



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 03:42 PM GMT

PDB ID : 4D4P
Title : Crystal Structure of the Kti11 Kti13 heterodimer Spacegroup P65
Authors : Glatt, S.; Mueller, C.W.
Deposited on : 2014-10-30
Resolution : 3.00 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

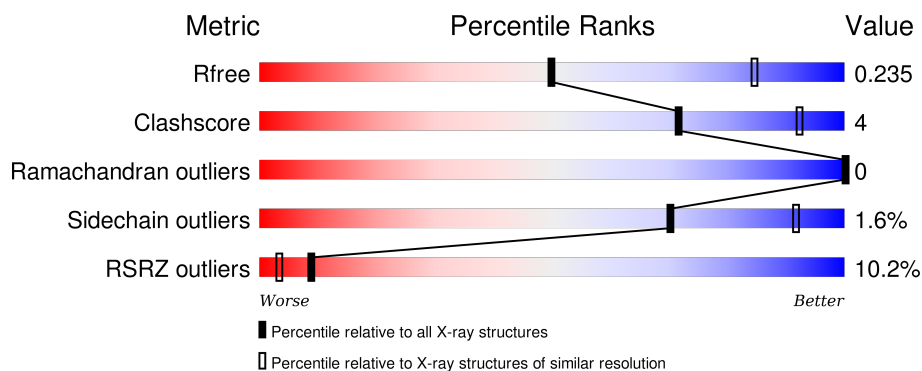
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1578 (3.00-3.00)
Clashscore	102246	1912 (3.00-3.00)
Ramachandran outliers	100387	1853 (3.00-3.00)
Sidechain outliers	100360	1856 (3.00-3.00)
RSRZ outliers	91569	1592 (3.00-3.00)

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	427	<div> <div>8%</div> <div>85%</div> <div>11%</div> <div>.</div> </div>
1	B	427	<div> <div>5%</div> <div>69%</div> <div>10%</div> <div>21%</div> </div>
1	C	427	<div> <div>%</div> <div>16%</div> <div>.</div> <div>82%</div> </div>
1	E	427	<div> <div>9%</div> <div>70%</div> <div>8%</div> <div>22%</div> </div>
1	G	427	<div> <div>14%</div> <div>86%</div> <div>9%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
1	H	427	<div><div><div></div><div></div><div></div><div></div><div></div></div><div>3%12%••83%</div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 12715 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 PROTEIN ATS1, DIPHTHAMIDE BIOSYNTHESIS PROTEIN 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	413	Total	C	N	O	S	0	0	0
			3178	1982	555	614	27			
1	B	336	Total	C	N	O	S	0	0	0
			2576	1603	471	484	18			
1	C	76	Total	C	N	O	S	0	0	0
			613	389	86	129	9			
1	E	334	Total	C	N	O	S	0	0	0
			2565	1597	469	481	18			
1	G	409	Total	C	N	O	S	0	0	0
			3152	1968	550	607	27			
1	H	74	Total	C	N	O	S	0	0	0
			602	382	84	127	9			

There are 72 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	EXPRESSION TAG	UNP P31386
A	0	ALA	-	EXPRESSION TAG	UNP P31386
A	334	GLY	-	LINKER	UNP P31386
A	335	SER	-	LINKER	UNP P31386
A	336	GLY	-	LINKER	UNP P31386
A	337	SER	-	LINKER	UNP P31386
A	338	GLY	-	LINKER	UNP P31386
A	339	SER	-	LINKER	UNP P31386
A	340	GLY	-	LINKER	UNP P31386
A	341	SER	-	LINKER	UNP P31386
A	342	GLY	-	LINKER	UNP P31386
A	343	SER	-	LINKER	UNP P31386
B	-1	GLY	-	EXPRESSION TAG	UNP P31386
B	0	ALA	-	EXPRESSION TAG	UNP P31386
B	334	GLY	-	LINKER	UNP P31386
B	335	SER	-	LINKER	UNP P31386

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Chain	Residue	Modelled	Actual	Comment	Reference
B	336	GLY	-	LINKER	UNP P31386
B	337	SER	-	LINKER	UNP P31386
B	338	GLY	-	LINKER	UNP P31386
B	339	SER	-	LINKER	UNP P31386
B	340	GLY	-	LINKER	UNP P31386
B	341	SER	-	LINKER	UNP P31386
B	342	GLY	-	LINKER	UNP P31386
B	343	SER	-	LINKER	UNP P31386
C	-1	GLY	-	EXPRESSION TAG	UNP P31386
C	0	ALA	-	EXPRESSION TAG	UNP P31386
C	334	GLY	-	LINKER	UNP P31386
C	335	SER	-	LINKER	UNP P31386
C	336	GLY	-	LINKER	UNP P31386
C	337	SER	-	LINKER	UNP P31386
C	338	GLY	-	LINKER	UNP P31386
C	339	SER	-	LINKER	UNP P31386
C	340	GLY	-	LINKER	UNP P31386
C	341	SER	-	LINKER	UNP P31386
C	342	GLY	-	LINKER	UNP P31386
C	343	SER	-	LINKER	UNP P31386
E	-1	GLY	-	EXPRESSION TAG	UNP P31386
E	0	ALA	-	EXPRESSION TAG	UNP P31386
E	334	GLY	-	LINKER	UNP P31386
E	335	SER	-	LINKER	UNP P31386
E	336	GLY	-	LINKER	UNP P31386
E	337	SER	-	LINKER	UNP P31386
E	338	GLY	-	LINKER	UNP P31386
E	339	SER	-	LINKER	UNP P31386
E	340	GLY	-	LINKER	UNP P31386
E	341	SER	-	LINKER	UNP P31386
E	342	GLY	-	LINKER	UNP P31386
E	343	SER	-	LINKER	UNP P31386
G	-1	GLY	-	EXPRESSION TAG	UNP P31386
G	0	ALA	-	EXPRESSION TAG	UNP P31386
G	334	GLY	-	LINKER	UNP P31386
G	335	SER	-	LINKER	UNP P31386
G	336	GLY	-	LINKER	UNP P31386
G	337	SER	-	LINKER	UNP P31386
G	338	GLY	-	LINKER	UNP P31386
G	339	SER	-	LINKER	UNP P31386
G	340	GLY	-	LINKER	UNP P31386
G	341	SER	-	LINKER	UNP P31386

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Chain	Residue	Modelled	Actual	Comment	Reference
G	342	GLY	-	LINKER	UNP P31386
G	343	SER	-	LINKER	UNP P31386
H	-1	GLY	-	EXPRESSION TAG	UNP P31386
H	0	ALA	-	EXPRESSION TAG	UNP P31386
H	334	GLY	-	LINKER	UNP P31386
H	335	SER	-	LINKER	UNP P31386
H	336	GLY	-	LINKER	UNP P31386
H	337	SER	-	LINKER	UNP P31386
H	338	GLY	-	LINKER	UNP P31386
H	339	SER	-	LINKER	UNP P31386
H	340	GLY	-	LINKER	UNP P31386
H	341	SER	-	LINKER	UNP P31386
H	342	GLY	-	LINKER	UNP P31386
H	343	SER	-	LINKER	UNP P31386

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	H	1	Total Fe 1 1	0	0
2	G	1	Total Fe 1 1	0	0
2	A	1	Total Fe 1 1	0	0
2	C	1	Total Fe 1 1	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).

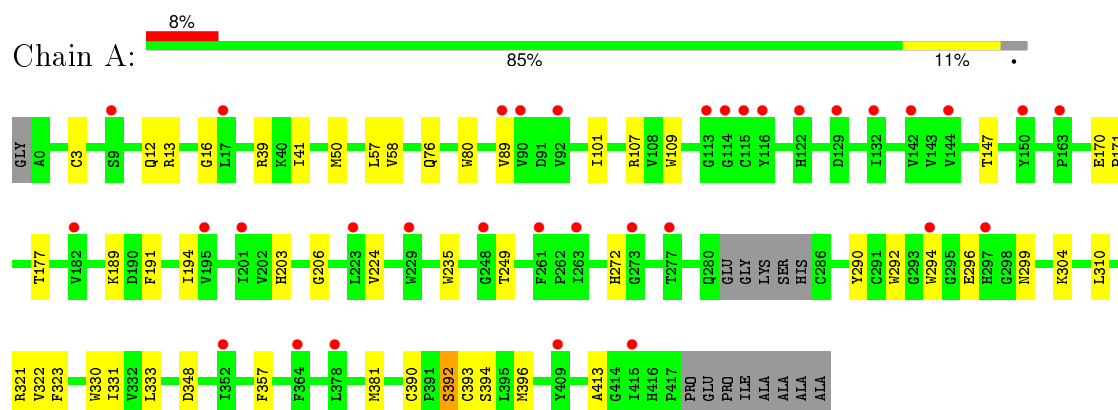


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		
3	E	1	Total	O	S	0	0
			5	4	1		

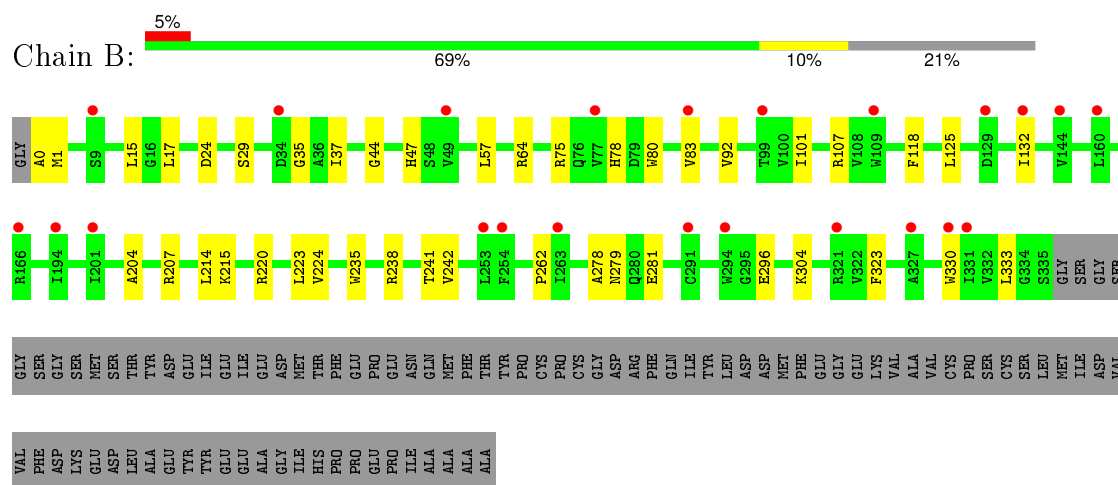
3 Residue-property plots

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.

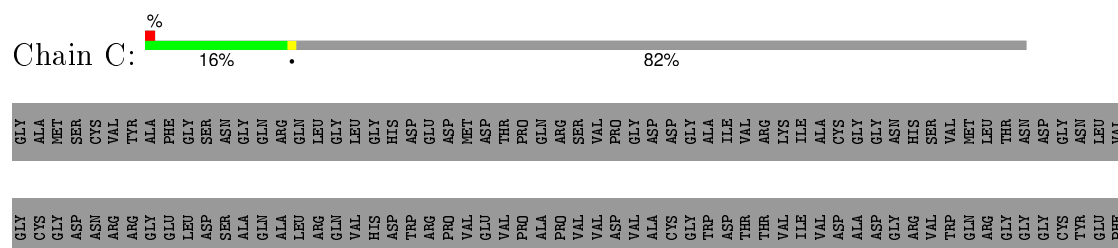
• Molecule 1: PROTEIN ATS1, DIPHTHAMIDE BIOSYNTHESIS PROTEIN 3

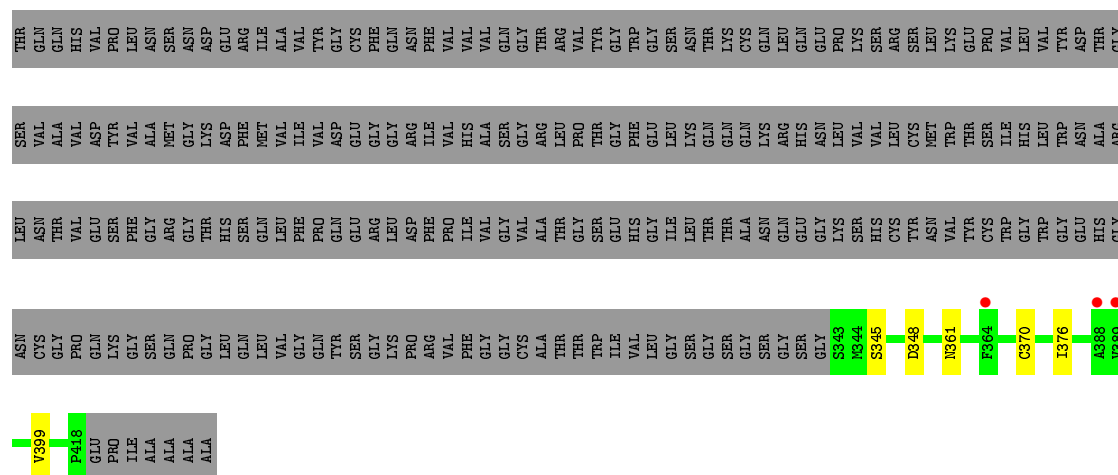


• Molecule 1: PROTEIN ATS1, DIPHTHAMIDE BIOSYNTHESIS PROTEIN 3

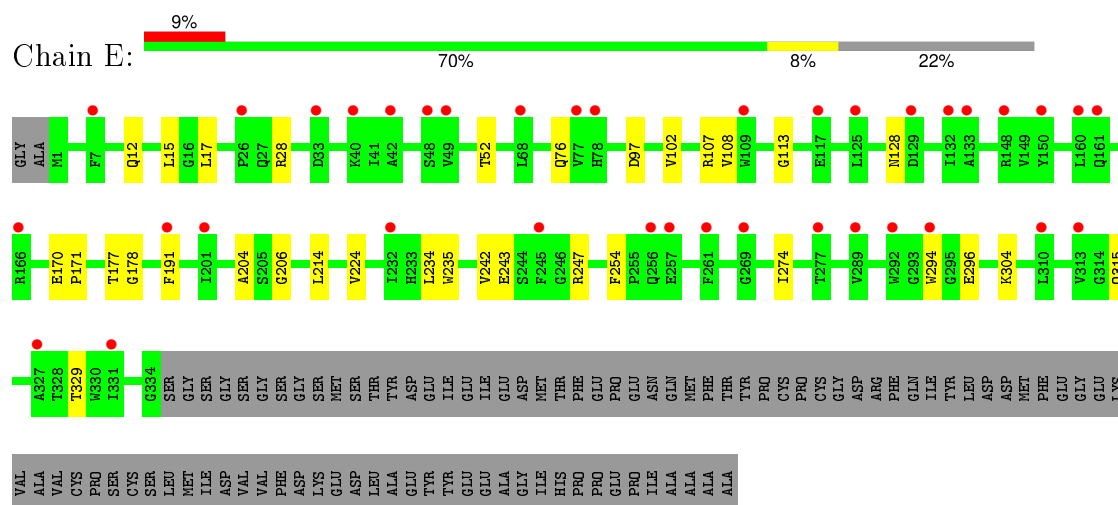


• Molecule 1: PROTEIN ATS1, DIPHTHAMIDE BIOSYNTHESIS PROTEIN 3

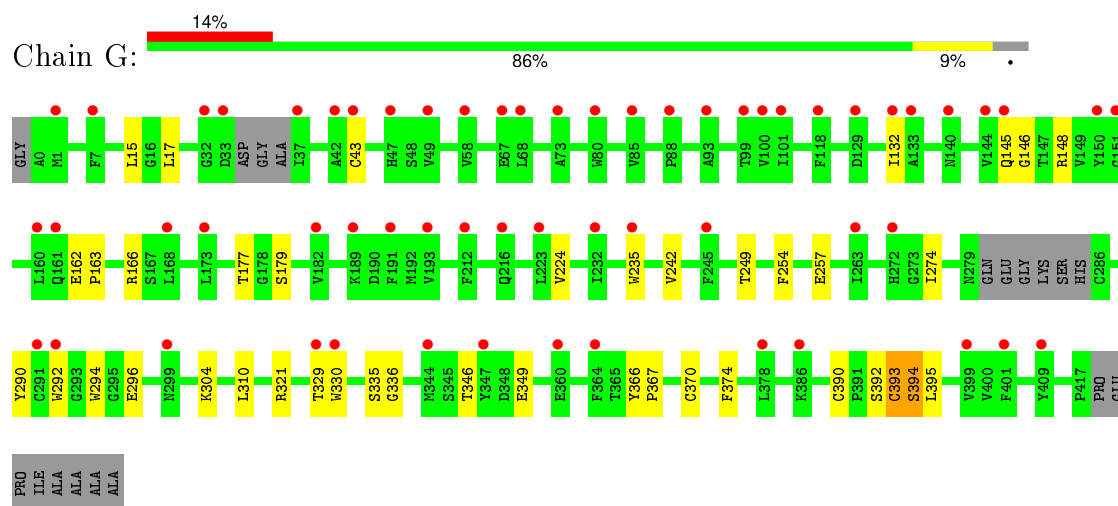




• Molecule 1: PROTEIN ATS1, DIPHTHAMIDE BIOSYNTHESIS PROTEIN 3



• Molecule 1: PROTEIN ATS1, DIPHTHAMIDE BIOSYNTHESIS PROTEIN 3



• Molecule 1: PROTEIN ATS1, DIPHTHAMIDE BIOSYNTHESIS PROTEIN 3



V377	V378	D379	D380	E383	GLY	E385	K386	V387	A388	V389	C390	P391	S392	C393	S394	V397	D398	V399	V400	F401	L406	A407	E408	Y409	Y410	E411	E412	F417	PRO	GLU	PRO	ILE	ALA	ALA	
ASN	CYS	GLY	PRO	GLN	LYS	GLY	SER	GLN	PRO	GLY	LEU	GLN	VAL	GLY	TYR	SER	GLY	LYS	PRO	VAL	PHE	GLY	CYS	ALA	THR	THR	THR	THR	ILE	VAL	HIS	LEU	GLY	SER	THR
LEU	ASN	THR	VAL	GLU	SER	PHE	GLY	ARG	GLY	THR	HIS	SER	GLN	LEU	PHE	GLY	ARG	ASP	PHE	PRO	ILE	VAL	GLY	ALA	THR	GLY	SER	GLU	HIS	LEU	GLY	THR	GLU	THR	GLU
SER	VAL	ALA	VAL	ASP	TYR	VAL	ALA	MET	GLY	LYS	ASP	PHE	MET	VAL	ILE	VAL	GLN	ASP	GLY	GLY	GLY	ILE	ARG	ALA	THR	GLY	PRO	THR	GLY	PHE	THR	GLN	GLY	TRP	GLY
THR	GLN	GLN	HIS	VAL	PRO	LEU	ASN	SER	ASP	GLY	ARG	ILE	ILE	ALA	VAL	TYR	GLY	CYS	PHE	GLN	PHE	ASP	THR	ARG	THR	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL	VAL
GLY	ALA	MET	SER	CYS	ARG	ARG	GLY	LEU	ALA	SER	ASN	GLY	GLN	ARG	LEU	VAL	GLN	VAL	VAL	VAL	GLU	ASP	THR	PRO	ALA	PRO	VAL	VAL	ASP	GLY	ALA	ILE	VAL	VAL	VAL
ASN	CYS	GLY	GLY	TYR	ASN	VAL	VAL	SER	VAL	VAL	CYS	MET	THR	TYR	THR	GLY	LEU	VAL	GLY	THR	GLN	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY	GLY
S943	M344	F357	F364	T365	Y366	P367	C370	G371	D372	R373	I376																								

4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	152.06Å 152.06Å 203.85Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	110.61 – 3.00 131.69 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.6 (110.61-3.00) 99.6 (131.69-3.00)	Depositor EDS
R_{merge}	0.01	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.40 (at 3.01Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.208 , 0.234 0.208 , 0.235	Depositor DCC
R_{free} test set	2659 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	95.3	Xtriage
Anisotropy	0.194	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 62.5	EDS
Estimated twinning fraction	0.043 for h,-h-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Outliers	0 of 53195 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12715	wwPDB-VP
Average B, all atoms (Å ²)	106.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FE, 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	0.23	0/3253	0.39	1/4414 (0.0%)
1	B	0.20	0/2637	0.37	0/3580
1	C	0.21	0/629	0.38	0/853
1	E	0.21	0/2626	0.37	0/3565
1	G	0.23	0/3226	0.39	0/4376
1	H	0.26	0/616	0.40	0/833
All	All	0.22	0/12987	0.38	1/17621 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	390	CYS	C-N-CD	-8.07	102.85	120.60

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	3178	0	3004	28	0
1	B	2576	0	2471	24	0
1	C	613	0	547	4	0
1	E	2565	0	2461	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	G	3152	0	2984	30	0
1	H	602	0	536	11	0
2	A	1	0	0	0	0
2	C	1	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	A	5	0	0	1	0
3	B	10	0	0	2	0
3	E	10	0	0	1	0
All	All	12715	0	12003	106	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 (106) 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:G:393:CYS:SG	1:G:395:LEU:HD23	2.00	1.00
1:E:296:GLU:OE1	1:G:394:SER:OG	1.99	0.81
1:G:224:VAL:HB	1:G:235:TRP:HB3	1.68	0.74
1:B:224:VAL:HB	1:B:235:TRP:HB3	1.68	0.74
1:G:395:LEU:N	1:G:395:LEU:HD22	2.03	0.73
1:A:224:VAL:HB	1:A:235:TRP:HB3	1.71	0.73
1:G:395:LEU:H	1:G:395:LEU:HD22	1.56	0.71
1:G:393:CYS:HB2	1:G:395:LEU:CD2	2.19	0.70
1:H:390:CYS:HB3	1:H:393:CYS:SG	2.32	0.69
1:H:393:CYS:SG	1:H:394:SER:N	2.68	0.66
1:A:189:LYS:NZ	1:C:348:ASP:OD2	2.30	0.64
1:A:294:TRP:HH2	1:C:370:CYS:HB3	1.61	0.63
1:A:296:GLU:HA	1:A:304:LYS:HB3	1.79	0.63
1:A:39:ARG:O	1:A:321:ARG:NH2	2.32	0.62
1:H:344:MET:HG3	1:H:387:VAL:HG21	1.81	0.62
1:E:107:ARG:NH1	3:E:1335:SO4:O3	2.33	0.61
1:E:224:VAL:HB	1:E:235:TRP:HB3	1.82	0.60
1:A:348:ASP:OD1	1:B:207:ARG:NH2	2.30	0.59
1:A:292:TRP:HB3	1:A:310:LEU:HD23	1.84	0.58
1:A:290:TYR:HB3	1:A:310:LEU:HB3	1.85	0.57
1:A:13:ARG:NH1	1:A:76:GLN:OE1	2.33	0.57
1:B:262:PRO:HG2	1:B:278:ALA:HB3	1.86	0.57
1:H:407:ALA:HA	1:H:410:TYR:HB2	1.86	0.57
1:A:107:ARG:NH1	3:A:1418:SO4:O1	2.37	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:393:CYS:CB	1:G:395:LEU:HD23	2.36	0.56
1:G:395:LEU:CD2	1:G:395:LEU:H	2.19	0.55
1:B:107:ARG:NH1	3:B:1336:SO4:O4	2.40	0.55
1:B:92:VAL:HG23	1:B:101:ILE:HG22	1.88	0.55
1:H:386:LYS:HG2	1:H:401:PHE:HE1	1.73	0.54
1:G:292:TRP:HB3	1:G:310:LEU:HD23	1.89	0.53
1:G:296:GLU:HA	1:G:304:LYS:HB3	1.92	0.52
1:B:0:ALA:HB1	1:B:37:ILE:HD11	1.90	0.52
1:B:220:ARG:HE	1:B:223:LEU:HD11	1.75	0.51
1:G:395:LEU:N	1:G:395:LEU:CD2	2.73	0.51
1:B:57:LEU:HB3	1:B:83:VAL:HB	1.92	0.51
1:E:15:LEU:HB3	1:E:17:LEU:HG	1.93	0.51
1:B:125:LEU:HD13	1:B:132:ILE:HD13	1.92	0.51
1:G:335:SER:OG	1:G:336:GLY:N	2.44	0.51
1:B:279:ASN:ND2	1:G:249:THR:O	2.42	0.51
1:E:12:GLN:OE1	1:E:76:GLN:NE2	2.43	0.51
1:C:345:SER:HB3	1:E:315:GLN:HB3	1.93	0.50
1:A:322:VAL:HG12	1:A:331:ILE:HG12	1.94	0.50
1:B:15:LEU:HB3	1:B:17:LEU:HG	1.93	0.50
1:G:294:TRP:HH2	1:H:370:CYS:HB3	1.76	0.49
1:B:215:LYS:H	1:B:215:LYS:HD2	1.76	0.49
1:A:191:PHE:HA	1:A:206:GLY:HA3	1.95	0.49
1:A:249:THR:O	1:E:315:GLN:NE2	2.32	0.49
1:B:323:PHE:HB2	1:B:330:TRP:HB2	1.95	0.49
1:G:390:CYS:SG	1:G:393:CYS:SG	3.11	0.49
1:A:57:LEU:HG	1:A:89:VAL:HG21	1.94	0.48
1:G:15:LEU:HB3	1:G:17:LEU:HG	1.95	0.48
1:A:147:THR:HG23	1:A:177:THR:HB	1.95	0.48
1:E:102:VAL:HG22	1:E:108:VAL:HG22	1.95	0.47
1:G:374:PHE:HE1	1:G:395:LEU:HB3	1.79	0.47
1:A:323:PHE:HB2	1:A:330:TRP:HB2	1.97	0.47
1:G:132:ILE:HG12	1:G:145:GLN:HG3	1.95	0.47
1:G:374:PHE:CE1	1:G:395:LEU:HB3	2.50	0.46
1:G:43:CYS:HG	1:G:330:TRP:HE1	1.62	0.46
1:E:296:GLU:HA	1:E:304:LYS:HB3	1.97	0.46
1:A:16:GLY:HA3	1:A:80:TRP:NE1	2.32	0.45
1:A:381:MET:HB2	1:A:381:MET:HE3	1.70	0.45
1:A:194:ILE:HD12	1:A:203:HIS:HB3	1.99	0.44
1:E:247:ARG:NH2	1:G:346:THR:O	2.50	0.44
1:H:390:CYS:HA	1:H:391:PRO:HD3	1.86	0.44
1:A:41:ILE:HG12	1:A:50:MET:HG2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:50:MET:HB2	1:A:58:VAL:HG13	2.00	0.44
1:B:238:ARG:NH1	3:B:1337:SO4:O3	2.51	0.44
1:B:57:LEU:HD23	1:B:57:LEU:HA	1.84	0.43
1:B:333:LEU:HD13	1:H:343:SER:HB3	1.99	0.43
1:B:64:ARG:HG2	1:B:75:ARG:HD2	1.99	0.43
1:B:24:ASP:HB3	1:B:304:LYS:HE2	2.00	0.43
1:G:146:GLY:O	1:G:148:ARG:N	2.47	0.43
1:C:376:ILE:HG21	1:C:399:VAL:HG21	2.01	0.43
1:E:274:ILE:HD13	1:E:329:THR:HG23	1.99	0.43
1:A:357:PHE:HZ	1:A:413:ALA:HB2	1.84	0.43
1:H:376:ILE:HG21	1:H:399:VAL:HG21	1.99	0.42
1:E:204:ALA:HB3	1:E:214:LEU:HD22	2.01	0.42
1:G:242:VAL:HB	1:G:254:PHE:CG	2.55	0.42
1:G:274:ILE:HD13	1:G:329:THR:HG23	2.01	0.42
1:H:372:ASP:OD1	1:H:373:ARG:N	2.45	0.42
1:B:44:GLY:HA3	1:B:47:HIS:CE1	2.54	0.42
1:E:191:PHE:HA	1:E:206:GLY:HA3	2.02	0.42
1:B:1:MET:HG3	1:B:35:GLY:HA2	2.01	0.42
1:B:296:GLU:HA	1:B:304:LYS:HB3	2.01	0.41
1:E:170:GLU:HA	1:E:171:PRO:HD3	1.88	0.41
1:A:272:HIS:CG	1:A:299:ASN:HD22	2.38	0.41
1:A:101:ILE:HG12	1:A:109:TRP:HB2	2.02	0.41
1:E:234:LEU:HB2	1:E:243:GLU:HB2	2.01	0.41
1:E:294:TRP:CZ2	1:G:395:LEU:HD21	2.55	0.41
1:G:177:THR:HB	1:G:179:SER:H	1.84	0.41
1:G:162:GLU:HA	1:G:163:PRO:HA	1.74	0.41
1:G:290:TYR:HB3	1:G:310:LEU:HB3	2.02	0.41
1:A:3:CYS:HB2	1:A:333:LEU:HB2	2.03	0.41
1:B:29:SER:OG	1:B:80:TRP:NE1	2.45	0.41
1:E:177:THR:N	1:E:178:GLY:HA2	2.36	0.41
1:B:241:THR:OG1	1:B:242:VAL:N	2.53	0.41
1:A:12:GLN:OE1	1:A:76:GLN:NE2	2.54	0.41
1:A:170:GLU:HA	1:A:171:PRO:HD3	1.93	0.41
1:E:97:ASP:O	1:E:113:GLY:N	2.54	0.41
1:G:366:TYR:HA	1:G:367:PRO:HD3	1.98	0.41
1:E:242:VAL:HB	1:E:254:PHE:CG	2.56	0.41
1:A:392:SER:C	1:A:393:CYS:SG	2.99	0.41
1:H:380:ASP:HB3	1:H:385:GLU:OE1	2.21	0.41
1:E:294:TRP:HH2	1:G:370:CYS:HB3	1.86	0.40
1:E:128:ASN:N	1:E:128:ASN:OD1	2.54	0.40
1:B:204:ALA:HB3	1:B:214:LEU:HD22	2.02	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	409/427 (96%)	384 (94%)	25 (6%)	0	100	100
1	B	334/427 (78%)	312 (93%)	22 (7%)	0	100	100
1	C	74/427 (17%)	72 (97%)	2 (3%)	0	100	100
1	E	332/427 (78%)	309 (93%)	23 (7%)	0	100	100
1	G	403/427 (94%)	367 (91%)	36 (9%)	0	100	100
1	H	70/427 (16%)	61 (87%)	9 (13%)	0	100	100
All	All	1622/2562 (63%)	1505 (93%)	117 (7%)	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	343/351 (98%)	340 (99%)	3 (1%)	84	95
1	B	275/351 (78%)	272 (99%)	3 (1%)	80	94
1	C	70/351 (20%)	69 (99%)	1 (1%)	74	93
1	E	274/351 (78%)	272 (99%)	2 (1%)	88	96
1	G	341/351 (97%)	334 (98%)	7 (2%)	61	89
1	H	69/351 (20%)	63 (91%)	6 (9%)	13	43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1372/2106 (65%)	1350 (98%)	22 (2%)	70 92

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	392	SER
1	A	394	SER
1	A	396	MET
1	B	78	HIS
1	B	118	PHE
1	B	281	GLU
1	C	361	ASN
1	E	28	ARG
1	E	52	THR
1	G	166	ARG
1	G	257	GLU
1	G	321	ARG
1	G	349	GLU
1	G	392	SER
1	G	393	CYS
1	G	394	SER
1	H	357	PHE
1	H	380	ASP
1	H	401	PHE
1	H	406	LEU
1	H	410	TYR
1	H	412	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	27	GLN
1	B	221	HIS

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 9 ligands modelled in this entry, 4 are monoatomic - leaving 5 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	SO4	A	1418	-	4,4,4	0.23	0	6,6,6	0.07	0
3	SO4	B	1336	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	B	1337	-	4,4,4	0.24	0	6,6,6	0.07	0
3	SO4	E	1335	-	4,4,4	0.23	0	6,6,6	0.08	0
3	SO4	E	1336	-	4,4,4	0.23	0	6,6,6	0.08	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	SO4	A	1418	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1336	-	-	0/0/0/0	0/0/0/0
3	SO4	B	1337	-	-	0/0/0/0	0/0/0/0
3	SO4	E	1335	-	-	0/0/0/0	0/0/0/0
3	SO4	E	1336	-	-	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.

4 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1418	SO4	1	0
3	B	1336	SO4	1	0
3	B	1337	SO4	1	0
3	E	1335	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	413/427 (96%)	0.81	33 (7%) 15 5	60, 97, 139, 214	0
1	B	336/427 (78%)	0.90	23 (6%) 20 7	65, 88, 129, 169	0
1	C	76/427 (17%)	0.87	3 (3%) 43 18	72, 85, 115, 135	0
1	E	334/427 (78%)	0.95	37 (11%) 7 3	66, 98, 147, 241	0
1	G	409/427 (95%)	0.96	59 (14%) 3 1	70, 113, 161, 239	0
1	H	74/427 (17%)	0.96	13 (17%) 2 1	77, 140, 189, 210	0
All	All	1642/2562 (64%)	0.90	168 (10%) 9 3	60, 99, 154, 241	0

All (168) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	160	LEU	7.5
1	E	129	ASP	5.9
1	G	37	ILE	5.0
1	G	33	ASP	5.0
1	G	99	THR	4.5
1	E	125	LEU	4.3
1	G	191	PHE	4.2
1	G	132	ILE	4.1
1	A	129	ASP	4.0
1	G	32	GLY	3.9
1	H	378	LEU	3.9
1	G	100	VAL	3.9
1	G	150	TYR	3.8
1	A	115	CYS	3.7
1	B	201	ILE	3.6
1	E	68	LEU	3.6
1	G	212	PHE	3.6
1	G	173	LEU	3.5
1	G	344	MET	3.5

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Mol	Chain	Res	Type	RSRZ
1	H	409	TYR	3.4
1	E	109	TRP	3.3
1	E	78	HIS	3.3
1	H	366	TYR	3.3
1	E	48	SER	3.2
1	G	68	LEU	3.2
1	G	193	VAL	3.1
1	G	47	HIS	3.0
1	G	168	LEU	3.0
1	G	129	ASP	3.0
1	A	150	TYR	3.0
1	H	400	VAL	3.0
1	H	364	PHE	3.0
1	E	148	ARG	2.9
1	C	389	VAL	2.9
1	B	331	ILE	2.9
1	E	294	TRP	2.9
1	G	85	VAL	2.9
1	B	49	VAL	2.9
1	G	263	ILE	2.9
1	G	58	VAL	2.8
1	B	330	TRP	2.8
1	B	166	ARG	2.8
1	H	389	VAL	2.8
1	E	117	GLU	2.8
1	G	291	CYS	2.8
1	G	118	PHE	2.8
1	B	263	ILE	2.7
1	A	163	PRO	2.7
1	A	132	ILE	2.7
1	G	140	ASN	2.7
1	G	401	PHE	2.7
1	A	116	TYR	2.7
1	G	399	VAL	2.7
1	E	160	LEU	2.7
1	G	133	ALA	2.7
1	E	150	TYR	2.7
1	H	401	PHE	2.7
1	A	89	VAL	2.6
1	G	67	GLU	2.6
1	B	291	CYS	2.6
1	B	144	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	G	7	PHE	2.6
1	E	132	ILE	2.6
1	G	1	MET	2.6
1	B	83	VAL	2.6
1	E	161	GLN	2.6
1	A	92	VAL	2.5
1	A	229	TRP	2.5
1	G	329	THR	2.5
1	E	292	TRP	2.5
1	B	132	ILE	2.5
1	A	144	VAL	2.5
1	A	261	PHE	2.5
1	G	151	GLY	2.5
1	G	216	GLN	2.5
1	A	114	GLY	2.5
1	A	352	ILE	2.5
1	A	415	ILE	2.5
1	G	330	TRP	2.5
1	B	129	ASP	2.5
1	G	235	TRP	2.5
1	H	393	CYS	2.5
1	H	367	PRO	2.4
1	A	113	GLY	2.4
1	G	145	GLN	2.4
1	G	299	ASN	2.4
1	E	245	PHE	2.4
1	G	378	LEU	2.4
1	G	409	TYR	2.4
1	A	90	VAL	2.4
1	E	232	ILE	2.4
1	A	409	TYR	2.4
1	A	182	VAL	2.4
1	B	321	ARG	2.4
1	G	364	PHE	2.4
1	G	182	VAL	2.4
1	B	194	ILE	2.3
1	G	232	ILE	2.3
1	G	292	TRP	2.3
1	E	201	ILE	2.3
1	G	49	VAL	2.3
1	B	109	TRP	2.3
1	E	42	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	E	33	ASP	2.3
1	G	223	LEU	2.3
1	A	142	VAL	2.3
1	A	263	ILE	2.3
1	H	397	ILE	2.3
1	E	261	PHE	2.3
1	G	161	GLN	2.3
1	B	9	SER	2.3
1	E	26	PRO	2.3
1	E	310	LEU	2.3
1	H	399	VAL	2.2
1	G	80	TRP	2.2
1	E	40	LYS	2.2
1	B	160	LEU	2.2
1	A	294	TRP	2.2
1	A	122	HIS	2.2
1	A	223	LEU	2.2
1	A	364	PHE	2.2
1	G	101	ILE	2.2
1	E	331	ILE	2.2
1	G	347	TYR	2.2
1	A	9	SER	2.2
1	B	254	PHE	2.2
1	A	248	GLY	2.2
1	G	93	ALA	2.2
1	E	269	GLY	2.2
1	A	195	VAL	2.2
1	G	144	VAL	2.2
1	G	42	ALA	2.2
1	B	253	LEU	2.2
1	A	273	GLY	2.1
1	B	294	TRP	2.1
1	E	133	ALA	2.1
1	G	245	PHE	2.1
1	E	256	GLN	2.1
1	G	73	ALA	2.1
1	E	166	ARG	2.1
1	G	360	GLU	2.1
1	H	357	PHE	2.1
1	E	289	VAL	2.1
1	A	297	HIS	2.1
1	C	388	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	E	327	ALA	2.1
1	B	327	ALA	2.1
1	G	272	HIS	2.1
1	B	77	VAL	2.1
1	E	277	THR	2.1
1	A	378	LEU	2.1
1	E	49	VAL	2.1
1	G	386	LYS	2.1
1	G	189	LYS	2.0
1	G	88	PRO	2.0
1	H	417	PRO	2.0
1	A	17	LEU	2.0
1	G	43	CYS	2.0
1	A	201	ILE	2.0
1	A	277	THR	2.0
1	E	77	VAL	2.0
1	E	313	VAL	2.0
1	E	191	PHE	2.0
1	E	257	GLU	2.0
1	B	34	ASP	2.0
1	B	99	THR	2.0
1	C	364	PHE	2.0
1	E	7	PHE	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	FE	H	501	1/1	0.91	0.21	-0.37	102,102,102,102	0
3	SO4	B	1337	5/5	0.94	0.24	-0.63	117,117,117,117	0
2	FE	G	501	1/1	0.97	0.16	-0.70	133,133,133,133	0
2	FE	A	501	1/1	0.93	0.18	-0.73	109,109,109,109	0
2	FE	C	501	1/1	0.99	0.19	-0.77	87,87,87,87	0
3	SO4	E	1336	5/5	0.94	0.16	-3.35	121,121,121,121	0
3	SO4	A	1418	5/5	0.82	0.20	-	156,156,156,156	0
3	SO4	B	1336	5/5	0.90	0.19	-	135,135,135,135	0
3	SO4	E	1335	5/5	0.89	0.14	-	163,163,163,163	0

6.5 Other polymers [i](#)

There are no such residues in this entry.