Full wwPDB X-ray Structure Validation Report ⓘ

Mar 18, 2024 – 11:41 AM JST

PDB ID	:	5YFD
Title	:	Crystal structure of a new DPP III family member
Authors	:	Xu, T.; Liu, J.
Deposited on	:	2017-09-20
Resolution	:	1.76 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
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

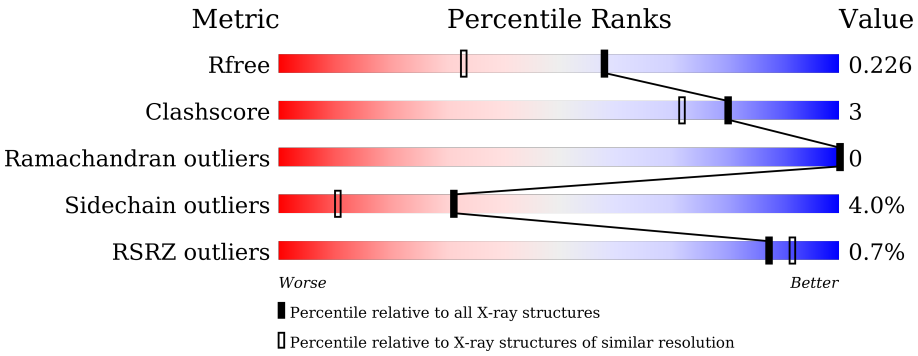
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

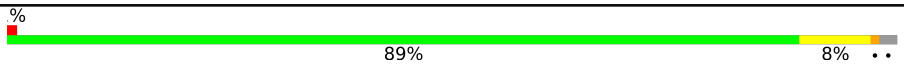
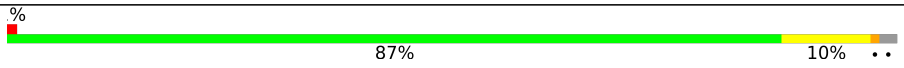
The reported resolution of this entry is 1.76 Å.

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}	130704	2340 (1.76-1.76)
Clashscore	141614	2466 (1.76-1.76)
Ramachandran outliers	138981	2437 (1.76-1.76)
Sidechain outliers	138945	2437 (1.76-1.76)
RSRZ outliers	127900	2298 (1.76-1.76)

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 of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. 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	703	
1	B	703	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 11736 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.

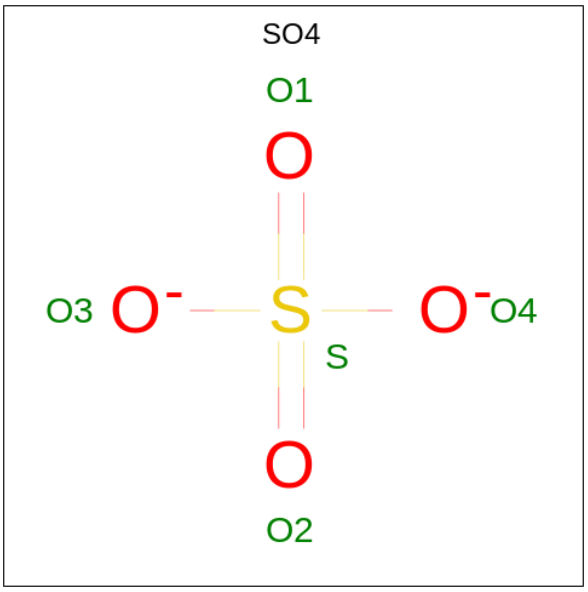
- Molecule 1 is a protein called Dipeptidyl peptidase 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	689	Total	C	N	O	S	0	5	0
			5421	3470	899	1044	8			
1	B	689	Total	C	N	O	S	0	12	0
			5454	3495	903	1048	8			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	696	LEU	-	expression tag	UNP B0S4Q0
A	697	GLU	-	expression tag	UNP B0S4Q0
A	698	HIS	-	expression tag	UNP B0S4Q0
A	699	HIS	-	expression tag	UNP B0S4Q0
A	700	HIS	-	expression tag	UNP B0S4Q0
A	701	HIS	-	expression tag	UNP B0S4Q0
A	702	HIS	-	expression tag	UNP B0S4Q0
A	703	HIS	-	expression tag	UNP B0S4Q0
B	696	LEU	-	expression tag	UNP B0S4Q0
B	697	GLU	-	expression tag	UNP B0S4Q0
B	698	HIS	-	expression tag	UNP B0S4Q0
B	699	HIS	-	expression tag	UNP B0S4Q0
B	700	HIS	-	expression tag	UNP B0S4Q0
B	701	HIS	-	expression tag	UNP B0S4Q0
B	702	HIS	-	expression tag	UNP B0S4Q0
B	703	HIS	-	expression tag	UNP B0S4Q0

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



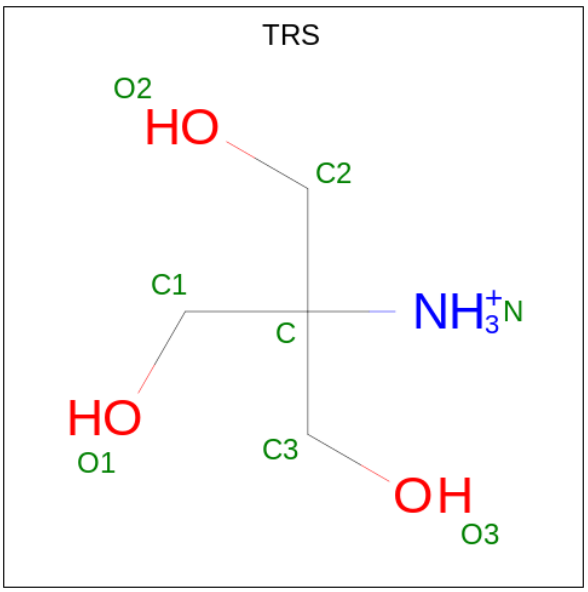
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	A	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0
2	B	1	Total O S 5 4 1	0	0

- Molecule 3 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cu 1 1	0	0
3	B	1	Total Cu 1 1	0	0

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code:

TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	B	1	Total	C	N	O	0	0
			8	4	1	3		

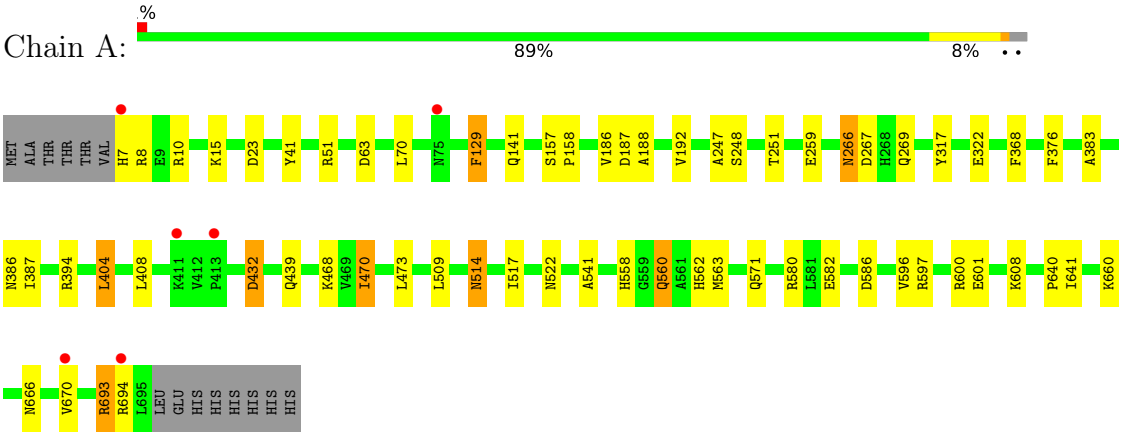
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	402	Total	O	0	0
			402	402		
5	B	404	Total	O	0	0
			404	404		

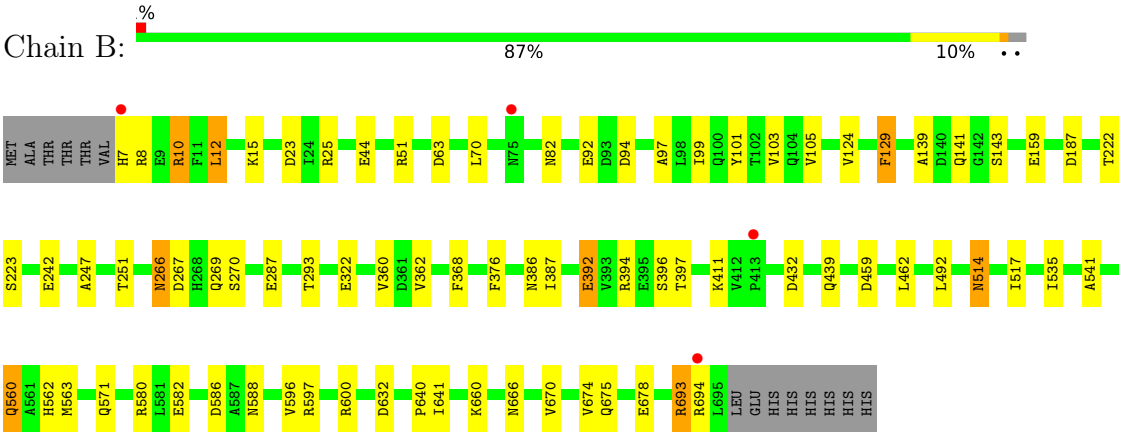
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes 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: Dipeptidyl peptidase 3



• Molecule 1: Dipeptidyl peptidase 3



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	58.46Å 207.14Å 58.99Å 90.00° 90.02° 90.00°	Depositor
Resolution (Å)	58.99 – 1.76 58.99 – 1.76	Depositor EDS
% Data completeness (in resolution range)	92.1 (58.99-1.76) 92.0 (58.99-1.76)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	11.38 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.8.0158	Depositor
R, R_{free}	0.180 , 0.217 0.191 , 0.226	Depositor DCC
R_{free} test set	6274 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	9.0	Xtriage
Anisotropy	0.224	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 19.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.016 for l,k,-h 0.478 for h,-k,-l 0.018 for l,-k,h	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	11736	wwPDB-VP
Average B, all atoms (Å^2)	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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, 0.333 respectively for untwinned datasets, and 0.375, 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, CU, TRS

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	0.95	3/5550 (0.1%)	1.00	18/7530 (0.2%)
1	B	0.97	8/5604 (0.1%)	1.02	24/7603 (0.3%)
All	All	0.96	11/11154 (0.1%)	1.01	42/15133 (0.3%)

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	92	GLU	CG-CD	8.43	1.64	1.51
1	B	92	GLU	CB-CG	6.56	1.64	1.52
1	B	678	GLU	CD-OE1	-6.44	1.18	1.25
1	B	322	GLU	CD-OE2	-5.88	1.19	1.25
1	B	223	SER	CB-OG	-5.78	1.34	1.42
1	B	242	GLU	CD-OE1	-5.74	1.19	1.25
1	A	601	GLU	CG-CD	5.64	1.60	1.51
1	A	322	GLU	CD-OE1	5.40	1.31	1.25
1	B	270	SER	CB-OG	-5.11	1.35	1.42
1	A	322	GLU	CD-OE2	-5.09	1.20	1.25
1	B	287	GLU	CD-OE1	5.01	1.31	1.25

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	693	ARG	NE-CZ-NH2	9.43	125.01	120.30
1	B	394	ARG	NE-CZ-NH2	8.44	124.52	120.30
1	B	92	GLU	OE1-CD-OE2	-8.27	113.38	123.30
1	A	394	ARG	NE-CZ-NH2	8.22	124.41	120.30
1	B	693	ARG	NE-CZ-NH2	7.87	124.23	120.30
1	B	597	ARG	NE-CZ-NH1	-7.61	116.49	120.30
1	B	10	ARG	NE-CZ-NH1	7.47	124.03	120.30
1	A	693	ARG	NE-CZ-NH1	-7.41	116.59	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	693	ARG	NE-CZ-NH1	-7.41	116.59	120.30
1	B	10	ARG	NE-CZ-NH2	-6.75	116.92	120.30
1	B	600	ARG	NE-CZ-NH2	-6.71	116.95	120.30
1	A	597	ARG	NE-CZ-NH2	-6.69	116.96	120.30
1	B	63	ASP	CB-CG-OD1	6.65	124.28	118.30
1	A	404	LEU	CB-CG-CD2	6.59	122.20	111.00
1	B	12	LEU	CB-CG-CD1	6.51	122.08	111.00
1	B	580	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	B	597	ARG	NE-CZ-NH2	6.41	123.50	120.30
1	A	10	ARG	NE-CZ-NH2	-6.31	117.14	120.30
1	A	580	ARG	NE-CZ-NH1	6.29	123.44	120.30
1	A	432	ASP	CB-CG-OD2	-6.20	112.72	118.30
1	B	492	LEU	CB-CG-CD2	6.10	121.37	111.00
1	A	10	ARG	NE-CZ-NH1	6.03	123.32	120.30
1	B	187	ASP	CB-CG-OD1	6.03	123.72	118.30
1	A	404	LEU	CB-CG-CD1	5.91	121.05	111.00
1	B	600	ARG	NE-CZ-NH1	5.90	123.25	120.30
1	B	25	ARG	NE-CZ-NH1	5.76	123.18	120.30
1	B	459	ASP	CB-CG-OD1	5.71	123.44	118.30
1	A	600	ARG	NE-CZ-NH2	-5.59	117.50	120.30
1	B	267	ASP	CB-CG-OD2	-5.51	113.34	118.30
1	A	597	ARG	NE-CZ-NH1	5.49	123.05	120.30
1	B	187	ASP	CB-CG-OD2	-5.48	113.37	118.30
1	A	51	ARG	NE-CZ-NH2	-5.42	117.59	120.30
1	B	51	ARG	NE-CZ-NH2	-5.38	117.61	120.30
1	B	432	ASP	CB-CG-OD2	-5.35	113.48	118.30
1	A	187	ASP	CB-CG-OD1	5.34	123.11	118.30
1	B	586	ASP	CB-CG-OD1	5.30	123.07	118.30
1	A	267	ASP	CB-CG-OD2	-5.20	113.62	118.30
1	B	129	PHE	CB-CG-CD1	5.16	124.41	120.80
1	A	129	PHE	CB-CG-CD1	5.15	124.40	120.80
1	A	63	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	586	ASP	CB-CG-OD1	5.12	122.91	118.30
1	B	392	GLU	CA-CB-CG	5.03	124.46	113.40

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	5421	0	5413	28	0
1	B	5454	0	5474	31	0
2	A	25	0	0	0	0
2	B	20	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	8	0	11	1	0
5	A	402	0	0	5	0
5	B	404	0	0	4	0
All	All	11736	0	10898	59	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 3.

All (59) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:608:LYS:NZ	5:A:901:HOH:O	1.81	1.13
1:B:360:VAL:HG11	5:B:909:HOH:O	1.59	0.99
1:A:186[A]:VAL:HG11	1:A:317:TYR:CE1	2.10	0.86
1:A:582:GLU:OE2	5:A:902:HOH:O	2.02	0.77
1:B:439:GLN:OE1	5:B:901:HOH:O	2.07	0.72
1:B:97:ALA:HB3	1:B:124[B]:VAL:HG13	1.73	0.70
1:A:571:GLN:HE22	1:A:640:PRO:HA	1.57	0.69
1:B:582:GLU:OE2	5:B:902:HOH:O	2.11	0.68
1:A:439:GLN:OE1	5:A:903:HOH:O	2.12	0.67
1:A:247:ALA:O	1:A:251:THR:HG23	1.94	0.67
1:B:571:GLN:HE22	1:B:640:PRO:HA	1.61	0.65
1:B:632[B]:ASP:OD1	5:B:903:HOH:O	2.16	0.61
1:B:293:THR:HG23	1:B:397[A]:THR:HG21	1.82	0.60
1:B:541:ALA:CB	1:B:596[A]:VAL:HG11	2.32	0.60
1:A:541:ALA:CB	1:A:596[A]:VAL:HG11	2.33	0.59
1:B:97:ALA:HB3	1:B:124[B]:VAL:CG1	2.32	0.59
1:A:383:ALA:HB1	1:A:408:LEU:HD11	1.85	0.58
1:B:139:ALA:O	1:B:143[A]:SER:OG	2.16	0.58
1:B:247:ALA:O	1:B:251[A]:THR:HG23	2.04	0.57
1:B:392:GLU:N	4:B:805:TRS:O1	2.31	0.57
1:A:70:LEU:HD13	1:A:141:GLN:HG3	1.88	0.56
1:B:70:LEU:HD13	1:B:141:GLN:HG3	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:571:GLN:NE2	1:A:641:ILE:H	2.04	0.55
1:B:560:GLN:NE2	1:B:563:MET:H	2.05	0.55
1:B:396:SER:OG	1:B:397[A]:THR:HG23	2.06	0.55
1:B:97:ALA:CB	1:B:124[B]:VAL:HG13	2.36	0.54
1:B:560:GLN:HE21	1:B:563:MET:H	1.57	0.53
1:A:558:HIS:HD2	5:A:1193:HOH:O	1.91	0.53
1:B:666:ASN:HD21	1:B:693:ARG:HE	1.55	0.52
1:B:560:GLN:HE22	1:B:562:HIS:HB2	1.75	0.52
1:A:186[A]:VAL:HG11	1:A:317:TYR:CZ	2.43	0.52
1:A:41:TYR:CZ	1:A:259:GLU:HG2	2.44	0.52
1:A:514:ASN:HD22	1:A:517:ILE:H	1.57	0.51
1:A:666:ASN:HD21	1:A:693:ARG:HE	1.57	0.51
1:A:560:GLN:NE2	1:A:563:MET:H	2.09	0.50
1:B:266:ASN:ND2	1:B:269:GLN:H	2.09	0.50
1:A:541:ALA:HB3	1:A:596[A]:VAL:HG11	1.93	0.50
1:B:571:GLN:NE2	1:B:641:ILE:H	2.10	0.49
1:A:560:GLN:HE21	1:A:563:MET:H	1.60	0.49
1:B:670:VAL:HG21	1:B:675:GLN:NE2	2.27	0.49
1:A:560:GLN:HE22	1:A:562:HIS:HB2	1.78	0.49
1:B:514:ASN:HD22	1:B:517:ILE:H	1.60	0.48
1:A:186[A]:VAL:HG11	1:A:317:TYR:CD1	2.49	0.48
1:B:541:ALA:HB3	1:B:596[A]:VAL:HG11	1.97	0.46
1:A:266:ASN:ND2	1:A:269:GLN:H	2.13	0.46
1:B:94:ASP:O	1:B:124[B]:VAL:HG11	2.16	0.46
1:A:41:TYR:CE1	1:A:259:GLU:HG2	2.51	0.45
1:B:541:ALA:HB1	1:B:596[A]:VAL:HG11	1.97	0.45
1:A:248:SER:O	1:A:251:THR:OG1	2.33	0.45
1:A:188:ALA:O	1:A:192:VAL:HG23	2.17	0.44
1:B:99:ILE:O	1:B:103:VAL:HG23	2.18	0.44
1:A:470:ILE:HA	5:A:1004:HOH:O	2.18	0.43
1:A:571:GLN:HE22	1:A:641:ILE:H	1.66	0.43
1:A:541:ALA:HB1	1:A:596[A]:VAL:HG11	2.01	0.42
1:B:101:TYR:CZ	1:B:105:VAL:HG21	2.55	0.42
1:B:535:ILE:HD13	1:B:535:ILE:HA	1.85	0.42
1:B:571:GLN:HE22	1:B:641:ILE:H	1.67	0.42
1:B:462:LEU:HD12	1:B:462:LEU:N	2.34	0.41
1:A:157:SER:HA	1:A:158:PRO:C	2.40	0.41

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	692/703 (98%)	676 (98%)	16 (2%)	0	100	100
1	B	699/703 (99%)	684 (98%)	15 (2%)	0	100	100
All	All	1391/1406 (99%)	1360 (98%)	31 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	586/594 (99%)	564 (96%)	22 (4%)	33	11
1	B	593/594 (100%)	567 (96%)	26 (4%)	28	8
All	All	1179/1188 (99%)	1131 (96%)	48 (4%)	31	10

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	7	HIS
1	A	8	ARG
1	A	15	LYS
1	A	23	ASP
1	A	129	PHE
1	A	266	ASN
1	A	368	PHE
1	A	376	PHE

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Mol	Chain	Res	Type
1	A	386	ASN
1	A	387	ILE
1	A	404	LEU
1	A	432	ASP
1	A	468	LYS
1	A	470	ILE
1	A	473	LEU
1	A	509	LEU
1	A	514	ASN
1	A	522	ASN
1	A	560	GLN
1	A	660	LYS
1	A	670	VAL
1	A	694	ARG
1	B	7	HIS
1	B	8[A]	ARG
1	B	8[B]	ARG
1	B	10	ARG
1	B	12	LEU
1	B	15	LYS
1	B	23	ASP
1	B	44	GLU
1	B	82	ASN
1	B	129	PHE
1	B	159	GLU
1	B	222[A]	THR
1	B	222[B]	THR
1	B	266	ASN
1	B	362	VAL
1	B	368	PHE
1	B	376	PHE
1	B	386	ASN
1	B	387	ILE
1	B	411	LYS
1	B	514	ASN
1	B	560	GLN
1	B	588	ASN
1	B	660	LYS
1	B	674	VAL
1	B	694	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	100	GLN
1	A	141	GLN
1	A	191	ASN
1	A	266	ASN
1	A	386	ASN
1	A	401	ASN
1	A	514	ASN
1	A	558	HIS
1	A	560	GLN
1	A	571	GLN
1	A	666	ASN
1	B	100	GLN
1	B	141	GLN
1	B	266	ASN
1	B	386	ASN
1	B	401	ASN
1	B	439	GLN
1	B	514	ASN
1	B	560	GLN
1	B	571	GLN
1	B	666	ASN
1	B	675	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 12 ligands modelled in this entry, 2 are monoatomic - leaving 10 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	$\#\|Z\| > 2$
2	SO4	A	805	-	4,4,4	0.64	0	6,6,6	0.35	0
2	SO4	A	801	-	4,4,4	0.54	0	6,6,6	0.53	0
2	SO4	A	803	-	4,4,4	0.51	0	6,6,6	0.26	0
2	SO4	B	801	-	4,4,4	0.41	0	6,6,6	0.84	0
2	SO4	A	802	-	4,4,4	0.44	0	6,6,6	0.67	0
4	TRS	B	805	-	7,7,7	1.37	1 (14%)	9,9,9	1.95	2 (22%)
2	SO4	A	804	-	4,4,4	1.56	1 (25%)	6,6,6	1.38	1 (16%)
2	SO4	B	803	-	4,4,4	0.47	0	6,6,6	0.28	0
2	SO4	B	802	-	4,4,4	0.44	0	6,6,6	0.81	0
2	SO4	B	804	-	4,4,4	0.47	0	6,6,6	0.33	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	TRS	B	805	-	-	5/9/9/9	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	804	SO4	O2-S	2.46	1.59	1.46
4	B	805	TRS	O1-C1	-2.27	1.34	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	805	TRS	C2-C-C1	3.72	122.35	110.81
4	B	805	TRS	O2-C2-C	3.25	121.30	111.00
2	A	804	SO4	O4-S-O1	-2.45	96.53	109.31

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	805	TRS	N-C-C3-O3
4	B	805	TRS	C3-C-C1-O1
4	B	805	TRS	N-C-C1-O1
4	B	805	TRS	C2-C-C1-O1
4	B	805	TRS	C1-C-C3-O3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	805	TRS	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, 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	689/703 (98%)	-0.20	6 (0%)	84	89	4, 9, 21, 42	0
1	B	689/703 (98%)	-0.17	4 (0%)	89	92	4, 8, 21, 38	0
All	All	1378/1406 (98%)	-0.19	10 (0%)	87	92	4, 9, 21, 42	0

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	413	PRO	3.8
1	B	413	PRO	3.1
1	A	75	ASN	3.1
1	B	75	ASN	2.9
1	B	7	HIS	2.5
1	A	7	HIS	2.5
1	B	694	ARG	2.4
1	A	670	VAL	2.4
1	A	411	LYS	2.2
1	A	694	ARG	2.1

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

There are no monosaccharides 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. 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	B-factors(Å^2)	Q<0.9
4	TRS	B	805	8/8	0.85	0.21	15,17,24,27	0
2	SO4	B	802	5/5	0.92	0.18	28,35,38,45	0
2	SO4	A	805	5/5	0.92	0.18	35,41,43,45	0
2	SO4	B	804	5/5	0.93	0.16	33,39,43,45	0
2	SO4	A	802	5/5	0.93	0.18	35,38,38,45	0
2	SO4	A	804	5/5	0.94	0.12	14,16,20,20	0
2	SO4	A	801	5/5	0.95	0.13	22,23,27,29	0
2	SO4	B	801	5/5	0.96	0.12	18,19,23,23	0
2	SO4	A	803	5/5	0.96	0.13	36,38,41,42	0
3	CU	B	806	1/1	0.97	0.05	16,16,16,16	1
2	SO4	B	803	5/5	0.97	0.15	35,38,42,45	0
3	CU	A	806	1/1	0.98	0.04	15,15,15,15	1

6.5 Other polymers (i)

There are no such residues in this entry.