Full wwPDB X-ray Structure Validation Report (i)

Jun 25, 2024 – 11:45 AM EDT

PDB ID	:	6H4I
Title	:	Usp28 catalytic domain apo
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Deposited on	:	2018-07-21
Resolution	:	3.22 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 (i) 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 (i)) were used in the production of this report:

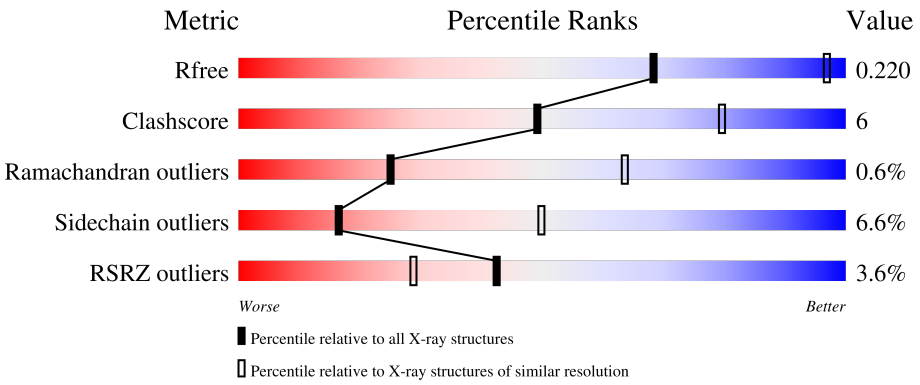
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.22 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	1335 (3.24-3.20)
Clashscore	141614	1460 (3.24-3.20)
Ramachandran outliers	138981	1437 (3.24-3.20)
Sidechain outliers	138945	1436 (3.24-3.20)
RSRZ outliers	127900	1291 (3.24-3.20)

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	560	2% 66% 15% • 19%
1	C	560	3% 63% 17% 19%

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	SO4	A	802	-	-	-	X

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 7310 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.

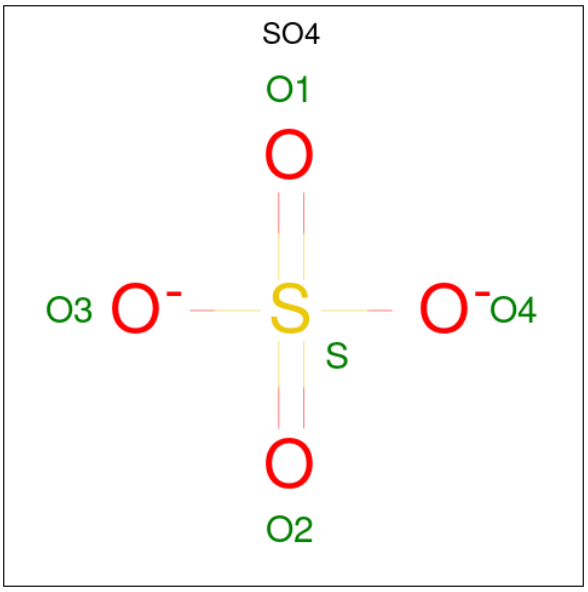
- Molecule 1 is a protein called Ubiquitin carboxyl-terminal hydrolase 28.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	456	3692	2354	625	690	10	13	0	0	0
1	C	451	3608	2305	603	678	9	13	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	148	GLY	ASN	conflict	UNP Q96RU2
C	148	GLY	ASN	conflict	UNP Q96RU2

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



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

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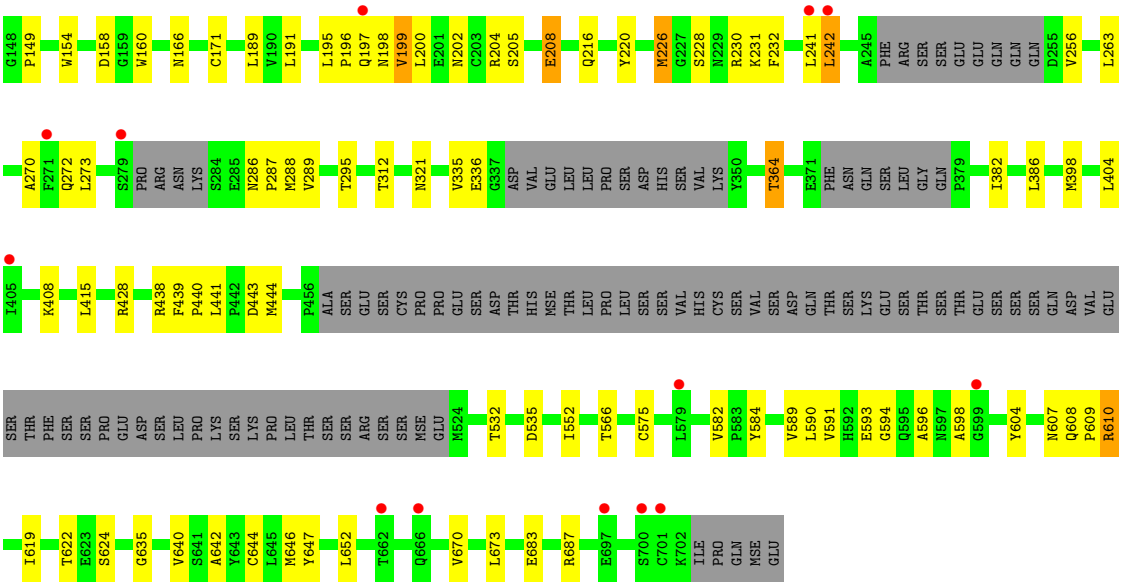
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	O	S		
2	A	1	5	4	1	0	0

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.

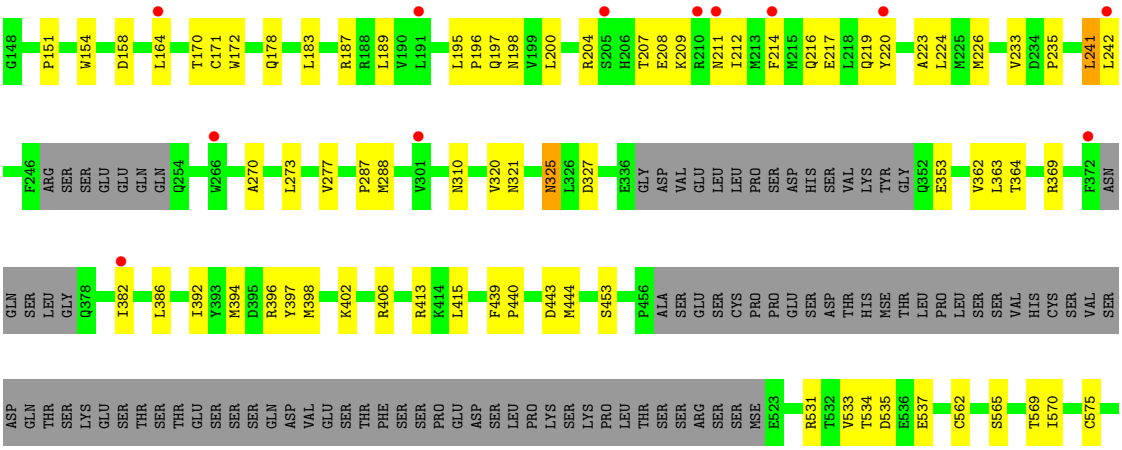
• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 28

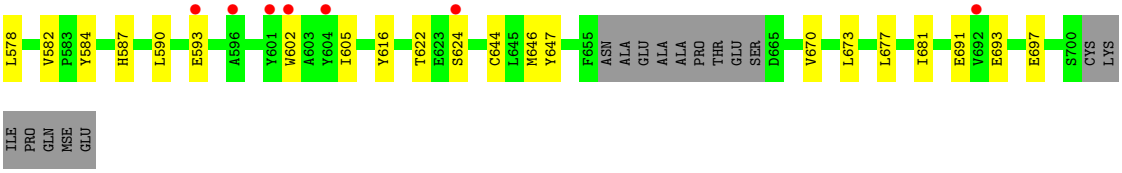
Chain A:



• Molecule 1: Ubiquitin carboxyl-terminal hydrolase 28

Chain C:




L578
V582
P583
Y584
H587
L590
E593
A596
Y601
W602
A603
Y604
I605
Y616
T622
E623
S624
C644
L645
M646
Y647
F655
ASN
ALA
GLU
ALA
ALA
PRO
THR
GLU
SER
D665
V670
L673
L677
I681
E691
V692
E693
E697
S700
CYS
LYS
ILE
PRO
GLN
MSE
GLU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α, β, γ	105.54Å 200.52Å 207.24Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.59 – 3.22 49.58 – 3.22	Depositor EDS
% Data completeness (in resolution range)	72.1 (49.59-3.22) 72.1 (49.58-3.22)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.70 (at 3.25Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.171 , 0.196 0.193 , 0.220	Depositor DCC
R_{free} test set	1096 reflections (4.23%)	wwPDB-VP
Wilson B-factor (Å^2)	109.5	Xtriage
Anisotropy	0.151	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 115.1	EDS
L-test for twinning[2]	$< \|L\| > = 0.44$, $< L^2 > = 0.27$	Xtriage
Estimated twinning fraction	0.028 for -h,-l,-k	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	7310	wwPDB-VP
Average B, all atoms (Å^2)	144.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.05% 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 (i)

5.1 Standard geometry (i)

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	0.47	0/3770	0.65	0/5092
1	C	0.47	0/3681	0.63	0/4976
All	All	0.47	0/7451	0.64	0/10068

There are no bond length outliers.

There are no bond angle outliers.

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	3692	0	3518	44	0
1	C	3608	0	3403	45	0
2	A	10	0	0	0	0
All	All	7310	0	6921	84	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 6.

All (84) 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:607:ASN:HD22	1:A:610:ARG:HB2	1.38	0.86
1:A:364:THR:HG23	1:A:646:MSE:HG3	1.67	0.76
1:A:205:SER:HB3	1:A:208:GLU:HB2	1.72	0.71
1:A:593:GLU:HA	1:A:640:VAL:HG12	1.73	0.70
1:C:440:PRO:HG2	1:C:443:ASP:HB2	1.77	0.67
1:A:440:PRO:HG2	1:A:443:ASP:HB2	1.82	0.61
1:C:183:LEU:HD11	1:C:646:MSE:HE1	1.82	0.61
1:A:590:LEU:HD12	1:A:644:CYS:HB3	1.83	0.59
1:A:231:LYS:HE2	1:C:569:THR:CG2	2.33	0.59
1:C:204:ARG:HB3	1:C:208:GLU:HB3	1.85	0.58
1:A:228:SER:OG	1:A:230:ARG:HG3	2.05	0.57
1:C:196:PRO:HG2	1:C:277:VAL:HG21	1.87	0.56
1:C:439:PHE:HB3	1:C:444:MSE:HE2	1.87	0.56
1:C:593:GLU:HG2	1:C:602:TRP:HE1	1.71	0.56
1:C:534:THR:HG23	1:C:537:GLU:H	1.71	0.56
1:A:683:GLU:O	1:A:687:ARG:HG2	2.06	0.55
1:A:216:GLN:O	1:A:220:TYR:HD1	1.90	0.55
1:A:589:VAL:HG13	1:A:604:TYR:HB2	1.89	0.55
1:A:652:LEU:HD12	1:A:652:LEU:H	1.71	0.55
1:A:295:THR:HG22	1:A:312:THR:HG22	1.88	0.55
1:A:154:TRP:HA	1:A:231:LYS:HD2	1.90	0.53
1:C:396:ARG:HD2	1:C:397:TYR:CE1	2.44	0.52
1:A:166:ASN:ND2	1:A:171:CYS:HB3	2.24	0.52
1:C:392:ILE:CG2	1:C:394:MSE:HE2	2.40	0.52
1:C:439:PHE:CG	1:C:440:PRO:HD2	2.44	0.52
1:C:590:LEU:HD12	1:C:644:CYS:HB3	1.92	0.51
1:A:398:MSE:HE3	1:A:582:VAL:HG21	1.92	0.51
1:C:170:THR:HB	1:C:172:TRP:CD1	2.46	0.51
1:A:232:PHE:CD1	1:A:619:ILE:HG23	2.46	0.50
1:A:270:ALA:HA	1:A:273:LEU:HD12	1.92	0.50
1:C:325:ASN:HD21	1:C:327:ASP:HB2	1.77	0.50
1:C:214:PHE:HA	1:C:241:LEU:HD13	1.94	0.50
1:A:439:PHE:HB3	1:A:444:MSE:HE2	1.94	0.48
1:C:364:THR:HG22	1:C:646:MSE:CG	2.43	0.48
1:C:364:THR:HG22	1:C:646:MSE:HG2	1.95	0.48
1:A:439:PHE:CG	1:A:440:PRO:HD2	2.49	0.48
1:C:216:GLN:O	1:C:220:TYR:HD1	1.97	0.47
1:A:242:LEU:HD11	1:A:263:LEU:HD12	1.95	0.47
1:A:189:LEU:HD21	1:A:287:PRO:HB2	1.97	0.47
1:A:584:TYR:HB3	1:A:647:TYR:HB3	1.97	0.47
1:A:670:VAL:O	1:A:673:LEU:HB2	2.15	0.46
1:A:196:PRO:HB2	1:A:198:ASN:OD1	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:272:GLN:HE21	1:A:286:ASN:HD22	1.63	0.46
1:C:270:ALA:HA	1:C:273:LEU:HD12	1.98	0.46
1:A:607:ASN:ND2	1:A:610:ARG:HB2	2.20	0.46
1:C:320:VAL:HG23	1:C:369:ARG:HG3	1.96	0.45
1:C:584:TYR:HB3	1:C:647:TYR:HB3	1.98	0.45
1:A:404:LEU:HD11	1:A:408:LYS:HE2	1.97	0.45
1:C:224:LEU:HB3	1:C:233:VAL:HG11	1.97	0.45
1:C:224:LEU:HA	1:C:681:ILE:HD11	1.98	0.45
1:C:398:MSE:HE2	1:C:582:VAL:HG11	1.98	0.45
1:C:590:LEU:HB2	1:C:644:CYS:HB3	1.99	0.45
1:C:151:PRO:HA	1:C:154:TRP:HD1	1.82	0.44
1:C:415:LEU:HB3	1:C:570:ILE:HD11	1.99	0.44
1:C:183:LEU:HD11	1:C:646:MSE:CE	2.47	0.44
1:C:392:ILE:HG23	1:C:394:MSE:HE2	2.00	0.44
1:C:362:VAL:CG1	1:C:646:MSE:HE3	2.48	0.44
1:A:149:PRO:HB3	1:C:562:CYS:SG	2.58	0.43
1:A:199:VAL:HA	1:A:202:ASN:HB2	2.00	0.43
1:A:591:VAL:HA	1:A:642:ALA:HA	2.00	0.43
1:A:321:ASN:OD1	1:A:382:ILE:HG23	2.19	0.43
1:C:189:LEU:HD21	1:C:287:PRO:HB2	2.00	0.43
1:A:160:TRP:HZ3	1:C:575:CYS:HB3	1.83	0.43
1:C:363:LEU:HD23	1:C:394:MSE:HE3	1.99	0.43
1:A:231:LYS:CE	1:C:569:THR:HG21	2.49	0.43
1:A:191:LEU:HD13	1:A:226:MSE:HE2	2.01	0.42
1:C:402:LYS:HE2	1:C:406:ARG:NH1	2.34	0.42
1:C:209:LYS:HA	1:C:212:ILE:HD12	2.01	0.42
1:C:164:LEU:HB3	1:C:235:PRO:HG3	2.02	0.42
1:C:587:HIS:CD2	1:C:646:MSE:HE2	2.54	0.42
1:A:191:LEU:HD11	1:A:226:MSE:HG3	2.01	0.42
1:A:590:LEU:HB2	1:A:644:CYS:HB3	2.01	0.42
1:A:596:ALA:C	1:A:598:ALA:H	2.23	0.42
1:A:608:GLN:N	1:A:609:PRO:HD2	2.35	0.41
1:A:231:LYS:HE2	1:C:569:THR:HG21	2.00	0.41
1:C:178:GLN:HG2	1:C:616:TYR:CD2	2.55	0.41
1:C:223:ALA:O	1:C:681:ILE:HD11	2.20	0.41
1:C:670:VAL:O	1:C:673:LEU:HB2	2.20	0.41
1:A:635:GLY:HA2	1:A:640:VAL:O	2.21	0.41
1:A:415:LEU:HD22	1:A:566:THR:HG23	2.02	0.41
1:A:441:LEU:HD22	1:A:552:ILE:HG13	2.03	0.41
1:A:197:GLN:HA	1:A:200:LEU:HB2	2.02	0.41
1:C:605:ILE:HB	1:C:616:TYR:CE1	2.57	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:219:GLN:HE21	1:C:677:LEU:HD11	1.86	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	444/560 (79%)	421 (95%)	22 (5%)	1 (0%)	47	79
1	C	439/560 (78%)	404 (92%)	31 (7%)	4 (1%)	17	55
All	All	883/1120 (79%)	825 (93%)	53 (6%)	5 (1%)	25	63

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	594	GLY
1	C	197	GLN
1	C	531	ARG
1	C	171	CYS
1	C	158	ASP

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.

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	396/501 (79%)	373 (94%)	23 (6%)	20	54
1	C	382/501 (76%)	354 (93%)	28 (7%)	14	46
All	All	778/1002 (78%)	727 (93%)	51 (7%)	16	50

All (51) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	158	ASP
1	A	195	LEU
1	A	199	VAL
1	A	204	ARG
1	A	208	GLU
1	A	226	MSE
1	A	241	LEU
1	A	242	LEU
1	A	256	VAL
1	A	288	MSE
1	A	289	VAL
1	A	335	VAL
1	A	336	GLU
1	A	364	THR
1	A	386	LEU
1	A	428	ARG
1	A	438	ARG
1	A	532	THR
1	A	535	ASP
1	A	575	CYS
1	A	610	ARG
1	A	622	THR
1	A	624	SER
1	C	187	ARG
1	C	195	LEU
1	C	198	ASN
1	C	200	LEU
1	C	207	THR
1	C	211	ASN
1	C	217	GLU
1	C	226	MSE
1	C	241	LEU

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Mol	Chain	Res	Type
1	C	242	LEU
1	C	288	MSE
1	C	310	ASN
1	C	321	ASN
1	C	325	ASN
1	C	353	GLU
1	C	382	ILE
1	C	386	LEU
1	C	413	ARG
1	C	453	SER
1	C	533	VAL
1	C	535	ASP
1	C	565	SER
1	C	578	LEU
1	C	622	THR
1	C	624	SER
1	C	691	GLU
1	C	693	GLU
1	C	697	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	152	ASN
1	A	166	ASN
1	A	272	GLN
1	A	315	GLN
1	A	325	ASN
1	A	607	ASN
1	C	211	ASN
1	C	219	GLN
1	C	315	GLN
1	C	325	ASN
1	C	617	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

2 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	802	-	4,4,4	0.16	0	6,6,6	0.14	0
2	SO4	A	801	-	4,4,4	0.18	0	6,6,6	0.15	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.

No monomer is involved in short contacts.

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	443/560 (79%)	0.36	13 (2%)	51	37	78, 125, 208, 236	0
1	C	438/560 (78%)	0.34	19 (4%)	35	23	80, 161, 224, 246	0
All	All	881/1120 (78%)	0.35	32 (3%)	42	29	78, 139, 221, 246	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	205	SER	6.2
1	A	271	PHE	5.5
1	C	604	TYR	3.5
1	C	211	ASN	3.4
1	C	692	VAL	3.1
1	A	701	CYS	3.0
1	A	242	LEU	3.0
1	C	266	TRP	3.0
1	C	191	LEU	2.9
1	C	596	ALA	2.8
1	C	242	LEU	2.8
1	C	602	TRP	2.8
1	C	164	LEU	2.8
1	A	700	SER	2.8
1	C	220	TYR	2.7
1	C	372	PHE	2.6
1	C	301	VAL	2.6
1	A	662	THR	2.6
1	A	666	GLN	2.5
1	C	624	SER	2.5
1	A	599	GLY	2.5
1	C	382	ILE	2.4
1	A	697	GLU	2.3
1	A	405	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	601	TYR	2.2
1	C	593	GLU	2.2
1	C	214	PHE	2.2
1	C	210	ARG	2.1
1	A	279	SER	2.1
1	A	579	LEU	2.1
1	A	241	LEU	2.1
1	A	197	GLN	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 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, 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	B-factors(Å^2)	Q<0.9
2	SO4	A	802	5/5	0.70	0.45	198,199,199,199	0
2	SO4	A	801	5/5	0.84	0.27	134,135,135,135	5

6.5 Other polymers (i)

There are no such residues in this entry.