Full wwPDB X-ray Structure Validation Report (i)

Jun 12, 2024 – 04:00 AM EDT

PDB ID	:	1WRB
Title	:	Crystal structure of the N-terminal RecA-like domain of DjVLGB, a pranarian Vasa-like RNA helicase
Authors	:	Kurimoto, K.; Muto, Y.; Obayashi, N.; Terada, T.; Shirouzu, M.; Yabuki, T.; Aoki, M.; Seki, E.; Matsuda, T.; Kigawa, T.; Okumura, H.; Tanaka, A.; Shibata, N.; Kashikawa, M.; Agata, K.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2004-10-14
Resolution	:	2.40 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
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:

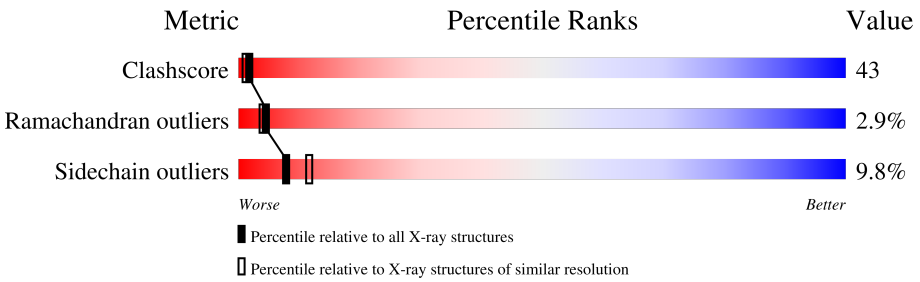
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.40 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	253	44% 41% 6% • 8%
1	B	253	39% 42% 11% 8%

2 Entry composition (i)

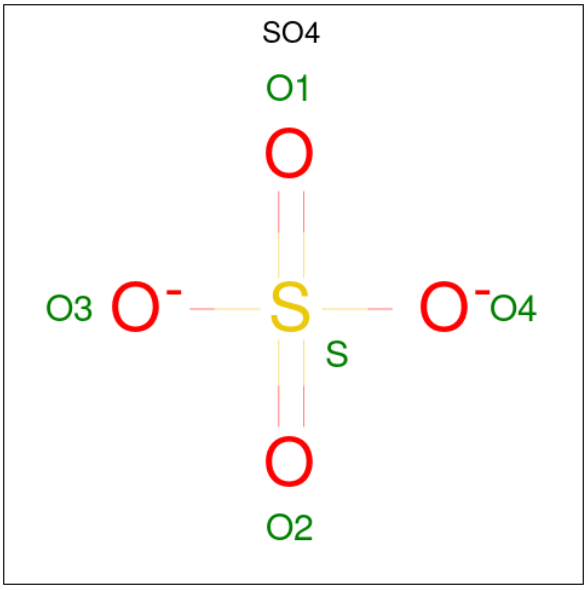
There are 3 unique types of molecules in this entry. The entry contains 3888 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DjVLGB.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	232	1823	1165	305	340	13	0	0	0
1	B	232	1823	1164	307	339	13	0	0	0

- 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
2	B	1	5	4	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	143	143	143	0	0
			Total	O		
3	B	89	89	89	0	0

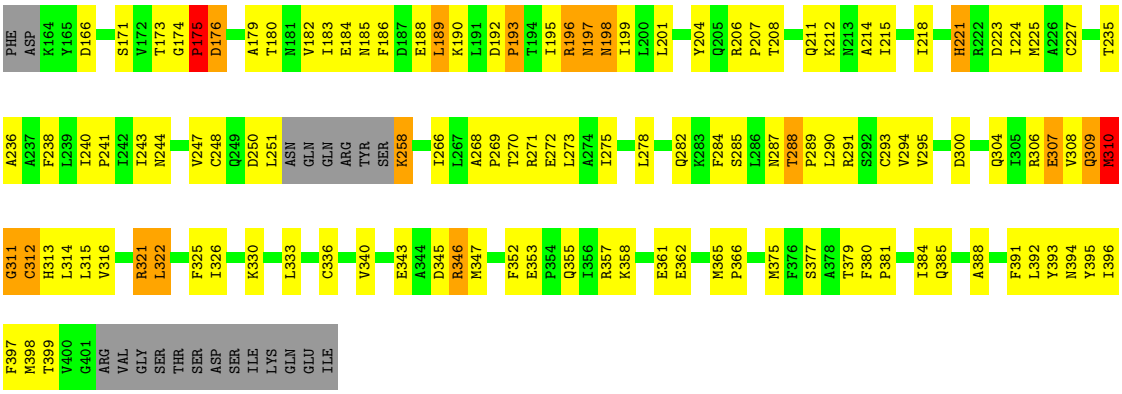
3 Residue-property plots (i)

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. 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. 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.

Note EDS was not executed.

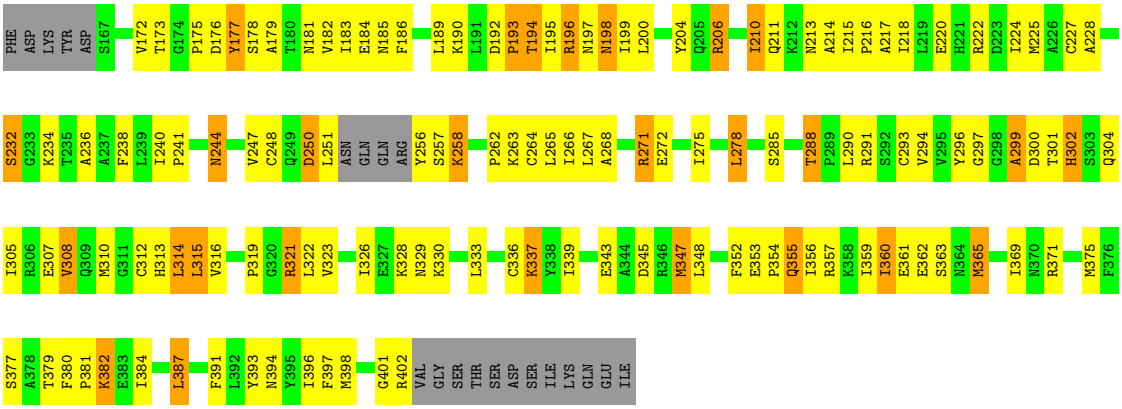
• Molecule 1: DjVLGB

Chain A: 44% 41% 6% • 8%



• Molecule 1: DjVLGB

Chain B: 39% 42% 11% 8%



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	138.24Å 138.24Å 47.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.40	Depositor
% Data completeness (in resolution range)	(Not available) (50.00-2.40)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.241 , 0.281	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3888	wwPDB-VP
Average B, all atoms (Å^2)	43.0	wwPDB-VP

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	0.36	0/1857	0.65	1/2516 (0.0%)
1	B	0.37	0/1857	0.64	1/2516 (0.0%)
All	All	0.37	0/3714	0.65	2/5032 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	198	ASN	N-CA-C	-5.57	95.95	111.00
1	B	198	ASN	N-CA-C	-5.20	96.97	111.00

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	1823	0	1857	144	0
1	B	1823	0	1858	176	0
2	A	5	0	0	0	0
2	B	5	0	0	0	0
3	A	143	0	0	11	0
3	B	89	0	0	14	0
All	All	3888	0	3715	320	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 43.

All (320) 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:193:PRO:HD2	1:A:244:ASN:HD21	1.02	1.13
1:A:193:PRO:HD2	1:A:244:ASN:ND2	1.64	1.10
1:B:193:PRO:HD3	1:B:244:ASN:HD22	0.94	1.06
1:B:193:PRO:HD3	1:B:244:ASN:ND2	1.73	1.02
1:A:288:THR:HG22	1:A:290:LEU:H	1.25	0.99
1:B:196:ARG:HA	1:B:196:ARG:HH11	1.31	0.93
1:A:193:PRO:CD	1:A:244:ASN:HD21	1.80	0.93
1:A:196:ARG:HE	1:A:243:ILE:HG22	1.33	0.92
1:A:388:ALA:HB1	3:A:1108:HOH:O	1.68	0.92
1:A:192:ASP:HB2	1:A:244:ASN:ND2	1.86	0.91
1:B:215:ILE:HG23	1:B:241:PRO:HG3	1.55	0.89
1:A:185:ASN:H	1:A:189:LEU:HD13	1.37	0.88
1:B:288:THR:HG22	1:B:290:LEU:H	1.39	0.86
1:A:345:ASP:OD1	1:A:379:THR:HG22	1.75	0.86
1:A:291:ARG:H	1:A:313:HIS:HD2	1.20	0.85
1:A:196:ARG:HE	1:A:243:ILE:CG2	1.88	0.84
1:A:193:PRO:HB3	3:A:1020:HOH:O	1.76	0.84
1:A:196:ARG:NH2	1:A:288:THR:HG21	1.95	0.81
1:B:216:PRO:O	1:B:220:GLU:HG3	1.78	0.81
1:B:217:ALA:HB1	1:B:396:ILE:CD1	2.10	0.81
1:B:176:ASP:HB3	1:B:396:ILE:HA	1.62	0.80
1:B:224:ILE:HG12	1:B:396:ILE:HD12	1.63	0.80
1:A:310:MET:O	1:A:312:CYS:N	2.16	0.79
1:B:182:VAL:HG12	1:B:216:PRO:HB3	1.64	0.79
1:A:291:ARG:H	1:A:313:HIS:CD2	2.03	0.76
1:A:196:ARG:NH2	1:A:285:SER:HA	2.00	0.76
1:B:210:ILE:HD11	1:B:232:SER:HB2	1.68	0.76
1:B:251:LEU:HD22	1:B:251:LEU:H	1.49	0.76
1:B:258:LYS:HD3	1:B:258:LYS:H	1.50	0.76
1:B:291:ARG:HG3	1:B:310:MET:HG3	1.68	0.76
1:B:353:GLU:HB3	1:B:354:PRO:HD3	1.68	0.75
1:B:293:CYS:SG	1:B:312:CYS:HB3	2.27	0.75
1:A:184:GLU:OE1	1:A:189:LEU:HB3	1.86	0.74
1:A:375:MET:HE3	1:A:392:LEU:HG	1.69	0.74
1:B:176:ASP:CG	1:B:396:ILE:HG23	2.07	0.74
1:A:357:ARG:HD3	1:A:391:PHE:HZ	1.52	0.73
1:B:176:ASP:CB	1:B:396:ILE:HA	2.17	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:CYS:HB2	1:A:312:CYS:SG	2.29	0.73
1:A:285:SER:O	1:A:288:THR:HB	1.89	0.72
1:A:293:CYS:SG	1:A:312:CYS:HB3	2.29	0.72
1:A:278:LEU:O	1:A:282:GLN:HG3	1.89	0.72
1:A:215:ILE:HG23	1:A:241:PRO:HG3	1.70	0.71
1:B:288:THR:CG2	1:B:290:LEU:H	2.04	0.71
1:B:182:VAL:HG23	3:B:1064:HOH:O	1.91	0.70
1:B:285:SER:O	1:B:288:THR:HB	1.92	0.70
1:B:196:ARG:HA	1:B:196:ARG:NH1	2.07	0.70
1:B:250:ASP:OD1	1:B:251:LEU:HD22	1.90	0.69
1:B:177:TYR:CD2	1:B:394:ASN:HB3	2.27	0.69
1:B:328:LYS:HD2	1:B:330:LYS:HZ3	1.57	0.69
1:A:197:ASN:HD22	1:A:197:ASN:N	1.91	0.68
1:B:256:TYR:CZ	1:B:310:MET:HA	2.27	0.68
1:A:309:GLN:O	1:A:311:GLY:N	2.26	0.68
1:A:291:ARG:HG3	1:A:310:MET:HB2	1.75	0.67
1:A:358:LYS:HD3	1:A:362:GLU:HB2	1.76	0.67
1:B:224:ILE:CG1	1:B:396:ILE:HD12	2.25	0.66
1:B:296:TYR:C	1:B:321:ARG:HG3	2.16	0.66
1:A:211:GLN:NE2	1:A:236:ALA:HB3	2.11	0.65
1:A:192:ASP:HB2	1:A:244:ASN:HD21	1.62	0.65
1:B:293:CYS:HG	1:B:312:CYS:HB3	1.61	0.65
1:B:217:ALA:CB	1:B:224:ILE:HD11	2.27	0.65
1:A:180:THR:O	1:A:182:VAL:HG23	1.98	0.64
1:B:179:ALA:HB1	3:B:1065:HOH:O	1.97	0.64
1:B:217:ALA:HB1	1:B:396:ILE:HD13	1.79	0.64
1:A:307:GLU:OE1	1:A:307:GLU:HA	1.95	0.64
1:A:186:PHE:HB3	1:A:188:GLU:HG2	1.80	0.64
1:A:304:GLN:O	1:A:308:VAL:HG23	1.98	0.64
1:B:176:ASP:OD2	1:B:396:ILE:HG12	1.97	0.63
1:B:360:ILE:HG21	1:B:391:PHE:CD2	2.34	0.63
1:B:217:ALA:HB3	1:B:224:ILE:HD11	1.79	0.63
1:B:258:LYS:HG2	3:B:1073:HOH:O	1.99	0.63
1:A:196:ARG:HH22	1:A:288:THR:HG21	1.62	0.62
1:A:225:MET:CE	1:A:388:ALA:HB2	2.29	0.62
1:B:210:ILE:HD11	1:B:232:SER:C	2.19	0.62
1:B:258:LYS:HA	1:B:308:VAL:HG13	1.81	0.62
1:A:392:LEU:HD12	3:A:1108:HOH:O	2.00	0.61
1:A:227:CYS:HA	1:A:377:SER:O	2.00	0.61
1:B:291:ARG:HE	1:B:310:MET:HG2	1.64	0.61
1:B:240:ILE:HB	1:B:241:PRO:HD3	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:291:ARG:H	1:B:313:HIS:CD2	2.19	0.61
1:A:243:ILE:O	1:A:247:VAL:HG13	1.99	0.61
1:B:195:ILE:HD12	1:B:195:ILE:H	1.66	0.61
1:A:240:ILE:HB	1:A:241:PRO:HD3	1.83	0.60
1:A:271:ARG:O	1:A:275:ILE:HG13	1.99	0.60
1:A:304:GLN:NE2	1:A:330:LYS:HE3	2.16	0.60
1:B:227:CYS:HA	1:B:377:SER:O	2.01	0.60
1:A:357:ARG:O	1:A:361:GLU:HG2	2.01	0.60
1:B:258:LYS:H	1:B:258:LYS:CD	2.14	0.60
1:A:186:PHE:H	1:A:189:LEU:CD1	2.15	0.60
1:A:186:PHE:HE1	1:A:206:ARG:HH22	1.50	0.60
1:B:173:THR:HG22	1:B:175:PRO:HD3	1.83	0.59
1:B:291:ARG:HG3	1:B:310:MET:CG	2.32	0.59
1:A:196:ARG:HH22	1:A:288:THR:CB	2.15	0.59
1:B:228:ALA:O	1:B:234:LYS:HD3	2.02	0.59
1:B:225:MET:SD	1:B:375:MET:HE2	2.42	0.59
1:B:196:ARG:HB3	3:B:1071:HOH:O	2.02	0.59
1:A:251:LEU:O	1:A:251:LEU:HD13	2.02	0.59
1:B:393:TYR:O	1:B:394:ASN:C	2.41	0.59
1:B:401:GLY:O	1:B:402:ARG:HB2	2.02	0.59
1:B:293:CYS:HG	1:B:312:CYS:CB	2.15	0.58
1:A:321:ARG:HD2	1:A:325:PHE:CE1	2.38	0.58
1:A:196:ARG:NE	1:A:243:ILE:HG22	2.11	0.58
1:A:174:GLY:N	1:A:175:PRO:HD3	2.19	0.58
1:A:196:ARG:HH22	1:A:288:THR:CG2	2.17	0.58
1:A:225:MET:HE2	1:A:388:ALA:HB2	1.84	0.58
1:A:357:ARG:HD3	1:A:391:PHE:CZ	2.36	0.57
1:B:291:ARG:NE	1:B:310:MET:HG2	2.19	0.57
1:B:193:PRO:HG2	3:B:1048:HOH:O	2.04	0.57
1:A:381:PRO:O	1:A:385:GLN:HG3	2.04	0.57
1:B:288:THR:HG22	1:B:290:LEU:N	2.17	0.57
1:B:177:TYR:CD2	1:B:222:ARG:NH2	2.73	0.57
1:B:182:VAL:HG12	1:B:182:VAL:O	2.05	0.57
1:B:355:GLN:O	1:B:359:ILE:HG13	2.05	0.57
1:B:293:CYS:SG	1:B:312:CYS:SG	3.03	0.56
1:B:210:ILE:HG13	3:B:1017:HOH:O	2.03	0.56
1:A:193:PRO:CG	1:A:248:CYS:SG	2.93	0.56
1:B:265:LEU:HD23	1:B:315:LEU:HD13	1.87	0.56
1:B:192:ASP:O	1:B:193:PRO:O	2.23	0.56
1:B:175:PRO:HD2	1:B:397:PHE:O	2.05	0.56
1:B:265:LEU:HD11	1:B:267:LEU:HG	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:266:ILE:HD13	1:B:314:LEU:HD11	1.87	0.56
1:A:225:MET:HB2	3:A:1108:HOH:O	2.06	0.56
1:B:214:ALA:O	1:B:218:ILE:HG13	2.06	0.56
1:A:288:THR:HG23	1:A:289:PRO:HD2	1.88	0.55
1:A:291:ARG:HG3	1:A:310:MET:CB	2.36	0.55
1:A:193:PRO:HD2	1:A:244:ASN:CG	2.23	0.55
1:B:175:PRO:O	1:B:176:ASP:HB3	2.07	0.55
1:A:293:CYS:HG	1:A:312:CYS:HB3	1.71	0.55
1:B:323:VAL:HG21	1:B:355:GLN:HB3	1.87	0.55
1:B:355:GLN:CD	1:B:355:GLN:H	2.08	0.55
1:B:343:GLU:C	1:B:345:ASP:N	2.57	0.55
1:A:293:CYS:SG	1:A:312:CYS:SG	3.05	0.55
1:A:183:ILE:C	1:A:183:ILE:HD12	2.27	0.55
1:B:193:PRO:HG3	1:B:248:CYS:SG	2.46	0.55
1:B:206:ARG:HG3	1:B:206:ARG:HH11	1.72	0.55
1:A:214:ALA:O	1:A:218:ILE:HG13	2.07	0.55
1:A:291:ARG:CG	1:A:310:MET:HB2	2.36	0.55
1:B:177:TYR:HB3	3:B:1051:HOH:O	2.07	0.55
1:B:210:ILE:HD11	1:B:232:SER:CB	2.35	0.55
1:A:227:CYS:HB2	1:A:399:THR:HG22	1.89	0.54
1:A:195:ILE:C	1:A:197:ASN:H	2.10	0.54
1:B:181:ASN:C	1:B:183:ILE:H	2.09	0.54
1:A:293:CYS:HG	1:A:312:CYS:CB	2.20	0.54
1:B:293:CYS:HB2	1:B:312:CYS:SG	2.48	0.54
1:B:337:LYS:HG3	1:B:369:ILE:CG2	2.38	0.54
1:B:348:LEU:HD22	1:B:384:ILE:HD13	1.89	0.54
1:A:291:ARG:HB2	1:A:312:CYS:HA	1.90	0.54
1:B:319:PRO:O	1:B:323:VAL:HG23	2.07	0.53
1:B:357:ARG:HG3	1:B:357:ARG:HH11	1.71	0.53
1:A:258:LYS:HB2	1:A:258:LYS:NZ	2.23	0.53
1:A:375:MET:HE3	1:A:392:LEU:CG	2.39	0.53
1:A:173:THR:O	1:A:398:MET:HA	2.08	0.53
1:B:293:CYS:SG	1:B:312:CYS:CB	2.96	0.53
1:B:211:GLN:HE21	1:B:236:ALA:HB3	1.74	0.53
1:B:183:ILE:N	1:B:183:ILE:HD12	2.24	0.53
1:A:175:PRO:O	1:A:176:ASP:HB2	2.10	0.52
1:A:196:ARG:NE	1:A:243:ILE:CG2	2.68	0.52
1:B:278:LEU:HG	1:B:294:VAL:HB	1.91	0.52
1:B:181:ASN:HA	1:B:183:ILE:HD13	1.92	0.52
1:A:208:THR:O	1:A:212:LYS:HG3	2.10	0.52
1:A:295:VAL:HG12	1:A:321:ARG:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:311:GLY:O	1:A:312:CYS:O	2.28	0.52
1:B:265:LEU:CD1	1:B:267:LEU:HG	2.40	0.52
1:B:343:GLU:C	1:B:345:ASP:H	2.13	0.52
1:A:288:THR:CG2	1:A:290:LEU:H	2.11	0.51
1:A:235:THR:HA	1:A:238:PHE:CE2	2.46	0.51
1:B:352:PHE:HA	1:B:355:GLN:HE21	1.75	0.51
1:B:354:PRO:HA	3:B:1034:HOH:O	2.09	0.51
1:A:174:GLY:HA2	1:A:398:MET:HA	1.92	0.51
1:A:195:ILE:C	1:A:197:ASN:N	2.63	0.51
1:A:198:ASN:HB3	3:A:1068:HOH:O	2.09	0.51
1:A:269:PRO:HG2	1:A:343:GLU:HB2	1.92	0.51
1:A:379:THR:HG23	1:A:381:PRO:HD3	1.91	0.51
1:B:357:ARG:HG2	1:B:361:GLU:OE1	2.11	0.51
1:B:401:GLY:O	1:B:402:ARG:CB	2.59	0.51
1:B:251:LEU:H	1:B:251:LEU:CD2	2.22	0.51
1:B:176:ASP:OD1	1:B:179:ALA:HB3	2.11	0.50
1:A:321:ARG:HD2	1:A:325:PHE:HE1	1.76	0.50
1:A:186:PHE:O	1:A:189:LEU:HB2	2.12	0.50
1:B:196:ARG:HH11	1:B:196:ARG:CA	2.15	0.50
1:B:190:LYS:HB2	1:B:190:LYS:NZ	2.27	0.50
1:A:345:ASP:HA	1:A:384:ILE:HD11	1.93	0.50
1:B:247:VAL:HB	3:B:1048:HOH:O	2.12	0.50
1:B:328:LYS:HB3	1:B:330:LYS:HD3	1.94	0.49
1:A:186:PHE:H	1:A:189:LEU:HD13	1.77	0.49
1:A:346:ARG:HG3	3:A:1078:HOH:O	2.11	0.49
1:B:379:THR:C	1:B:381:PRO:HD3	2.33	0.49
1:A:207:PRO:HB2	1:A:212:LYS:HG2	1.95	0.49
1:B:186:PHE:O	1:B:189:LEU:HB3	2.12	0.49
1:B:290:LEU:HD22	1:B:313:HIS:CD2	2.47	0.49
1:A:333:LEU:O	1:A:365:MET:HA	2.13	0.49
1:B:328:LYS:O	1:B:330:LYS:HD2	2.13	0.49
1:A:185:ASN:O	1:A:207:PRO:HD2	2.12	0.48
1:B:271:ARG:NH1	1:B:272:GLU:OE2	2.46	0.48
1:A:306:ARG:NH2	1:A:309:GLN:OE1	2.46	0.48
1:B:182:VAL:HG11	1:B:220:GLU:OE2	2.13	0.48
1:B:352:PHE:O	1:B:356:ILE:HG13	2.13	0.48
1:B:210:ILE:O	1:B:214:ALA:HB3	2.14	0.48
1:B:257:SER:O	1:B:308:VAL:HG13	2.13	0.48
1:A:288:THR:HG23	1:A:289:PRO:CD	2.43	0.48
1:B:211:GLN:NE2	1:B:236:ALA:HB3	2.28	0.48
1:B:222:ARG:CB	1:B:396:ILE:HD11	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:290:LEU:HA	1:B:313:HIS:HD2	1.77	0.48
1:A:201:LEU:HG	3:A:1095:HOH:O	2.14	0.48
1:A:195:ILE:O	1:A:197:ASN:N	2.46	0.48
1:A:336:CYS:O	1:A:366:PRO:HD2	2.13	0.48
1:B:196:ARG:C	1:B:198:ASN:H	2.17	0.48
1:A:192:ASP:HA	3:A:1121:HOH:O	2.13	0.48
1:A:266:ILE:CD1	1:A:340:VAL:HB	2.43	0.48
1:B:193:PRO:CB	3:B:1031:HOH:O	2.62	0.48
1:B:297:GLY:C	1:B:299:ALA:H	2.17	0.48
1:A:190:LYS:HE2	1:A:215:ILE:HG21	1.96	0.47
1:A:392:LEU:HB3	1:A:395:TYR:HB3	1.95	0.47
1:B:184:GLU:HB2	1:B:189:LEU:HD23	1.95	0.47
1:A:174:GLY:N	1:A:175:PRO:CD	2.78	0.47
1:A:186:PHE:H	1:A:189:LEU:HD12	1.79	0.47
1:A:322:LEU:HD22	1:A:326:ILE:HG13	1.95	0.47
1:B:294:VAL:HA	1:B:316:VAL:O	2.15	0.47
1:A:244:ASN:O	1:A:247:VAL:HG22	2.14	0.47
1:B:305:ILE:HG22	1:B:305:ILE:O	2.14	0.47
1:B:172:VAL:HG11	1:B:213:ASN:ND2	2.29	0.47
1:B:195:ILE:HD12	1:B:195:ILE:N	2.30	0.47
1:B:290:LEU:HD22	1:B:313:HIS:HD2	1.80	0.47
1:B:222:ARG:HB2	1:B:396:ILE:HD11	1.96	0.47
1:B:293:CYS:CB	1:B:312:CYS:HG	2.28	0.47
1:A:186:PHE:HE1	1:A:206:ARG:NH2	2.11	0.47
1:A:186:PHE:CE1	1:A:206:ARG:NH2	2.83	0.47
1:A:293:CYS:SG	1:A:312:CYS:CB	3.01	0.47
1:A:211:GLN:HE21	1:A:236:ALA:HB3	1.79	0.46
1:B:300:ASP:O	1:B:301:THR:HB	2.14	0.46
1:B:173:THR:O	1:B:398:MET:HA	2.16	0.46
1:A:293:CYS:CB	1:A:312:CYS:SG	3.01	0.46
1:A:314:LEU:HD23	1:A:314:LEU:C	2.36	0.46
1:B:256:TYR:CE1	1:B:310:MET:HA	2.51	0.46
1:B:262:PRO:HG2	1:B:315:LEU:HD12	1.98	0.46
1:B:328:LYS:HB3	1:B:330:LYS:NZ	2.31	0.46
1:B:304:GLN:OE1	1:B:330:LYS:HE2	2.15	0.46
1:A:266:ILE:HD13	1:A:340:VAL:HB	1.98	0.46
1:B:264:CYS:SG	1:B:314:LEU:HD22	2.55	0.46
1:A:196:ARG:HH22	1:A:288:THR:HB	1.81	0.45
1:A:352:PHE:HA	1:A:355:GLN:OE1	2.16	0.45
1:B:215:ILE:HG23	1:B:241:PRO:CG	2.38	0.45
1:A:353:GLU:O	1:A:357:ARG:HG2	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:380:PHE:CE2	1:A:385:GLN:HG2	2.51	0.45
1:B:333:LEU:HD11	1:B:359:ILE:HG23	1.99	0.45
1:A:190:LYS:HB2	1:A:190:LYS:NZ	2.32	0.45
1:A:199:ILE:CG2	1:A:204:TYR:HB2	2.47	0.45
1:B:182:VAL:HG12	1:B:216:PRO:CB	2.41	0.45
1:B:375:MET:HE1	1:B:387:LEU:HB3	1.99	0.45
1:A:304:GLN:HE22	1:A:330:LYS:HG3	1.82	0.45
1:B:382:LYS:HB3	3:B:1036:HOH:O	2.16	0.45
1:A:196:ARG:CZ	1:A:285:SER:HA	2.46	0.45
1:B:196:ARG:HH21	1:B:247:VAL:HB	1.82	0.45
1:B:217:ALA:CB	1:B:396:ILE:HD13	2.46	0.45
1:B:268:ALA:O	1:B:319:PRO:HD3	2.17	0.45
1:A:179:ALA:HB1	3:A:1041:HOH:O	2.16	0.45
1:A:293:CYS:HG	1:A:312:CYS:HG	1.62	0.45
1:B:177:TYR:HD1	1:B:178:SER:HG	1.60	0.45
1:A:174:GLY:HA2	1:A:397:PHE:O	2.17	0.45
1:A:258:LYS:HB2	1:A:258:LYS:HZ3	1.81	0.45
1:A:186:PHE:HB2	1:A:189:LEU:HD12	1.97	0.44
1:B:217:ALA:HB1	1:B:224:ILE:HD11	1.99	0.44
1:B:381:PRO:HD2	1:B:384:ILE:CG1	2.47	0.44
1:A:393:TYR:O	1:A:394:ASN:C	2.55	0.44
1:B:293:CYS:HG	1:B:312:CYS:HG	1.58	0.44
1:A:294:VAL:HA	1:A:316:VAL:O	2.17	0.44
1:B:193:PRO:HB2	3:B:1031:HOH:O	2.17	0.44
1:B:326:ILE:HG21	1:B:362:GLU:HG2	2.00	0.44
1:B:293:CYS:HB2	1:B:312:CYS:HG	1.82	0.44
1:B:271:ARG:O	1:B:275:ILE:HG13	2.18	0.44
1:B:380:PHE:N	1:B:381:PRO:HD3	2.32	0.43
1:B:365:MET:SD	1:B:365:MET:N	2.81	0.43
1:B:339:ILE:HD11	1:B:363:SER:OG	2.17	0.43
1:B:238:PHE:O	1:B:241:PRO:HD2	2.19	0.42
1:B:251:LEU:HD22	1:B:251:LEU:N	2.28	0.42
1:A:197:ASN:N	1:A:197:ASN:ND2	2.63	0.42
1:B:291:ARG:H	1:B:313:HIS:HD2	1.65	0.42
1:B:185:ASN:H	1:B:189:LEU:HD23	1.84	0.42
1:A:196:ARG:CZ	1:A:284:PHE:O	2.67	0.42
1:B:353:GLU:HB3	1:B:354:PRO:CD	2.45	0.42
1:A:204:TYR:CZ	1:A:236:ALA:HB2	2.55	0.42
1:B:193:PRO:HB2	1:B:194:THR:H	1.68	0.42
1:B:196:ARG:NH1	1:B:196:ARG:CA	2.78	0.42
1:A:291:ARG:HA	3:A:1072:HOH:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:328:LYS:HB3	1:B:330:LYS:HZ3	1.85	0.41
1:B:329:ASN:CG	1:B:329:ASN:O	2.58	0.41
1:B:357:ARG:HG3	1:B:357:ARG:NH1	2.34	0.41
1:B:357:ARG:HB2	3:B:1034:HOH:O	2.20	0.41
1:A:221:HIS:ND1	1:A:221:HIS:N	2.68	0.41
1:B:337:LYS:HG3	1:B:369:ILE:HG21	2.02	0.41
1:A:269:PRO:HG3	1:A:347:MET:HG3	2.01	0.41
1:A:285:SER:OG	1:A:290:LEU:HD23	2.21	0.41
1:A:311:GLY:O	1:A:312:CYS:C	2.59	0.41
1:B:190:LYS:HB2	1:B:190:LYS:HZ1	1.86	0.41
1:B:195:ILE:O	1:B:197:ASN:N	2.54	0.41
1:A:208:THR:OG1	1:A:211:GLN:HG3	2.21	0.41
1:A:290:LEU:HD12	1:A:313:HIS:CD2	2.55	0.41
1:B:181:ASN:C	1:B:183:ILE:N	2.73	0.41
1:B:371:ARG:CZ	3:B:1067:HOH:O	2.69	0.41
1:A:268:ALA:HA	1:A:269:PRO:HD3	1.80	0.41
1:A:396:ILE:HG23	3:A:1085:HOH:O	2.20	0.41
1:B:175:PRO:CD	1:B:397:PHE:O	2.69	0.41
1:B:195:ILE:H	1:B:195:ILE:CD1	2.33	0.41
1:B:290:LEU:HA	1:B:313:HIS:CD2	2.55	0.41
1:B:300:ASP:C	1:B:302:HIS:H	2.24	0.41
1:B:347:MET:HG2	1:B:356:ILE:HD11	2.03	0.41
1:A:199:ILE:HG23	1:A:204:TYR:HB2	2.03	0.41
1:A:225:MET:HG3	1:A:397:PHE:CE1	2.56	0.41
1:A:269:PRO:HD2	1:A:273:LEU:HD23	2.02	0.41
1:A:288:THR:CG2	1:A:289:PRO:N	2.83	0.41
1:B:322:LEU:O	1:B:326:ILE:HG13	2.20	0.41
1:A:270:THR:HB	1:A:272:GLU:OE1	2.21	0.41
1:B:177:TYR:O	1:B:222:ARG:NH2	2.41	0.41
1:B:183:ILE:N	1:B:183:ILE:CD1	2.84	0.40
1:B:199:ILE:CG2	1:B:204:TYR:HB2	2.51	0.40
1:B:234:LYS:HB2	1:B:234:LYS:HE3	1.82	0.40
1:A:223:ASP:C	1:A:224:ILE:HG13	2.41	0.40
1:B:263:LYS:HA	1:B:336:CYS:HA	2.03	0.40
1:B:210:ILE:HD11	1:B:232:SER:O	2.21	0.40
1:B:258:LYS:HA	1:B:308:VAL:CG1	2.48	0.40
1:B:258:LYS:CD	1:B:258:LYS:N	2.84	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	228/253 (90%)	207 (91%)	13 (6%)	8 (4%)	3 3
1	B	228/253 (90%)	206 (90%)	17 (8%)	5 (2%)	6 7
All	All	456/506 (90%)	413 (91%)	30 (7%)	13 (3%)	4 4

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	250	ASP
1	A	310	MET
1	A	311	GLY
1	A	312	CYS
1	B	193	PRO
1	B	299	ALA
1	A	176	ASP
1	A	309	GLN
1	B	196	ARG
1	B	250	ASP
1	A	175	PRO
1	A	196	ARG
1	B	308	VAL

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	205/225 (91%)	188 (92%)	17 (8%)	11 17

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	205/225 (91%)	182 (89%)	23 (11%)	6 8
All	All	410/450 (91%)	370 (90%)	40 (10%)	8 11

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	ASP
1	A	171	SER
1	A	175	PRO
1	A	189	LEU
1	A	193	PRO
1	A	197	ASN
1	A	221	HIS
1	A	258	LYS
1	A	287	ASN
1	A	288	THR
1	A	300	ASP
1	A	307	GLU
1	A	310	MET
1	A	315	LEU
1	A	321	ARG
1	A	322	LEU
1	A	346	ARG
1	B	177	TYR
1	B	194	THR
1	B	200	LEU
1	B	206	ARG
1	B	210	ILE
1	B	232	SER
1	B	244	ASN
1	B	258	LYS
1	B	271	ARG
1	B	278	LEU
1	B	288	THR
1	B	302	HIS
1	B	307	GLU
1	B	314	LEU
1	B	315	LEU
1	B	321	ARG
1	B	337	LYS
1	B	347	MET
1	B	355	GLN

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Mol	Chain	Res	Type
1	B	360	ILE
1	B	365	MET
1	B	382	LYS
1	B	387	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	197	ASN
1	A	244	ASN
1	A	287	ASN
1	A	313	HIS
1	A	394	ASN
1	B	244	ASN
1	B	313	HIS
1	B	355	GLN
1	B	372	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)

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	B	1002	-	4,4,4	0.41	0	6,6,6	0.05	0
2	SO4	A	1001	-	4,4,4	0.32	0	6,6,6	0.17	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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.