)	5 (3%)	51	72
1	F	179/204 (88%)	173 (97%)	6 (3%)	44	65
1	G	179/204 (88%)	174 (97%)	5 (3%)	51	72
1	H	179/204 (88%)	173 (97%)	6 (3%)	44	65
All	All	1432/1632 (88%)	1387 (97%)	45 (3%)	47	69

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	80	SER
1	H	127	ARG
1	H	148	ASP
1	H	158	ARG
1	H	185	THR
1	H	205	PHE
1	A	80	SER
1	A	127	ARG
1	A	148	ASP
1	A	158	ARG
1	A	185	THR
1	A	205	PHE
1	B	80	SER
1	B	127	ARG
1	B	148	ASP
1	B	158	ARG
1	B	185	THR
1	B	205	PHE
1	C	80	SER
1	C	127	ARG
1	C	148	ASP
1	C	158	ARG
1	C	185	THR
1	D	80	SER
1	D	127	ARG
1	D	148	ASP
1	D	158	ARG

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Mol	Chain	Res	Type
1	D	185	THR
1	D	205	PHE
1	E	80	SER
1	E	127	ARG
1	E	148	ASP
1	E	158	ARG
1	E	185	THR
1	F	80	SER
1	F	127	ARG
1	F	148	ASP
1	F	158	ARG
1	F	185	THR
1	F	205	PHE
1	G	80	SER
1	G	127	ARG
1	G	148	ASP
1	G	158	ARG
1	G	185	THR

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

Mol	Chain	Res	Type
1	E	6	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](#)

8 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	301	-	4,4,4	0.58	0	6,6,6	0.29	0
2	SO4	B	301	-	4,4,4	0.57	0	6,6,6	0.21	0
2	SO4	C	301	-	4,4,4	0.79	0	6,6,6	0.47	0
2	SO4	D	301	-	4,4,4	0.90	0	6,6,6	0.76	0
2	SO4	E	301	-	4,4,4	0.50	0	6,6,6	0.61	0
2	SO4	F	301	-	4,4,4	0.58	0	6,6,6	0.23	0
2	SO4	G	301	-	4,4,4	0.74	0	6,6,6	0.75	0
2	SO4	H	301	-	4,4,4	0.72	0	6,6,6	0.49	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	SO4	A	301	-	-	0/0/0/0	0/0/0/0
2	SO4	B	301	-	-	0/0/0/0	0/0/0/0
2	SO4	C	301	-	-	0/0/0/0	0/0/0/0
2	SO4	D	301	-	-	0/0/0/0	0/0/0/0
2	SO4	E	301	-	-	0/0/0/0	0/0/0/0
2	SO4	F	301	-	-	0/0/0/0	0/0/0/0
2	SO4	G	301	-	-	0/0/0/0	0/0/0/0
2	SO4	H	301	-	-	0/0/0/0	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 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	301	SO4	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	SO4	1	0
2	G	301	SO4	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	233/262 (88%)	-0.10	9 (3%)	43	44	18, 31, 69, 118	4 (1%)
1	B	233/262 (88%)	0.37	20 (8%)	13	13	21, 45, 88, 140	4 (1%)
1	C	233/262 (88%)	0.11	11 (4%)	35	36	22, 39, 71, 100	4 (1%)
1	D	233/262 (88%)	0.03	14 (6%)	25	25	15, 28, 69, 115	4 (1%)
1	E	233/262 (88%)	-0.15	7 (3%)	54	53	15, 28, 62, 121	4 (1%)
1	F	233/262 (88%)	0.20	12 (5%)	31	31	18, 38, 73, 107	4 (1%)
1	G	233/262 (88%)	0.03	9 (3%)	43	44	19, 33, 66, 89	4 (1%)
1	H	233/262 (88%)	-0.04	12 (5%)	31	31	18, 31, 71, 131	4 (1%)
All	All	1864/2096 (88%)	0.06	94 (5%)	32	33	15, 34, 73, 140	32 (1%)

All (94) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	186	PRO	26.9
1	F	186	PRO	22.9
1	F	185	THR	22.2
1	C	186	PRO	20.3
1	C	185	THR	20.1
1	A	186	PRO	18.6
1	D	186	PRO	17.8
1	G	186	PRO	15.0
1	B	185	THR	14.4
1	G	185	THR	14.4
1	B	186	PRO	14.3
1	E	185	THR	13.4
1	H	186	PRO	13.3
1	B	203	ALA	12.2
1	F	203	ALA	12.1
1	D	185	THR	10.8

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Mol	Chain	Res	Type	RSRZ
1	A	185	THR	10.2
1	G	203	ALA	9.2
1	H	203	ALA	8.9
1	D	203	ALA	8.7
1	A	203	ALA	8.7
1	H	185	THR	8.6
1	E	203	ALA	8.1
1	H	205	PHE	8.1
1	C	203	ALA	7.6
1	D	205	PHE	6.1
1	A	205	PHE	5.8
1	E	205	PHE	5.6
1	H	204	LYS	4.1
1	D	2	TYR	4.1
1	B	1	ALA	3.9
1	D	40	ARG	3.9
1	C	45	GLN	3.8
1	B	40	ARG	3.8
1	D	41	LYS	3.8
1	B	205	PHE	3.7
1	F	40	ARG	3.5
1	B	51	GLY	3.5
1	F	2	TYR	3.4
1	F	76	GLU	3.4
1	F	205	PHE	3.4
1	F	1	ALA	3.3
1	G	205	PHE	3.2
1	A	208	ALA	3.2
1	C	205	PHE	3.2
1	H	41	LYS	3.2
1	C	41	LYS	3.2
1	H	2	TYR	3.1
1	B	204	LYS	3.1
1	G	1	ALA	3.1
1	H	40	ARG	3.0
1	D	204	LYS	3.0
1	C	102	GLU	3.0
1	B	45	GLN	2.7
1	A	51	GLY	2.7
1	B	52	ARG	2.7
1	D	1	ALA	2.7
1	A	41	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	41	LYS	2.6
1	C	2	TYR	2.6
1	B	39	ARG	2.6
1	B	6	ASN	2.6
1	H	208	ALA	2.5
1	D	184	ASP	2.5
1	B	2	TYR	2.5
1	D	45	GLN	2.5
1	E	1	ALA	2.5
1	A	48	ALA	2.4
1	B	86	ALA	2.4
1	E	40	ARG	2.4
1	G	84	LEU	2.3
1	F	48	ALA	2.3
1	H	184	ASP	2.3
1	C	42	GLU	2.3
1	B	177	ALA	2.2
1	E	204	LYS	2.2
1	D	85	PHE	2.2
1	B	184	ASP	2.2
1	G	133	ILE	2.2
1	B	133	ILE	2.2
1	G	134	LEU	2.2
1	C	39	ARG	2.1
1	B	16	SER	2.1
1	D	212	GLY	2.1
1	G	2	TYR	2.1
1	B	5	LEU	2.1
1	D	134	LEU	2.1
1	H	86	ALA	2.1
1	H	45	GLN	2.0
1	A	39	ARG	2.0
1	F	41	LYS	2.0
1	F	51	GLY	2.0
1	C	208	ALA	2.0
1	F	45	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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(\AA^2)	Q<0.9
2	SO4	D	301	5/5	0.82	0.22	0.66	62,78,96,96	0
2	SO4	G	301	5/5	0.85	0.17	0.05	72,81,85,92	0
2	SO4	A	301	5/5	0.93	0.17	0.04	81,81,88,90	0
2	SO4	C	301	5/5	0.81	0.18	-0.34	89,91,99,106	0
2	SO4	F	301	5/5	0.91	0.15	-1.47	91,92,97,106	0
2	SO4	H	301	5/5	0.88	0.24	-	72,80,104,109	0
2	SO4	E	301	5/5	0.96	0.12	-	72,73,81,86	0
2	SO4	B	301	5/5	0.77	0.24	-	102,105,117,120	0

6.5 Other polymers [i](#)

There are no such residues in this entry.