



# Full wwPDB X-ray Structure Validation Report ⓘ

Sep 25, 2017 – 02:16 PM EDT

PDB ID : 5VBN  
Title : Crystal Structure of human DNA polymerase epsilon B-subunit in complex with C-terminal domain of catalytic subunit  
Authors : Baranovskiy, A.G.; Gu, J.; Suwa, Y.; Babayeva, N.D.; Tahirov, T.H.  
Deposited on : unknown  
Resolution : 2.35 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](mailto: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.

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

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : **FAILED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20030345

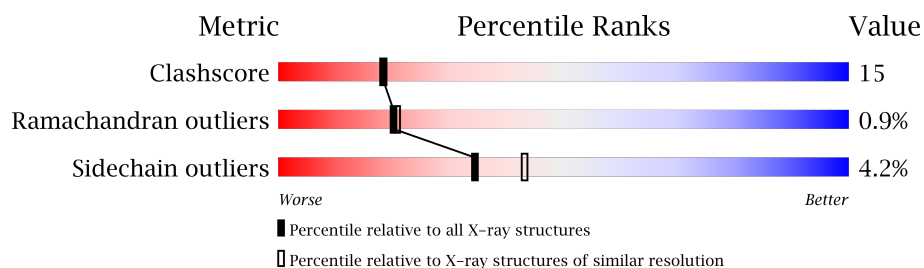
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.35 Å.




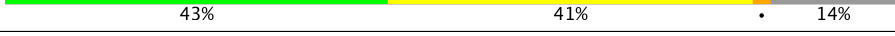
Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	1626 (2.38-2.34)
Ramachandran outliers	110173	1605 (2.38-2.34)
Sidechain outliers	110143	1606 (2.38-2.34)

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  $\geq 3$ , 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.

Note EDS failed to run properly.

Mol	Chain	Length	Quality of chain
1	A	527	
1	E	527	
2	B	145	
2	F	145	

## 2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 9058 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 DNA polymerase epsilon subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	427	Total	C	N	O	S	0	0	0
			3425	2219	565	624	17			
1	E	427	Total	C	N	O	S	0	0	0
			3425	2219	565	624	17			

- Molecule 2 is a protein called DNA polymerase epsilon catalytic subunit A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	125	Total	C	N	O	S	0	0	0
			991	631	161	184	15			
2	F	125	Total	C	N	O	S	0	0	0
			991	631	161	184	15			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	2	Total Zn 2 2	0	0
4	F	2	Total Zn 2 2	0	0

- Molecule 5 is water.

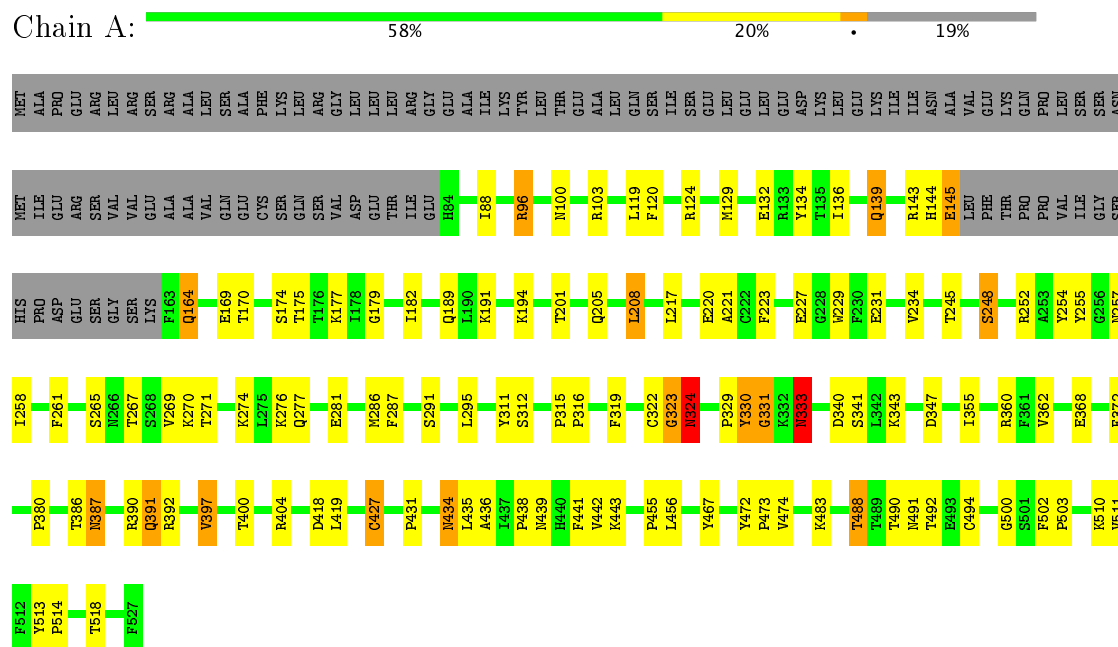
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	108	Total O 108 108	0	0
5	B	6	Total O 6 6	0	0
5	E	94	Total O 94 94	0	0
5	F	4	Total O 4 4	0	0

### 3 Residue-property plots

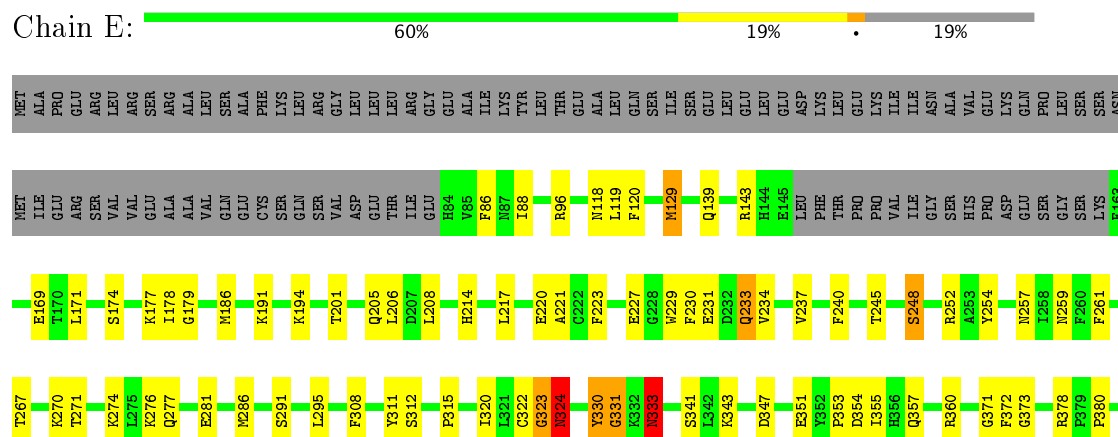
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS failed to run properly.

- Molecule 1: DNA polymerase epsilon subunit 2



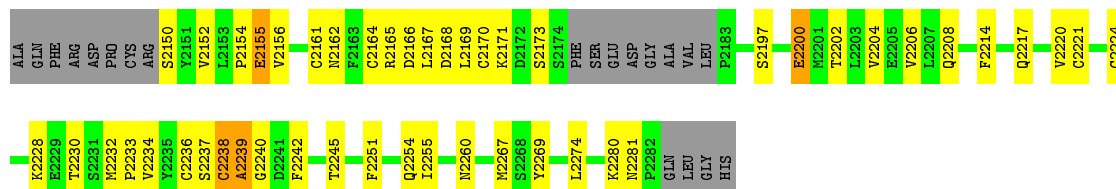
- Molecule 1: DNA polymerase epsilon subunit 2





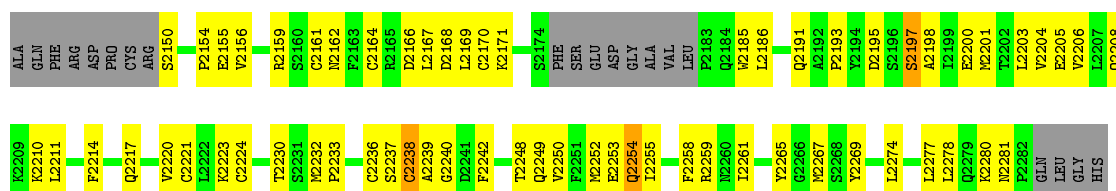
• Molecule 2: DNA polymerase epsilon catalytic subunit A

Chain B: 53% 30% 14%



• Molecule 2: DNA polymerase epsilon catalytic subunit A

Chain F: 43% 41% 14%



## 4 Data and refinement statistics

EDS failed to run properly - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	92.26Å 201.46Å 78.34Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	39.75 – 2.35	Depositor
% Data completeness (in resolution range)	94.7 (39.75-2.35)	Depositor
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.57 (at 2.34Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.225 , 0.264	Depositor
Wilson B-factor (Å <sup>2</sup> )	37.3	Xtriage
Anisotropy	0.592	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	9058	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	46.0	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 34.31 % 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 6.9667e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  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: ZN, 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	0.48	0/3526	0.70	3/4794 (0.1%)
1	E	0.46	0/3526	0.69	3/4794 (0.1%)
2	B	0.39	0/1010	0.68	1/1365 (0.1%)
2	F	0.40	0/1010	0.68	1/1365 (0.1%)
All	All	0.45	0/9072	0.69	8/12318 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	331	GLY	N-CA-C	6.93	130.44	113.10
1	A	331	GLY	N-CA-C	6.91	130.38	113.10
1	E	324	ASN	N-CA-C	-6.37	93.79	111.00
1	A	324	ASN	N-CA-C	-6.31	93.95	111.00
1	E	323	GLY	N-CA-C	5.65	127.22	113.10
1	A	323	GLY	N-CA-C	5.62	127.16	113.10
2	F	2239	ALA	N-CA-C	-5.09	97.25	111.00
2	B	2239	ALA	N-CA-C	-5.00	97.50	111.00

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts ⓘ

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	3425	0	3361	100	0
1	E	3425	0	3361	86	0
2	B	991	0	977	39	0
2	F	991	0	977	52	0
3	A	5	0	0	0	0
3	E	5	0	0	0	0
4	B	2	0	0	0	0
4	F	2	0	0	0	0
5	A	108	0	0	4	0
5	B	6	0	0	0	0
5	E	94	0	0	2	0
5	F	4	0	0	0	0
All	All	9058	0	8676	261	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 15.

All (261) 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:513:TYR:HB2	1:A:518:THR:HG22	1.55	0.85
1:E:513:TYR:HB2	1:E:518:THR:HG22	1.57	0.84
2:B:2167:LEU:HD22	2:B:2169:LEU:HD23	1.58	0.84
1:A:488:THR:HG22	1:A:510:LYS:HZ1	1.41	0.83
1:E:343:LYS:HE3	1:E:388:GLU:OE1	1.80	0.81
2:F:2255:ILE:HG23	2:F:2274:LEU:HD22	1.61	0.80
2:B:2200:GLU:OE1	2:B:2269:TYR:HB3	1.84	0.78
2:F:2236:CYS:SG	2:F:2237:SER:N	2.57	0.78
1:E:418:ASP:OD1	1:E:483:LYS:HE3	1.85	0.77
2:B:2238:CYS:HB2	2:B:2240:GLY:H	1.51	0.76
1:A:139:GLN:HG2	1:A:143:ARG:HH12	1.52	0.75
2:B:2155:GLU:HB3	2:B:2164:CYS:SG	2.26	0.75
2:F:2155:GLU:HB3	2:F:2164:CYS:SG	2.27	0.74
1:A:488:THR:HG22	1:A:510:LYS:NZ	2.03	0.74
1:A:513:TYR:HB2	1:A:518:THR:CG2	2.18	0.74
2:F:2238:CYS:HB2	2:F:2240:GLY:H	1.52	0.74
1:E:434:ASN:HD22	1:E:434:ASN:C	1.91	0.73
1:E:143:ARG:NH1	1:E:254:TYR:HB3	2.04	0.72
1:E:119:LEU:HB2	2:F:2281:ASN:HD21	1.55	0.72
1:E:86:PHE:CE1	1:E:360:ARG:HD3	2.26	0.70
1:A:144:HIS:O	1:A:145:GLU:HG3	1.91	0.70
1:A:434:ASN:C	1:A:434:ASN:HD22	1.93	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:502:PHE:HB3	1:E:503:PRO:HD3	1.73	0.69
1:A:217:LEU:HD22	1:A:427:CYS:SG	2.33	0.69
2:F:2186:LEU:HD22	2:F:2191:GLN:O	1.92	0.69
2:B:2154:PRO:HA	2:B:2166:ASP:OD1	1.93	0.68
1:A:277:GLN:O	1:A:281:GLU:HG3	1.93	0.68
1:E:513:TYR:HB2	1:E:518:THR:CG2	2.23	0.68
2:B:2255:ILE:HG23	2:B:2274:LEU:HD22	1.74	0.68
1:E:277:GLN:O	1:E:281:GLU:HG3	1.94	0.67
2:F:2167:LEU:HD22	2:F:2169:LEU:HD23	1.74	0.67
2:F:2186:LEU:HD23	2:F:2193:PRO:HA	1.77	0.67
1:A:502:PHE:HB3	1:A:503:PRO:HD3	1.77	0.66
2:F:2150:SER:HB3	2:F:2171:LYS:HZ3	1.60	0.65
1:E:119:LEU:HG	2:F:2280:LYS:HB3	1.76	0.65
1:A:418:ASP:CG	1:A:483:LYS:HE3	2.16	0.65
1:A:380:PRO:HD3	1:A:400:THR:HG22	1.79	0.65
2:F:2200:GLU:CG	2:F:2267:MET:HB3	2.28	0.64
1:E:143:ARG:HH12	1:E:254:TYR:HB3	1.61	0.64
1:E:418:ASP:CG	1:E:483:LYS:HE3	2.18	0.64
1:E:245:THR:HG22	1:E:492:THR:HG21	1.78	0.63
1:A:119:LEU:HG	2:B:2280:LYS:HB3	1.80	0.63
1:A:286:MET:HE3	1:A:511:VAL:HG13	1.80	0.63
2:F:2159:ARG:NH2	2:F:2198:ALA:HB2	2.14	0.62
1:E:286:MET:HE1	1:E:311:TYR:CE2	2.34	0.61
1:A:271:THR:O	1:A:271:THR:HG22	2.01	0.60
1:E:333:ASN:N	1:E:333:ASN:HD22	2.00	0.58
1:A:119:LEU:HB2	2:B:2281:ASN:HD21	1.68	0.58
2:B:2236:CYS:SG	2:B:2237:SER:N	2.76	0.58
1:E:129:MET:SD	1:E:456:LEU:HD21	2.44	0.58
1:E:86:PHE:HE1	1:E:360:ARG:HD3	1.69	0.58
2:F:2200:GLU:CD	2:F:2267:MET:HB3	2.24	0.58
1:E:353:PRO:O	1:E:357:GLN:HG3	2.04	0.58
2:B:2150:SER:HA	2:B:2170:CYS:SG	2.43	0.58
2:B:2214:PHE:O	2:B:2217:GLN:HG2	2.04	0.57
1:A:169:GLU:HB3	1:A:201:THR:HB	1.86	0.57
2:F:2150:SER:HA	2:F:2170:CYS:HB2	1.87	0.57
1:E:387:ASN:OD1	1:E:390:ARG:NH2	2.38	0.57
2:F:2195:ASP:OD2	2:F:2197:SER:HB3	2.05	0.56
1:A:120:PHE:CD1	2:B:2281:ASN:ND2	2.74	0.56
1:A:139:GLN:CG	1:A:143:ARG:HH12	2.17	0.56
1:A:257:ASN:HB3	1:A:267:THR:HG23	1.86	0.56
1:E:387:ASN:HA	1:E:390:ARG:NH2	2.21	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:248:SER:HB2	1:E:252:ARG:NH2	2.21	0.56
2:B:2150:SER:HB2	2:B:2168:ASP:OD1	2.06	0.56
2:F:2150:SER:HB3	2:F:2171:LYS:NZ	2.20	0.56
1:A:286:MET:HE2	1:A:311:TYR:CZ	2.40	0.56
1:A:474:VAL:CG1	1:A:494:CYS:HB2	2.37	0.55
2:F:2161:CYS:O	2:F:2162:ASN:HB2	2.07	0.55
1:A:261:PHE:CZ	1:A:404:ARG:HB3	2.42	0.55
1:E:177:LYS:HD3	1:E:231:GLU:CD	2.27	0.55
2:F:2250:VAL:O	2:F:2254:GLN:NE2	2.40	0.55
1:E:271:THR:O	1:E:271:THR:HG22	2.07	0.55
1:E:387:ASN:HA	1:E:390:ARG:HH21	1.72	0.55
1:A:139:GLN:HG2	1:A:143:ARG:NH1	2.22	0.54
1:A:144:HIS:O	1:A:145:GLU:CG	2.56	0.54
2:B:2161:CYS:O	2:B:2162:ASN:HB2	2.07	0.54
1:E:436:ALA:HB3	1:E:439:ASN:HD22	1.72	0.54
1:A:315:PRO:HB3	1:A:355:ILE:HD13	1.90	0.54
1:E:474:VAL:CG1	1:E:494:CYS:HB2	2.38	0.54
1:E:333:ASN:HB2	5:E:782:HOH:O	2.06	0.54
1:A:132:GLU:O	1:A:136:ILE:HD13	2.08	0.53
1:A:100:ASN:OD1	1:A:103:ARG:N	2.36	0.53
1:A:286:MET:HE3	1:A:511:VAL:CG1	2.39	0.53
2:F:2200:GLU:O	2:F:2204:VAL:HG23	2.08	0.53
2:F:2249:GLN:O	2:F:2253:GLU:HG3	2.08	0.53
1:E:205:GLN:HG2	1:E:234:VAL:HG22	1.90	0.53
1:A:248:SER:HB2	1:A:252:ARG:NH2	2.24	0.52
1:E:323:GLY:O	1:E:324:ASN:HB2	2.09	0.52
1:A:177:LYS:HB2	1:A:231:GLU:OE2	2.10	0.52
1:A:286:MET:HE2	1:A:311:TYR:CE2	2.45	0.52
1:A:291:SER:HA	1:A:322:CYS:HB2	1.90	0.52
1:A:387:ASN:HA	1:A:390:ARG:NH2	2.23	0.52
1:E:434:ASN:HD22	1:E:435:LEU:N	2.08	0.52
1:E:220:GLU:O	1:E:455:PRO:HD3	2.09	0.52
1:E:415:PHE:CD1	1:E:451:LEU:HD22	2.44	0.52
1:E:261:PHE:CZ	1:E:404:ARG:HB3	2.45	0.52
1:A:434:ASN:ND2	1:A:434:ASN:C	2.62	0.52
2:F:2230:THR:OG1	2:F:2233:PRO:HG3	2.08	0.52
1:A:269:VAL:HG22	5:A:713:HOH:O	2.09	0.52
2:B:2150:SER:HA	2:B:2170:CYS:HB2	1.92	0.52
1:A:191:LYS:HB2	1:A:194:LYS:HD2	1.92	0.51
2:B:2230:THR:OG1	2:B:2233:PRO:HG3	2.09	0.51
1:E:217:LEU:HD23	1:E:423:MET:HE2	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:436:ALA:HB3	1:A:439:ASN:HD22	1.76	0.51
1:A:274:LYS:O	1:A:277:GLN:HB3	2.10	0.51
2:B:2251:PHE:O	2:B:2254:GLN:HB2	2.10	0.51
1:E:120:PHE:CD1	2:F:2281:ASN:ND2	2.79	0.51
1:E:330:TYR:CD2	1:E:330:TYR:N	2.77	0.51
1:A:208:LEU:CD2	1:A:208:LEU:H	2.24	0.51
1:A:323:GLY:O	1:A:324:ASN:HB2	2.11	0.51
1:A:333:ASN:HD22	1:A:333:ASN:N	2.08	0.51
1:A:220:GLU:O	1:A:221:ALA:HB3	2.11	0.51
1:E:220:GLU:O	1:E:221:ALA:HB3	2.11	0.51
2:F:2150:SER:HA	2:F:2170:CYS:SG	2.51	0.51
1:E:88:ILE:CD1	1:E:397:VAL:HG11	2.41	0.51
2:B:2204:VAL:O	2:B:2208:GLN:HG3	2.11	0.50
1:A:270:LYS:HG3	5:A:731:HOH:O	2.10	0.50
2:B:2200:GLU:CG	2:B:2267:MET:HB3	2.42	0.50
2:F:2206:VAL:O	2:F:2210:LYS:HG3	2.11	0.50
1:A:419:LEU:HD23	1:A:441:PHE:HZ	1.77	0.50
1:E:434:ASN:ND2	1:E:434:ASN:C	2.62	0.50
1:A:329:PRO:HG2	1:A:368:GLU:OE1	2.12	0.50
2:B:2150:SER:HB3	2:B:2171:LYS:NZ	2.26	0.50
1:A:434:ASN:HD22	1:A:435:LEU:N	2.10	0.50
1:E:308:PHE:O	1:E:355:ILE:HD11	2.12	0.50
2:F:2220:VAL:O	2:F:2242:PHE:HA	2.12	0.50
2:F:2261:ILE:O	2:F:2265:TYR:HD1	1.94	0.50
1:A:330:TYR:CD1	1:A:330:TYR:N	2.80	0.50
1:E:312:SER:O	1:E:315:PRO:HD3	2.12	0.50
2:B:2220:VAL:HG23	2:B:2245:THR:CG2	2.42	0.49
1:A:340:ASP:HA	1:A:343:LYS:HE3	1.93	0.49
1:E:291:SER:HA	1:E:322:CYS:HB2	1.94	0.49
1:E:177:LYS:HG3	1:E:231:GLU:HB2	1.95	0.49
2:B:2228:LYS:HE3	2:B:2233:PRO:HG2	1.94	0.49
1:A:179:GLY:O	1:A:229:TRP:HB3	2.14	0.48
1:E:380:PRO:HD3	1:E:400:THR:HG22	1.95	0.48
1:A:205:GLN:HG2	1:A:234:VAL:HG22	1.95	0.48
1:E:333:ASN:ND2	1:E:333:ASN:N	2.60	0.48
2:F:2154:PRO:HA	2:F:2166:ASP:OD1	2.12	0.48
1:A:217:LEU:HD23	1:A:431:PRO:HG3	1.95	0.48
1:A:120:PHE:HD1	2:B:2281:ASN:ND2	2.11	0.48
2:F:2232:MET:N	2:F:2233:PRO:HD2	2.29	0.48
1:E:186:MET:HB2	1:E:223:PHE:CE2	2.48	0.48
2:F:2150:SER:HB2	2:F:2168:ASP:OD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:2255:ILE:HG23	2:F:2274:LEU:CD2	2.40	0.48
1:A:372:PHE:CD1	2:B:2208:GLN:HG2	2.49	0.48
1:E:492:THR:O	1:E:492:THR:HG22	2.13	0.48
1:E:438:PRO:O	1:E:442:VAL:HG23	2.14	0.47
2:B:2167:LEU:CD2	2:B:2169:LEU:HD23	2.38	0.47
1:E:373:GLY:HA2	1:E:378:ARG:HD2	1.96	0.47
2:F:2159:ARG:NH1	2:F:2195:ASP:OD1	2.47	0.47
1:A:438:PRO:O	1:A:442:VAL:HG23	2.14	0.47
1:E:320:ILE:HD12	1:E:320:ILE:N	2.29	0.47
1:A:347:ASP:OD1	1:A:392:ARG:NH1	2.42	0.47
1:A:88:ILE:HD12	1:A:397:VAL:HG11	1.96	0.47
1:A:324:ASN:HD21	1:A:368:GLU:HG3	1.79	0.47
1:A:372:PHE:CE1	2:B:2208:GLN:HG2	2.50	0.47
2:B:2220:VAL:O	2:B:2242:PHE:HA	2.15	0.47
1:A:217:LEU:HD23	1:A:431:PRO:CG	2.45	0.47
1:E:257:ASN:HB3	1:E:267:THR:CG2	2.45	0.47
1:E:399:THR:OG1	1:E:400:THR:N	2.48	0.47
1:A:490:THR:O	1:A:490:THR:HG23	2.15	0.46
1:E:354:ASP:HB2	5:E:759:HOH:O	2.15	0.46
1:A:443:LYS:HG2	1:A:491:ASN:ND2	2.30	0.46
1:E:169:GLU:HB3	1:E:201:THR:HB	1.96	0.46
1:E:252:ARG:CZ	1:E:270:LYS:HG2	2.45	0.46
2:F:2259:ARG:HA	2:F:2274:LEU:HD13	1.97	0.46
1:A:96:ARG:NH2	1:A:132:GLU:OE1	2.46	0.46
1:E:206:LEU:HD22	1:E:237:VAL:CG2	2.46	0.46
1:E:371:GLY:O	2:F:2208:GLN:NE2	2.48	0.46
1:A:258:ILE:HD12	1:A:258:ILE:N	2.31	0.46
1:A:360:ARG:HD3	5:A:737:HOH:O	2.14	0.46
1:A:287:PHE:HE1	1:A:514:PRO:HG3	1.80	0.46
2:B:2202:THR:O	2:B:2206:VAL:HG23	2.15	0.46
1:A:265:SER:OG	1:A:267:THR:O	2.28	0.46
1:A:333:ASN:ND2	1:A:333:ASN:N	2.63	0.46
1:E:387:ASN:CA	1:E:390:ARG:HH21	2.28	0.46
2:F:2150:SER:HA	2:F:2170:CYS:CB	2.45	0.46
2:F:2186:LEU:HD23	2:F:2193:PRO:CA	2.44	0.46
1:E:415:PHE:HD1	1:E:451:LEU:HD22	1.82	0.45
1:E:415:PHE:CE1	1:E:451:LEU:HB3	2.52	0.45
2:B:2232:MET:N	2:B:2233:PRO:HD2	2.31	0.45
1:A:245:THR:HG22	1:A:492:THR:HG21	1.97	0.45
1:E:286:MET:HE3	1:E:311:TYR:OH	2.15	0.45
2:F:2200:GLU:OE1	2:F:2269:TYR:HB3	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:472:TYR:HA	1:E:473:PRO:C	2.37	0.45
1:A:255:TYR:O	1:A:258:ILE:HD13	2.17	0.45
1:A:295:LEU:HB2	1:A:341:SER:HB3	1.98	0.45
1:A:96:ARG:HG3	1:A:467:TYR:CE2	2.51	0.45
1:E:143:ARG:NH1	1:E:254:TYR:CB	2.78	0.45
1:A:220:GLU:O	1:A:455:PRO:HD3	2.16	0.45
1:E:230:PHE:CZ	1:E:233:GLN:HA	2.52	0.45
2:B:2238:CYS:HB2	2:B:2239:ALA:H	1.29	0.44
1:E:510:LYS:HD3	1:E:521:ASP:OD1	2.17	0.44
2:B:2156:VAL:HG21	2:B:2167:LEU:HD12	1.99	0.44
2:B:2150:SER:HA	2:B:2170:CYS:CB	2.47	0.44
1:A:316:PRO:HG2	1:A:319:PHE:CE1	2.53	0.44
1:E:347:ASP:O	1:E:351:GLU:HG3	2.18	0.44
1:E:274:LYS:O	1:E:277:GLN:HB3	2.17	0.44
2:F:2203:LEU:HD22	2:F:2258:PHE:HE1	1.82	0.44
2:F:2156:VAL:HG21	2:F:2167:LEU:HD12	2.00	0.44
1:A:391:GLN:HE21	1:A:391:GLN:HB3	1.62	0.44
1:E:257:ASN:HB3	1:E:267:THR:HG23	1.99	0.44
1:A:124:ARG:NH1	2:B:2234:VAL:HG11	2.32	0.44
1:A:191:LYS:HB2	1:A:194:LYS:HB2	2.00	0.44
1:A:88:ILE:HD13	1:A:362:VAL:HG22	2.00	0.44
1:E:490:THR:O	1:E:490:THR:HG23	2.18	0.43
1:A:312:SER:O	1:A:315:PRO:HD3	2.18	0.43
1:E:286:MET:CE	1:E:311:TYR:CE2	3.01	0.43
1:A:145:GLU:CD	1:A:145:GLU:C	2.76	0.43
1:E:343:LYS:HE3	1:E:388:GLU:CD	2.38	0.43
2:F:2201:MET:O	2:F:2205:GLU:HG3	2.17	0.43
2:F:2248:THR:O	2:F:2252:MET:HG2	2.18	0.43
1:A:343:LYS:HA	5:A:778:HOH:O	2.16	0.43
1:A:88:ILE:CD1	1:A:397:VAL:HG11	2.48	0.43
1:A:472:TYR:HA	1:A:473:PRO:C	2.39	0.43
1:A:96:ARG:HG2	1:A:96:ARG:HH11	1.84	0.43
1:E:119:LEU:HB2	2:F:2281:ASN:ND2	2.27	0.43
1:E:179:GLY:O	1:E:229:TRP:HB3	2.19	0.43
1:E:191:LYS:HB2	1:E:194:LYS:HB2	2.00	0.43
1:A:119:LEU:HG	2:B:2280:LYS:CB	2.48	0.43
1:A:129:MET:SD	1:A:456:LEU:HD21	2.59	0.43
1:A:143:ARG:HD2	1:A:254:TYR:CE2	2.54	0.42
1:A:492:THR:O	1:A:492:THR:HG22	2.17	0.42
2:F:2204:VAL:O	2:F:2208:GLN:HG3	2.18	0.42
1:A:189:GLN:HG2	1:A:191:LYS:O	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:340:ASP:O	1:A:343:LYS:HB2	2.19	0.42
1:A:169:GLU:HG2	1:A:170:THR:N	2.35	0.42
1:E:208:LEU:C	1:E:208:LEU:HD12	2.39	0.42
1:A:164:GLN:HE21	1:A:164:GLN:HB3	1.60	0.42
1:A:386:THR:O	1:A:390:ARG:HD3	2.20	0.42
2:B:2152:VAL:HA	2:B:2167:LEU:O	2.19	0.42
1:E:217:LEU:HD23	1:E:423:MET:CE	2.50	0.42
2:F:2214:PHE:O	2:F:2217:GLN:HG2	2.19	0.42
2:F:2223:LYS:HD2	2:F:2238:CYS:HB3	2.02	0.42
2:B:2152:VAL:CG2	2:B:2166:ASP:HB3	2.50	0.41
2:F:2221:CYS:HB3	2:F:2224:CYS:O	2.19	0.41
1:A:488:THR:CG2	1:A:510:LYS:HZ1	2.19	0.41
1:A:418:ASP:OD1	1:A:483:LYS:HE3	2.20	0.41
2:F:2211:LEU:HD22	2:F:2277:LEU:HD11	2.02	0.41
1:E:171:LEU:HD22	1:E:178:ILE:HD12	2.03	0.41
2:F:2200:GLU:HA	2:F:2267:MET:HE1	2.02	0.41
2:B:2221:CYS:HB3	2:B:2224:CYS:O	2.21	0.41
1:E:88:ILE:HD12	1:E:397:VAL:HG11	2.02	0.41
1:E:118:ASN:HB3	2:F:2281:ASN:OD1	2.21	0.41
1:A:295:LEU:CB	1:A:341:SER:HB3	2.51	0.41
1:E:295:LEU:HB2	1:E:341:SER:HB3	2.03	0.41
1:E:88:ILE:HD13	1:E:397:VAL:HG11	2.03	0.41
2:B:2167:LEU:HD23	2:B:2167:LEU:C	2.41	0.41
1:E:214:HIS:HD2	1:E:240:PHE:O	2.03	0.41
2:F:2185:TRP:CH2	2:F:2265:TYR:CD2	3.09	0.40
2:F:2169:LEU:HD11	2:F:2203:LEU:HD21	2.04	0.40
1:E:120:PHE:HD1	2:F:2281:ASN:ND2	2.19	0.40
1:A:134:TYR:HB2	1:A:223:PHE:CE2	2.56	0.40
1:E:372:PHE:CD1	2:F:2208:GLN:HG2	2.56	0.40
1:A:274:LYS:HE2	1:A:274:LYS:HB3	1.87	0.40
2:B:2150:SER:HB3	2:B:2171:LYS:HZ2	1.87	0.40
1:A:419:LEU:HD23	1:A:441:PHE:CZ	2.55	0.40
1:A:291:SER:HB3	1:A:500:GLY:O	2.22	0.40
1:E:291:SER:HB3	1:E:500:GLY:O	2.21	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	423/527 (80%)	401 (95%)	18 (4%)	4 (1%)	20	21
1	E	423/527 (80%)	402 (95%)	17 (4%)	4 (1%)	20	21
2	B	121/145 (83%)	111 (92%)	9 (7%)	1 (1%)	22	24
2	F	121/145 (83%)	111 (92%)	9 (7%)	1 (1%)	22	24
All	All	1088/1344 (81%)	1025 (94%)	53 (5%)	10 (1%)	20	21

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	333	ASN
2	B	2238	CYS
1	E	333	ASN
2	F	2238	CYS
1	A	174	SER
1	A	331	GLY
1	E	174	SER
1	E	331	GLY
1	A	324	ASN
1	E	324	ASN

### 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	383/471 (81%)	365 (95%)	18 (5%)	30	38

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	E	383/471 (81%)	368 (96%)	15 (4%)	37	47
2	B	115/131 (88%)	109 (95%)	6 (5%)	27	33
2	F	115/131 (88%)	112 (97%)	3 (3%)	51	64
All	All	996/1204 (83%)	954 (96%)	42 (4%)	34	43

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	96	ARG
1	A	139	GLN
1	A	145	GLU
1	A	164	GLN
1	A	175	THR
1	A	182	ILE
1	A	208	LEU
1	A	227	GLU
1	A	248	SER
1	A	276	LYS
1	A	330	TYR
1	A	333	ASN
1	A	387	ASN
1	A	391	GLN
1	A	397	VAL
1	A	427	CYS
1	A	434	ASN
1	A	488	THR
2	B	2155	GLU
2	B	2165	ARG
2	B	2173	SER
2	B	2197	SER
2	B	2200	GLU
2	B	2260	ASN
1	E	96	ARG
1	E	129	MET
1	E	139	GLN
1	E	227	GLU
1	E	233	GLN
1	E	248	SER
1	E	259	ASN
1	E	276	LYS
1	E	330	TYR

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Mol	Chain	Res	Type
1	E	333	ASN
1	E	387	ASN
1	E	391	GLN
1	E	397	VAL
1	E	424	CYS
1	E	434	ASN
2	F	2197	SER
2	F	2254	GLN
2	F	2278	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	GLN
1	A	333	ASN
1	A	334	GLN
1	A	357	GLN
1	A	391	GLN
1	A	434	ASN
1	A	439	ASN
2	B	2184	GLN
2	B	2208	GLN
2	B	2263	GLN
1	E	139	GLN
1	E	214	HIS
1	E	259	ASN
1	E	297	GLN
1	E	333	ASN
1	E	334	GLN
1	E	357	GLN
1	E	391	GLN
1	E	410	GLN
1	E	426	ASN
1	E	434	ASN
1	E	439	ASN
2	F	2184	GLN
2	F	2208	GLN
2	F	2254	GLN
2	F	2263	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 4 are monoatomic - leaving 2 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	601	-	4,4,4	0.37	0	6,6,6	0.20	0
3	SO4	E	601	-	4,4,4	0.29	0	6,6,6	0.13	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	601	-	-	0/0/0/0	0/0/0/0
3	SO4	E	601	-	-	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.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

EDS failed to run properly - this section is therefore empty.

### 6.2 Non-standard residues in protein, DNA, RNA chains

EDS failed to run properly - this section is therefore empty.

### 6.3 Carbohydrates

EDS failed to run properly - this section is therefore empty.

### 6.4 Ligands

EDS failed to run properly - this section is therefore empty.

### 6.5 Other polymers

EDS failed to run properly - this section is therefore empty.