Full wwPDB X-ray Structure Validation Report (i)

Jun 13, 2024 – 09:11 AM EDT

PDB ID	:	4EZW
Title	:	Crystal structure of the substrate binding domain of E.coli DnaK in complex with the designer peptide NRLLLTG
Authors	:	Zahn, M.; Straeter, N.
Deposited on	:	2012-05-03
Resolution	:	1.80 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:

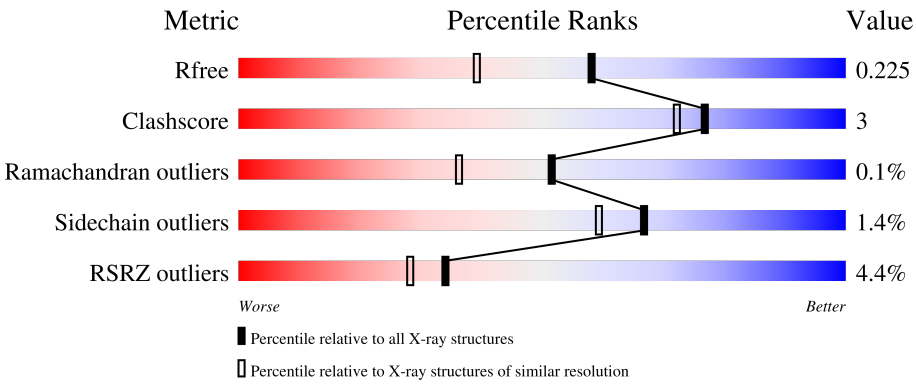
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	2.36.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 1.80 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	5950 (1.80-1.80)
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)
RSRZ outliers	127900	5850 (1.80-1.80)

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	219	6%, 88%, 9%
1	B	219	3%, 88%, 10%
1	C	219	3%, 92%, 6%
1	D	219	4%, 90%, 8%
2	E	7	14%, 100%

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Mol	Chain	Length	Quality of chain
2	F	7	14% 100%
2	G	7	29% 86% 14%
2	H	7	14% 100%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 7447 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.

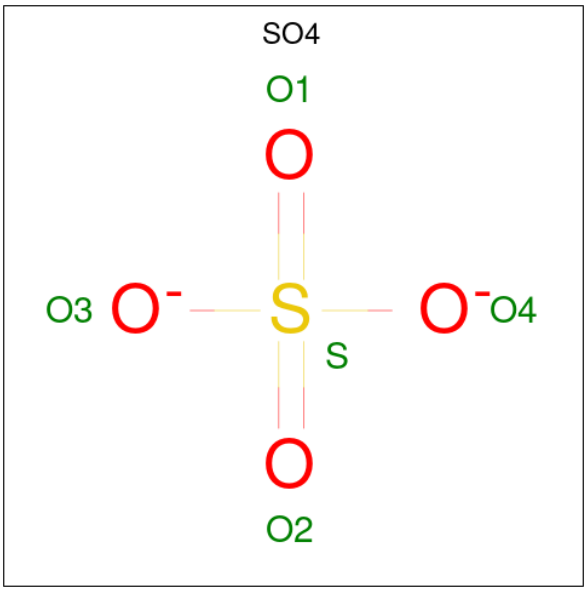
- Molecule 1 is a protein called Chaperone protein DnaK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	214	1626	1000	285	335	6	0	1	0
1	B	215	1635	1005	287	337	6	0	1	0
1	C	215	1644	1011	289	338	6	0	2	0
1	D	216	1661	1022	292	340	7	0	4	0

- Molecule 2 is a protein called synthetic peptide NRLLLTG.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	E	7	55	34	11	10	0	0	0
2	F	7	55	34	11	10	0	0	0
2	G	7	55	34	11	10	0	0	0
2	H	7	55	34	11	10	0	0	0

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	165	Total O 165 165	0	0
4	B	175	Total O 175 175	0	0
4	C	140	Total O 140 140	0	0

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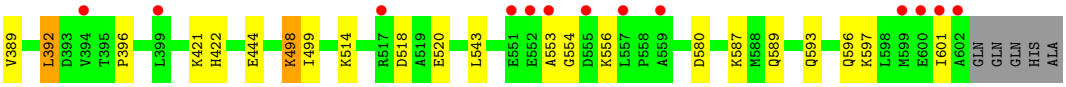
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	117	Total O 117 117	0	0
4	E	4	Total O 4 4	0	0
4	F	6	Total O 6 6	0	0
4	G	6	Total O 6 6	0	0
4	H	3	Total O 3 3	0	0

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.

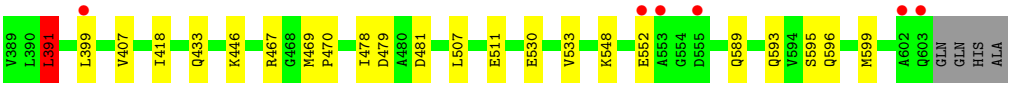
• Molecule 1: Chaperone protein DnaK

Chain A:



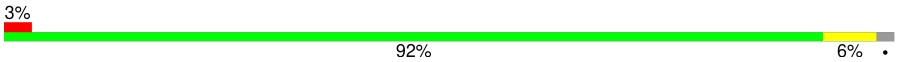
• Molecule 1: Chaperone protein DnaK

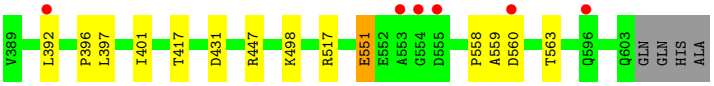
Chain B:



• Molecule 1: Chaperone protein DnaK

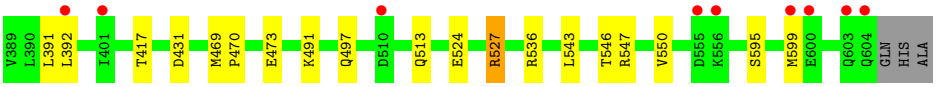
Chain C:





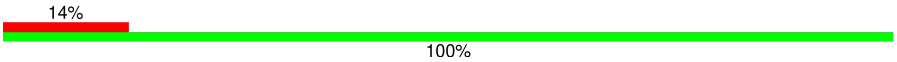
• Molecule 1: Chaperone protein DnaK

Chain D:

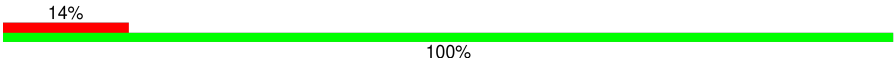


• Molecule 2: synthetic peptide NRLLLTG

Chain E:



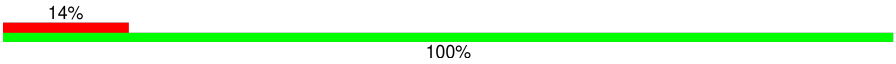
• Molecule 2: synthetic peptide NRLLLTG

Chain F: 

• Molecule 2: synthetic peptide NRLLLTG

Chain G:

• Molecule 2: synthetic peptide NRLLLTG

Chain H: 

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α, β, γ	157.12Å 78.03Å 89.48Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	24.70 – 1.80 24.69 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.6 (24.70-1.80) 99.6 (24.69-1.80)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.68 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.6.0117	Depositor
R, R_{free}	0.193 , 0.226 0.192 , 0.225	Depositor DCC
R_{free} test set	2048 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å^2)	25.8	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 41.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.48$, $< L^2 > = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7447	wwPDB-VP
Average B, all atoms (Å^2)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 35.48 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 5.7998e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[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	1.04	1/1643 (0.1%)	1.04	2/2214 (0.1%)
1	B	1.03	0/1652	1.06	5/2226 (0.2%)
1	C	0.97	0/1665	1.04	4/2244 (0.2%)
1	D	0.96	0/1688	1.02	2/2275 (0.1%)
2	E	1.13	0/54	1.12	0/70
2	F	0.99	0/54	1.42	0/70
2	G	1.03	0/54	1.27	0/70
2	H	0.83	0/54	1.07	0/70
All	All	1.00	1/6864 (0.0%)	1.04	13/9239 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	444	GLU	CD-OE1	-6.71	1.18	1.25

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	467	ARG	NE-CZ-NH1	8.84	124.72	120.30
1	D	536	ARG	NE-CZ-NH2	-7.80	116.40	120.30
1	D	431	ASP	CB-CG-OD1	6.62	124.26	118.30
1	C	431	ASP	CB-CG-OD1	6.61	124.25	118.30
1	A	543	LEU	CA-CB-CG	6.55	130.37	115.30
1	C	447	ARG	NE-CZ-NH2	-6.13	117.23	120.30
1	B	391	LEU	CB-CG-CD1	5.56	120.45	111.00
1	C	431	ASP	CB-CG-OD2	-5.53	113.33	118.30
1	C	397	LEU	CB-CG-CD1	-5.51	101.62	111.00
1	B	479	ASP	CB-CG-OD1	5.37	123.14	118.30
1	B	467	ARG	NE-CZ-NH2	-5.33	117.64	120.30
1	A	580	ASP	CB-CG-OD1	5.29	123.06	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	481	ASP	CB-CG-OD1	5.08	122.87	118.30

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	1626	0	1645	12	0
1	B	1635	0	1653	11	0
1	C	1644	0	1659	9	0
1	D	1661	0	1683	10	0
2	E	55	0	64	0	0
2	F	55	0	64	0	0
2	G	55	0	64	1	0
2	H	55	0	64	0	0
3	A	20	0	0	0	0
3	B	10	0	0	0	0
3	C	5	0	0	0	0
3	D	10	0	0	0	0
4	A	165	0	0	5	0
4	B	175	0	0	1	0
4	C	140	0	0	2	0
4	D	117	0	0	1	0
4	E	4	0	0	0	0
4	F	6	0	0	0	0
4	G	6	0	0	0	0
4	H	3	0	0	0	0
All	All	7447	0	6896	41	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 (41) 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:520:GLU:HG3	4:A:957:HOH:O	1.60	1.01
1:C:551:GLU:OE1	1:C:551:GLU:HA	1.79	0.81
1:A:422:HIS:HD2	4:A:928:HOH:O	1.70	0.75
1:C:559:ALA:O	1:C:563:THR:HG23	1.87	0.74
1:D:469[B]:MET:HB3	1:D:470:PRO:HD3	1.76	0.65
1:B:589:GLN:HE21	1:B:593:GLN:HE21	1.45	0.64
1:D:392:LEU:HD13	1:D:417:THR:HG22	1.80	0.62
1:A:553:ALA:HB2	1:A:601:ILE:HG21	1.86	0.57
1:B:595:SER:O	1:B:599:MET:HG2	2.04	0.56
1:B:391:LEU:HD22	4:D:863:HOH:O	2.07	0.55
1:A:421:LYS:HG2	4:A:854:HOH:O	2.07	0.54
1:B:548:LYS:O	1:B:552:GLU:HG2	2.08	0.54
1:C:517:ARG:HD2	4:C:814:HOH:O	2.08	0.53
1:D:497:GLN:HA	1:D:497:GLN:OE1	2.08	0.53
1:D:524:GLU:OE1	1:D:527:ARG:NH1	2.42	0.53
1:D:392:LEU:HD13	1:D:417:THR:CG2	2.39	0.52
1:A:514:LYS:HE3	1:A:518:ASP:OD1	2.10	0.52
1:C:392:LEU:HD13	1:C:417:THR:HG22	1.92	0.50
1:B:596:GLN:HG2	4:B:909:HOH:O	2.14	0.47
1:A:498:LYS:HE3	1:A:498:LYS:HB3	1.53	0.47
1:A:589:GLN:O	1:A:593:GLN:HG2	2.14	0.47
1:D:391:LEU:C	1:D:391:LEU:HD23	2.35	0.47
1:D:543:LEU:O	1:D:547:ARG:HG3	2.14	0.47
1:A:396:PRO:HB3	1:C:392:LEU:HD12	1.98	0.46
1:A:389:VAL:HG13	4:A:921:HOH:O	2.16	0.46
1:B:469:MET:HB3	1:B:470:PRO:HD3	1.97	0.45
1:D:595:SER:O	1:D:599:MET:HG2	2.16	0.45
1:D:546:THR:O	1:D:550:VAL:HG23	2.17	0.45
4:C:844:HOH:O	2:G:2:ARG:HD2	2.16	0.44
1:A:587:LYS:HE2	4:A:825:HOH:O	2.18	0.43
1:A:499:ILE:HD13	1:A:499:ILE:HG21	1.82	0.42
1:B:418:ILE:HD13	1:B:418:ILE:HG21	1.78	0.42
1:B:446:LYS:HD2	1:B:530:GLU:OE2	2.19	0.42
1:C:498:LYS:HE2	1:C:498:LYS:HB3	1.88	0.42
1:D:473:GLU:HB2	1:D:491:LYS:HE3	2.02	0.42
1:B:407:VAL:HG23	1:B:533:VAL:HG11	2.02	0.41
1:B:507:LEU:HB3	1:B:511:GLU:HB2	2.02	0.41
1:C:558:PRO:HB2	1:C:560:ASP:OD1	2.21	0.40
1:B:399:LEU:CD1	1:B:478:ILE:HD11	2.51	0.40
1:A:392:LEU:HD11	1:C:396:PRO:HB3	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	213/219 (97%)	211 (99%)	1 (0%)	1 (0%)	29	15
1	B	214/219 (98%)	213 (100%)	1 (0%)	0	100	100
1	C	215/219 (98%)	212 (99%)	3 (1%)	0	100	100
1	D	218/219 (100%)	215 (99%)	3 (1%)	0	100	100
2	E	5/7 (71%)	5 (100%)	0	0	100	100
2	F	5/7 (71%)	5 (100%)	0	0	100	100
2	G	5/7 (71%)	5 (100%)	0	0	100	100
2	H	5/7 (71%)	5 (100%)	0	0	100	100
All	All	880/904 (97%)	871 (99%)	8 (1%)	1 (0%)	51	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	554	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	178/181 (98%)	173 (97%)	5 (3%)	43	30
1	B	179/181 (99%)	177 (99%)	2 (1%)	73	68
1	C	180/181 (99%)	179 (99%)	1 (1%)	86	84
1	D	183/181 (101%)	181 (99%)	2 (1%)	73	68

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	E	6/6 (100%)	6 (100%)	0	100	100
2	F	6/6 (100%)	6 (100%)	0	100	100
2	G	6/6 (100%)	6 (100%)	0	100	100
2	H	6/6 (100%)	6 (100%)	0	100	100
All	All	744/748 (100%)	734 (99%)	10 (1%)	67	62

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	392	LEU
1	A	498	LYS
1	A	556	LYS
1	A	596	GLN
1	A	597	LYS
1	B	391	LEU
1	B	433	GLN
1	C	551	GLU
1	D	513	GLN
1	D	527	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	422	HIS
1	B	593	GLN
2	F	1	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)

9 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	$\#\|Z\| > 2$
3	SO4	B	702	-	4,4,4	0.94	0	6,6,6	0.49	0
3	SO4	C	701	-	4,4,4	0.51	0	6,6,6	0.51	0
3	SO4	A	701	-	4,4,4	0.58	0	6,6,6	0.85	0
3	SO4	D	702	-	4,4,4	0.46	0	6,6,6	0.29	0
3	SO4	A	703	-	4,4,4	0.52	0	6,6,6	0.32	0
3	SO4	A	704	-	4,4,4	0.72	0	6,6,6	0.54	0
3	SO4	D	701	-	4,4,4	0.26	0	6,6,6	0.78	0
3	SO4	B	701	-	4,4,4	0.29	0	6,6,6	0.25	0
3	SO4	A	702	-	4,4,4	0.59	0	6,6,6	0.62	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	214/219 (97%)	0.18	13 (6%)	21	16	15, 25, 59, 82	0
1	B	215/219 (98%)	-0.02	6 (2%)	53	47	18, 25, 46, 58	0
1	C	215/219 (98%)	-0.05	6 (2%)	53	47	17, 28, 51, 69	0
1	D	216/219 (98%)	0.02	9 (4%)	36	30	19, 29, 55, 66	0
2	E	7/7 (100%)	0.79	1 (14%)	2	1	20, 25, 43, 56	0
2	F	7/7 (100%)	0.83	1 (14%)	2	1	20, 24, 47, 52	0
2	G	7/7 (100%)	0.99	2 (28%)	0	0	24, 25, 47, 65	0
2	H	7/7 (100%)	0.81	1 (14%)	2	1	24, 28, 50, 64	0
All	All	888/904 (98%)	0.06	39 (4%)	34	28	15, 27, 53, 82	0

All (39) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	G	1	ASN	6.6
1	B	602	ALA	5.7
2	H	1	ASN	4.7
1	A	555	ASP	4.6
1	A	552	GLU	4.5
1	A	600	GLU	4.1
1	C	555	ASP	3.9
2	E	1	ASN	3.9
2	F	1	ASN	3.8
1	A	602	ALA	3.6
1	A	601	ILE	3.6
1	B	555	ASP	3.5
1	A	553	ALA	3.4
1	A	599	MET	3.3
1	D	555	ASP	3.1
1	D	392	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	392	LEU	2.9
1	B	552	GLU	2.9
1	A	559	ALA	2.8
1	B	603	GLN	2.8
1	D	600	GLU	2.8
1	D	599	MET	2.8
1	D	510	ASP	2.7
1	D	603	GLN	2.6
1	D	556	LYS	2.5
1	A	557	LEU	2.5
1	C	554	GLY	2.4
1	B	399	LEU	2.4
2	G	7	GLY	2.4
1	A	551	GLU	2.4
1	C	596	GLN	2.3
1	D	604	GLN	2.2
1	B	553	ALA	2.2
1	A	394	VAL	2.1
1	D	401	ILE	2.1
1	C	560	ASP	2.1
1	C	553	ALA	2.1
1	A	399	LEU	2.1
1	A	517	ARG	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.

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	SO4	A	704	5/5	0.72	0.20	59,65,77,82	0
3	SO4	D	702	5/5	0.84	0.34	65,69,84,90	0
3	SO4	C	701	5/5	0.85	0.16	77,77,86,90	0
3	SO4	B	702	5/5	0.92	0.18	48,48,70,71	0
3	SO4	B	701	5/5	0.95	0.12	46,46,59,67	0
3	SO4	A	703	5/5	0.96	0.20	67,71,77,84	0
3	SO4	A	702	5/5	0.97	0.19	64,67,73,74	0
3	SO4	D	701	5/5	0.98	0.09	41,42,46,49	0
3	SO4	A	701	5/5	0.98	0.11	45,45,56,60	0

6.5 Other polymers (i)

There are no such residues in this entry.